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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 52.9038 Seconds
(without alignment)
116.273 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78
Sequence: 1 SIKRDNDYKPM 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21:*

1: geneeqp19809:*

2: geneeqp19908:*

3: geneeqp20008:*

4: geneeqp20018:*

5: geneeqp20028:*

6: geneeqp20038:*

7: geneeqp20048:*

8: geneeqp20058:*

9: geneeqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	14	3	AA52510 House dus
2	78	100.0	14	5	AAU96314 Der HMW-m
3	37	47.4	17	5	ABJ01203 Human Sox
4	34	43.6	20	3	AA83556 5/20 natl
5	34	43.6	20	3	AA83556 5/20 natl
6	34	43.6	20	4	AAU04769 Peanut wt
7	34	43.6	20	4	AAU04769 Peanut wt
8	34	43.6	20	4	AAU04769 Peanut wt
9	32	41.0	10	8	ADK08378 Human pap
10	32	41.0	11	2	AA830009 CAEV 16 E2
11	32	41.0	11	2	AA830009 CAEV 16 E2
12	32	41.0	11	2	AA830009 CAEV 16 E2
13	32	41.0	11	2	AA830009 CAEV 16 E2
14	32	41.0	11	2	AA830009 CAEV 16 E2
15	32	41.0	11	2	AA830009 CAEV 16 E2
16	32	41.0	11	2	AA830009 CAEV 16 E2
17	32	41.0	11	2	AA830009 CAEV 16 E2
18	32	41.0	11	2	AA830009 CAEV 16 E2
19	32	41.0	11	2	AA830009 CAEV 16 E2
20	32	41.0	11	2	AA830009 CAEV 16 E2
21	32	41.0	11	2	AA830009 CAEV 16 E2
22	32	41.0	11	2	AA830009 CAEV 16 E2
23	32	41.0	11	2	AA830009 CAEV 16 E2
24	32	41.0	11	2	AA830009 CAEV 16 E2

25	30	38.5	20	4	AAU04770 Native an
26	30	38.5	20	4	AAU05095 Anaphylac
27	30	38.5	20	4	AAU05095 Anaphylac
28	30	38.5	20	4	AAU05095 Anaphylac
29	30	38.5	20	4	AAU05095 Anaphylac
30	30	38.5	20	4	AAU05095 Anaphylac
31	30	38.5	20	4	AAU05095 Anaphylac
32	30	38.5	20	4	AAU05095 Anaphylac
33	30	38.5	20	4	AAU05095 Anaphylac
34	30	38.5	20	4	AAU05095 Anaphylac
35	30	38.5	20	4	AAU05095 Anaphylac
36	30	38.5	20	4	AAU05095 Anaphylac
37	30	38.5	20	4	AAU05095 Anaphylac
38	30	38.5	20	4	AAU05095 Anaphylac
39	30	38.5	20	4	AAU05095 Anaphylac
40	30	38.5	20	4	AAU05095 Anaphylac
41	30	38.5	20	4	AAU05095 Anaphylac
42	30	38.5	20	4	AAU05095 Anaphylac
43	30	38.5	20	4	AAU05095 Anaphylac
44	30	38.5	20	4	AAU05095 Anaphylac
45	30	38.5	20	4	AAU05095 Anaphylac
46	30	38.5	20	4	AAU05095 Anaphylac
47	30	38.5	20	4	AAU05095 Anaphylac
48	30	38.5	20	4	AAU05095 Anaphylac
49	30	38.5	20	4	AAU05095 Anaphylac
50	30	38.5	20	4	AAU05095 Anaphylac
51	30	38.5	20	4	AAU05095 Anaphylac
52	30	38.5	20	4	AAU05095 Anaphylac
53	30	38.5	20	4	AAU05095 Anaphylac
54	30	38.5	20	4	AAU05095 Anaphylac
55	30	38.5	20	4	AAU05095 Anaphylac
56	30	38.5	20	4	AAU05095 Anaphylac
57	30	38.5	20	4	AAU05095 Anaphylac
58	30	38.5	20	4	AAU05095 Anaphylac
59	30	38.5	20	4	AAU05095 Anaphylac
60	30	38.5	20	4	AAU05095 Anaphylac
61	30	38.5	20	4	AAU05095 Anaphylac
62	30	38.5	20	4	AAU05095 Anaphylac
63	30	38.5	20	4	AAU05095 Anaphylac
64	30	38.5	20	4	AAU05095 Anaphylac
65	30	38.5	20	4	AAU05095 Anaphylac
66	30	38.5	20	4	AAU05095 Anaphylac
67	30	38.5	20	4	AAU05095 Anaphylac
68	30	38.5	20	4	AAU05095 Anaphylac
69	30	38.5	20	4	AAU05095 Anaphylac
70	30	38.5	20	4	AAU05095 Anaphylac
71	30	38.5	20	4	AAU05095 Anaphylac
72	30	38.5	20	4	AAU05095 Anaphylac
73	30	38.5	20	4	AAU05095 Anaphylac
74	30	38.5	20	4	AAU05095 Anaphylac
75	30	38.5	20	4	AAU05095 Anaphylac
76	30	38.5	20	4	AAU05095 Anaphylac
77	30	38.5	20	4	AAU05095 Anaphylac
78	30	38.5	20	4	AAU05095 Anaphylac
79	30	38.5	20	4	AAU05095 Anaphylac
80	30	38.5	20	4	AAU05095 Anaphylac
81	30	38.5	20	4	AAU05095 Anaphylac
82	30	38.5	20	4	AAU05095 Anaphylac
83	30	38.5	20	4	AAU05095 Anaphylac
84	30	38.5	20	4	AAU05095 Anaphylac
85	30	38.5	20	4	AAU05095 Anaphylac
86	30	38.5	20	4	AAU05095 Anaphylac
87	30	38.5	20	4	AAU05095 Anaphylac
88	30	38.5	20	4	AAU05095 Anaphylac
89	30	38.5	20	4	AAU05095 Anaphylac
90	30	38.5	20	4	AAU05095 Anaphylac
91	30	38.5	20	4	AAU05095 Anaphylac
92	30	38.5	20	4	AAU05095 Anaphylac
93	30	38.5	20	4	AAU05095 Anaphylac
94	30	38.5	20	4	AAU05095 Anaphylac
95	30	38.5	20	4	AAU05095 Anaphylac
96	30	38.5	20	4	AAU05095 Anaphylac
97	30	38.5	20	4	AAU05095 Anaphylac

98	27	34.6	20	4	AAM33354	Peptide #
99	27	34.6	20	4	AAU04768	Native an
100	27	34.6	20	4	ABR24400	Protein #

ALIGNMENTS

RESULT 1
AAVS2510

ID AAVS2510 standard; peptide; 14 AA.

AC AAVS2510;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B N-terminal fragment.

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

XX house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides
PT used to modify an animal's hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

CC Sequences AAVS2510-Y5252 represent proteolytic fragments of
CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW-
CC map) composition. The HMW-map composition was isolated from a D. farinae
CC homogenate by gel filtration, with each fraction being analysed for the
CC presence of proteins that bound to IGE present in mite-allergic dog
CC antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and
CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids
CC encoding them, may be used in therapeutic compositions to modify an
CC animal's hypersensitivity reaction to mite allergens. Animals that may be
CC treated include mammals and birds, especially felines, canines, equines,
CC humans, other pets, and work or domestic animals. The proteins or
CC fragments may also be used to diagnose allergies via a skin test. The
CC proteins and peptides can also be used to raise antibodies, which have a
CC variety of potential uses. For example, they can be used as vaccines to
CC passively immunise animals against dust mite hypersensitivity, as
CC positive controls in test kits and as tools to recover desired dust mite
CC allergens from a mixture of proteins

SQ Sequence 14 AA;

Query Match 100.0%; Score 78; DB 3; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.3e-06;

Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	SIKRDNDYSKNPM	14
DB	1	SIKRDNDYSKNPM	14

RESULT 2
AAU96314

ID AAU96314 standard; peptide; 14 AA.

AC AAU96314;

DT 15-JUL-2002 (first entry)

DE Der HMW-map polypeptide #1.

XX Der HMW-map; American house dust mite; anti-allergic; mite; IGE;

XX mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US028730.

XX 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated
XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of
XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic
XX acid. The Der HMW-map protein is useful for eliciting an immune response
XX against Der HMW-map protein. The protein or a reagent comprising a non-
XX proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX cat) susceptible to or having an allergic response to a mite. A
XX therapeutic composition is useful for desensitising a host animal to an
XX allergic response to a mite. The DNA and protein can be used in the
XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
XX of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting
XX binding of proteins to IGE, to prevent immunocomplex formation, thus
XX reducing hypersensitivity responses to mite allergens, and as vaccines
XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX represent Der HMW-map polypeptides of the invention

SQ Sequence 14 AA;

Query Match 100.0%; Score 78; DB 5; Length 14;

Best Local Similarity 100.0%; Pred. No. 1.3e-06; Mismatches 0; Indels 0; Gaps 0;

QY	1	SIKRDNDYSKNPM	14
DB	1	SIKRDNDYSKNPM	14

RESULT 3

ID AB01203 standard; peptide; 17 AA.

AC AB01203;

DT 13-SEP-2002 (first entry)

XX Human Sox-10 transcriptional regulator peptide fragment.


```

XX Human; cancer; neoplastic disease; tumour specific marker; cytostatic;
XX transcription factor.
XX
XX Homo sapiens.
XX
XX WO200240716-A2.
XX
XX 23-MAY-2002.
XX
XX 13-NOV-2001; 2001WO-US043461.
XX
XX 16-NOV-2000; 2000US-0249508P.
XX
XX (CEMI-) CEMINES LLC.
XX
XX Palm K;
XX
XX WPI, 2002-537346/57.
XX
XX Determining the presence of neoplastic molecular markers, by identifying
XX PT the presence of markers in host test sample using array of neoplastic
XX PT molecular marker specific reagents and analysing the array of the
XX PT reagents.
XX
XX Example 3; Page 12; 41pp; English.
XX
XX The present invention relates to a method for determining the presence of
XX CC neoplastic molecular markers in a host, involving the use of neoplastic
XX CC molecular marker specific reagents to detect such markers and analysing
XX CC the array of reagents, allowing the identification of the neoplastic
XX CC disease present. This can be used to determine the best treatment for
XX CC cancers, in particular neural cell, lung and prostate tumours. The
XX CC present sequence is a peptide derived from a transcription factor capable
XX CC of acting as a marker of the invention
XX
XX Sequence 17 AA:
XX
XX Query Match          47.4%; Score 37; DB 5; Length 17;
XX Best Local Similarity 54.5%; Pred. No. 25;
XX Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0
XX
XX      3 KDDANDYSKRP 13
XX      | : | | | | |
XX Db       1 KDHDPDYKYRP 11
XX
XX RESULT 4
XX AAB33556
XX ID AAB33556 standard; peptide; 20 AA.
XX
XX AC AAB33556;
XX
XX DT 12-SEP-2003 (revised)
XX DT 22-JAN-2001 (first entry)
XX
XX DE 5/20 native Ara h 2 peptide #10.
XX
XX Allergy; allergic reaction; allergen; anaphylactic antigen; peanut;
XX KM Ara h 1; Ara h 2; Ara h 3; epitope; binding; immunoglobulin E; IgE;
XX KM food antigen; sensitising; immune response; anti-allergic.
XX
XX OS Arachis hypogaea.
XX
XX PN WO200051647-A2.
XX
XX PD 08-SEP-2000.
XX
XX PF 03-MAR-2000; 2000WO-US005655.
XX
XX PR 03-MAR-1999; 99US-0122860P.
XX PR 06-DEC-1999; 99US-00455294.
XX

```

PA	(MOON) MOUNT SINAI SCHOOL MEDICINE.
PI	
XX	Sampson HA;
XX	
DR	WPI; 2000-611341/58.
XX	
PT	Non-human animal sensitized to an antigen, useful as an animal model for studying allergic reactions to allergens, such as those in food and in the environment.
PT	
XX	
PS	Example 5; Page 62; 124pp; English.
XX	
CC	The present invention describes an animal model which can be used for studying allergic reactions to allergens. The animal is sensitized to a selected antigen by administering the antigen itself or a nucleic acid encoding the antigen, where preferably the antigen is an anaphylactic antigen. The sensitized animal can then be used to screen for compounds which may help to prevent, ameliorate, or cure allergic conditions in humans. The animal model can be used for studying allergic reactions to allergens, such as those in food (peanuts, fruit, berry, nut, bean, milk, dairy products), or in the environment (weed pollen, grass pollen, tree pollen, mite, animal, animal dander, fungal, and insect antigens).
CC	AA833478 to AA833601 represent sequences which are used in examples from the present invention to specifically examine the peanut allergy, and the peanut anaphylactic antigens Ara h 1 to 3. (Updated on 12-SEP-2003 to standardise OS field)
CC	
XX	
SQ	Sequence 20 AA;
Query Match	43.6%; Score 34; DB 3; Length 20;
Best Local Similarity	41.7%; Pred. NO. 99;
Matches 5; Conservative	4; Mismatches 3; Indels 0; Gaps 0;
OY	2 IKRDHNDYSKNP 13 :: : ::
Db	5 IQRDEDSYRDP 16
RESULT 5	
AA823107	
ID	AA823107 standard; peptide; 20 AA.
XX	
XX	AA823107;
AC	
DT	29-JAN-2001 (first entry)
XX	
DE	Peanut wild-type Ara h 2 20 residue peptide #10.
XX	
KM	Ara h 2 protein; peanut; epitope; antigen; allergy; anaphylaxis; asthma; immunomodulation; umethylated Cpg oligonucleotide; antiallergic.
KW	
XX	Arachis hypogaea.
OS	
XX	WO200054803-A2.
PN	
PD	21-SEP-2000.
XX	
PP	16-MAR-2000; 2000WO-US007213.
XX	
PR	16-MAR-1999; 99US-0124595P.
XX	
PR	17-MAR-1999; 99US-0125071P.
XX	
PA	(PANA-) PANACEA PHARM LLC.
XX	
PI	Soetin HB, Caplan MJ;
XX	
DR	WPI; 2000-628168/60.
XX	
PT	Immunostimulatory composition for treating or preventing an allergic reaction leading to conditions such as asthma or anaphylaxis, comprises oligonucleotides with unmethylated Cpg sequences and antigens derived from allergens.
PT	
XX	

PS Example 3; Page 67; 103pp; English.

XX The invention relates to an immunomodulatory composition comprising a Cpg

CC oligonucleotide of the sequence 5' purine-purine-C-G-pyrimidine-

CC pyrimidine 3', where C and G are unmodified, and at least one antigen

CC derived from an allergen that causes anaphylaxis. The composition is

CC useful for treating allergy in an individual. The composition prevents or

CC modulates an individual's immune response to an antigen which leads to

CC asthma and/or anaphylaxis. Individuals susceptible to anaphylactic shock

CC upon exposure to allergens from foods (e.g., peanut), venom or rubber may

CC be treated using the composition. Sequences ABB23098-B23125 represent a

CC series of 20-residue peptides from wild-type peanut Ara h 2 protein used

CC in an exemplification of the invention

XX

SQ Sequence 20 AA;

Query Match 43.6%; Score 34; DB 3; Length 20;

Best Local Similarity 41.7%; Pred. No. 99;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNDYSKNP 13

DB 5 IQRDEDSYERDP 16

RESULT 6

AAU04769

ID AAU04769 standard; peptide; 20 AA.

XX

AC AAU04769;

XX

DT 23-OCT-2001 (first entry)

XX

DE Native anaphylactic antigen Ara h 2 peptide #10.

XX

KM Ara h 2; anaphylactic antigen; immunoglobulin E; IGF; immunogenic;

KW allergy; mast cell; basophil; mouse; epitope.

XX

OS Mus sp.

XX

PN WO200140264-A2.

XX

PD 07-JUN-2001.

XX

PF 06-DEC-2000; 2000WO-US033124.

XX

PR 06-DEC-1999; 99US-00455294.

PR 23-JUN-2000; 2000US-0213765P.

PR 27-SEP-2000; 2000US-0235797P.

XX

PA (PANA-) PANACEA PHARM LLC.

PA (UYAR-) UNIV ARKANSAS.

PA (MOUN) MOUNT SINAI SCHOOL MEDICINE NEW YORK.

PI Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;

XX

XX WPI; 2001-381378/40.

DR

XX

PT Antigenic fragments useful for reducing anaphylactic risk and reducing

PT the severity and/or number of allergic symptoms in individuals sensitive

PT to antigens, have reduced ability to bind Immunoglobulin E.

XX

XX

PS Claim 40; Page 52; 100pp; English.

XX

CC The sequence represents the amino acid sequence of native anaphylactic

CC antigen Ara h 2 peptide #10. Ara h 2 is an anaphylactic antigen (A) which

CC was used to design antigenic peptides having a reduced ability to bind

CC IGE as compared with the intact (A), or having a sequence substantially

CC identical to a portion of sequence of an antigen that includes at least

CC one IGE binding site, where at least one IGE binding site of the peptide

CC is altered. The antigenic peptides are used in a composition which is

CC useful for reducing risk or severity of allergic reaction to an antigen.

CC This is done by identifying an individual at risk of allergic reaction to

CC an antigen by identifying prior display of allergic symptoms when exposed

CC to the antigen, or a familial relationship with an individual who

CC previously displayed allergic symptoms when exposed to the antigen.

CC Following this an antigen-specific IGE present on one or more mast cells

CC or basophils in the individual's serum is identified. The individual is

CC then contacted with a peptide corresponding to a portion of the antigen,

CC which is selected, formulated, and delivered so that binding of the

CC peptide to antigen-specific IGE is reduced as compared with IGE binding

CC of intact antigen. The composition is also useful for treating and

CC preventing allergic reactions

XX

SQ Sequence 20 AA;

Query Match 43.6%; Score 34; DB 4; Length 20;

Best Local Similarity 41.7%; Pred. No. 99;

Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNDYSKNP 13

DB 5 IQRDEDSYERDP 16

RESULT 7

AAU05094

ID AAU05094 standard; peptide; 20 AA.

XX

AC AAU05094;

XX

DT 24-OCT-2001 (first entry)

XX

DE Anaphylactic peanut antigen Ara h 2, native peptide #10.

XX

KM Anaphylactic antigen; Ara h 2; peanut; desensitisation; antigen; allergy;

KW immunotherapy; rush immunotherapy; anaphylaxis; asthma; food allergen;

KW milk allergen; shellfish allergen; latex; drug; environmental allergen;

KW grass pollen; ovalbumin; insect venom; peanut oil; immunoglobulin E; IGE.

XX

OS Arachis sp.

XX

PN WO200139799-A2.

XX

PD 07-JUN-2001.

XX

PF 06-DEC-2000; 2000WO-US033125.

XX

PR 06-DEC-1999; 99US-00455294.

PR 23-JUN-2000; 2000US-0213765P.

PR 27-SEP-2000; 2000US-0235797P.

XX

PA (PANA-) PANACEA PHARM LLC.

PA

PI Caplan M;

XX

XX WPI; 2001-408258/43.

DR

XX

PT Preventing allergic response against antigens, e.g. food and

PT environmental allergens such as peanut allergen or grass pollen, latex or

PT drug, comprises administering agent, e.g. a peptide, that blocks antigen

PT binding sites on offending IGE.

XX

XX

PS Example 2; Page 46; 76pp; English.

XX

CC The sequence represents the amino acid sequence of anaphylactic peanut

CC antigen Ara h 2, native peptide #10. The peptide is used in active or

CC passive desensitisation of an individual to an antigen; for alleviating

CC or preventing allergic reactions and for decreasing the risk of allergic

CC reactions during immunotherapy or rush immunotherapy, anaphylaxis and

CC asthma. The antigen may be a food allergen (e.g., peanut or milk

CC allergen), shellfish allergen, environmental allergen (e.g. grass pollen

CC or tree pollen), latex, drug, pollen, ovalbumin, an insect venom antigen

CC or predominantly linear epitopes. The protein is useful for protecting an

CC individual against subsequent inadvertent or intentional exposure to

CC antigen, e.g. receiving blocking agent before eating a chocolate bar

CC which may inadvertently contain peanut components or before eating foods
CC prepared using peanut oil. Administration of the blocking agent does not
CC result in cross-linking of anti-antigenic IgE. After exposure to the
CC agent, the individual's antigen sensitivity is at least temporarily
CC reduced. Only those IgE molecules that bind the offending antigen and
CC contribute to the risk of an allergic response are blocked

XX Sequence 20 AA;

Query Match 43.6%; Score 34; DB 4; Length 20;
Best Local Similarity 41.7%; Pred. No. 99;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 IKRDNDYSKNP 13
|:|:|:|:|:
Db 5 IQRDEDSYERDP 16

RESULT 8

AAW24076 standard; peptide; 12 AA.

AC AAW24076;
DT 16-OCT-2003 (revised)
DT 25-MAR-2003 (revised)
DT 17-NOV-1997 (first entry)
XX PD498 alkaline protease peptide fragment B.
DE PD498 alkaline protease; heterologous protein production; detergent;
KM vector; promoter; signal sequence; primer; amplification.

XX Bacillus sp; strain PD498.
OS MO9634963-AA.
XX 07-NOV-1996.
PD 01-MAY-1996; 96MO-US006097.
PF 03-MAY-1995; 95US-00434255.

XX (NOVO) NOVO NORDISK BIOTECH INC.
PA (NOVO) NOVO-NORDISK AS.
XX Sloma AP, Outtrup H, Dammann CHG, Aaslyng DA;
PI WPI; 1996-506165/50.

DR WPI; 1996-506165/50.
XX Alkaline protease nucleic acid coding sequence - used to develop prods
PT for use in detergents and for the recombinant expression of
XX polypeptide(s).

PS Example 6.2; Page 35; 67pp; English.

XX AAW24075-76 are peptide fragments of a protease, used to design
CC degenerate primers (AA185623-24) for the amplification of a 180 bp gene
CC fragment. The gene fragment can be used to isolate a full length gene
CC encoding the protease, which was isolated from Bacillus sp. PD498. The
CC protease has the properties: (a) a molecular weight of about 34 kd as
CC determined by SDS-PAGE; (b) pI of about 9.3; (c) pH optimum in the range
CC of pH 9-11 at about 25 degrees C and with casein as substrate; (d)
CC temperature optimum in the range of about 40-55 degrees C at a pH of
CC about 9.5 and with casein as substrate; and (e) obtainable from Bacillus
CC sp. Group I. This alkaline protease is useful in detergent compositions.
CC The promoter and signal sequences of the protease gene and its encoded
CC product, can be used for the recombinant expression of heterologous
CC polypeptides. In particular nucleic acid constructs and vectors for this
CC purpose are also claimed. NB. The specification is unclear as to the
CC numbering of the sequences in the sequence ID listing. (Updated on 25-MAR
CC -2003 to correct PI field.) (Updated on 16-OCT-2003 to standardise OS
CC field)

XX Sequence 12 AA;

QY 5 DHNDYSKNPM 14
|:|:|:|:|:
Db 2 DFDYDNNPM 11
Query Match 42.3%; Score 33; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 81;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

RESULT 9

ADK08378 standard; peptide; 10 AA.

AC ADK08378;
DT 06-MAY-2004 (first entry)
XX Human papillomavirus peptide #433.
DE Human papillomavirus peptide #433.
XX pathogenic virus; alternative reading frame; antigenic determinant;
KM viricide; vaccine; therapeutic agent; infection; HPV.

XX Human papillomavirus.
OS WO2004011650-A2.
XX 05-FEB-2004.
PD 24-JUL-2003; 2003WO-EP008112.

XX 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX (INTE-) INTERCELL AG.

XX Matner F, Schmidt W, Habel A;
PI WPI; 2004-169243/16.
DR 24-JUL-2003; 2003WO-EP008112.

XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.

PS Claim 18; Page 178; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a viricide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.

XX Sequence 10 AA;

Query Match 41.0%; Score 32; DB 8; Length 10;
Best Local Similarity 66.7%; Pred. No. 98;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12
|:|:|:|:|:
Db 2 RDNDYWKH 10

RESULT 10

AAK30715 standard; peptide; 11 AA.

```

XX AC AAR30715;
XX DT 27-AUG-2003 (revised)
XX DT 25-MAR-2003 (revised)
XX DT 19-MAY-1993 (first entry)
XX DE HPV 16 E2-1170 peptide (amino acids 25-35) .
XX KM HPV; E1; E2; ELISA; diagnosis; vaccine; antibody.
XX OS Human papillomavirus.
XX PN BP523395-A2.
XX PD 20-JAN-1993.
XX PF 20-JUN-1992; 92EP-00110430.
XX PR 18-JUL-1991; 91DE-04123760.
XX PA (BEHV ) BEHRINGMERKE AG.
XX PI Mueller M, Giesmann L;
XX DR WPI; 1993-019476/03.
XX PT Peptide(s) corresp. to regions of HPV 16 E1 and E2 proteins - useful for
XX PT prevention, diagnosis and treatment of cervical tumours.
XX PS Claim 2; Page 13; 20pp; German.
XX CC The sero-reactive region is useful in the prevention, diagnosis and
XX CC therapy of HPV16-derived tumours and in the development of an ELISA.
XX CC (Updated on 25-MAR-2003 to correct PN field.) (Updated on 27-AUG-2003 to
XX CC correct OS field.)
XX SQ Sequence 11 AA;

Query Match          41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12
   ||| |||
   3 RDHIDYMKH 11

Db

RESULT 11
AAW30009
ID AAW30009 standard; peptide; 11 AA.
XX
XX AAW30009;
AC
XX
XX 17-OCT-2003 (revised)
XX DT 07-APR-1998 (first entry)
XX
XX CAEV immunogen pol 1033.
DE
XX
XX Immunogen; CAEV; caprine arthritis encephalomyelitis virus; HIV vaccine;
XX KM protective immune response; human; HIV-1; B-lymphocyte; T-lymphocyte;
XX KM diagnosis.
XX OS Caprine arthritis-encephalitis virus.
XX PA
XX PN WO9733615-A2.
XX PD 18-SEP-1997.
XX PF 14-MAR-1997; 97WO-US004020.
XX PR 15-MAR-1996; 96US-00616854.
XX PR 15-MAR-1996; 96US-00616855.

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XX PA (UYSC-) UNIV SOUTHERN CALIFORNIA.
XX PI Douvas A, Ehresmann G;
XX DR WPI; 1997-470647/43.
XX
XX PT Vaccine containing caprine arthritis-encephalomyelitis virus immunogen -
XX PT used to generate immune response against CAEV that is cross-reactive with
XX PT human immunodeficiency virus.
XX PS Claim 4; Page 8; 71pp; English.
XX
XX CC This sequence represents a caprine arthritis encephalomyelitis virus
XX CC (CAEV) immunogen. This sequence, along with a carrier, can be used as a
XX CC vaccine of the invention. The immunogen is used to stimulate protective
XX CC immune responses against CAEV which, in humans, are cross-reactive with
XX CC human immunodeficiency virus (HIV-1), i.e. it protects against HIV-1
XX CC infection or reduces severity of existing infections. An immune response
XX CC can also be induced by exposure, particularly in vitro, of T- or B-
XX CC lymphocytes to the immunogen, followed by expansion of the stimulated
XX CC cells and return to the patient. Assays using CAEV specific antibodies
XX CC recognising this sequence are used for diagnosis, to screen blood for
XX CC contamination by CAEV and to monitor the effect of vaccination. CAEV-
XX CC based vaccines can protect against HIV without the risks attendant on
XX CC using HIV-based vaccines. The assays are simple, inexpensive and suitable
XX CC for large scale screening. (Updated on 17-OCT-2003 to standardise OS
XX CC field)
XX SQ Sequence 11 AA;

Query Match          41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNHYSKN 12
   ||| |||
   1 KRINNKYNKN 10

Db

RESULT 12
AAB86994
ID AAB86994 standard; peptide; 11 AA.
XX
XX AAB86994;
AC
XX
XX 09-JAN-2002 (first entry)
XX DT
XX DE HPV 16 E2 protein fragment SEQ ID 3.
XX
XX Sero-reactive; E2 protein; antiviral; antitumor; vaccine; infection;
XX KM cancer; detection.
XX KM Human papillomavirus.
XX OS
XX PN EP136500-A2.
XX PD 26-SEP-2001.
XX
XX 20-JUN-1992; 2001EP-00102056.
XX PF 18-JUL-1991; 91DE-04123760.
XX PR 20-JUN-1992; 92EP-00110430.
XX
XX (DADE-) DADE BEHRING MARBURG GMBH.
XX PA
XX PI Mueller M, Giesmann L;
XX DR WPI; 2001-591567/67.
XX
XX Sero-reactive regions of human papilloma virus 16 E2 protein, and the
XX PT specific antibodies, useful in vaccines and diagnosis.

```

PS Claim 1, Page 10, 17pp; German.
XX
CC This invention describes novel seroreactive regions (A) from the E2
CC protein of human papilloma virus 16 (HPV 16). The products of the
CC invention have antiviral and antitumor activity. Peptides (I) that
CC include at least one (A) are used (i) to prepare vaccines against HPV 16
CC infection (and associated cancers) and (ii) for diagnosis (detection of
CC E2-specific antibodies). Monoclonal antibodies raised against (I) are
CC useful for diagnosis, by detecting HPV 16-specific E2 protein. This
CC sequence represents a fragment of the human papillomavirus E2 protein
CC which is used in the method of the invention
XX
SQ Sequence 11 AA;
XX
Query Match 41.0%; Score 32; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4 RDHNDVSKN 12
DB 3 RDHIDYWKH 11
XX
RESULT 13
ADU68123
ID ADU68123 standard; peptide; 15 AA.
XX
AC ADU68123;
XX
DT 10-FEB-2005 (first entry)
XX
DE Human papillomavirus-derived epitope peptide SeqID82.
XX
KM epitope mapping; T-cell; antiviral; cytostatic; vaccine;
XX vaccine, antiviral; benign tumor; tumor.
XX
OS Human papillomavirus.
XX
PN WO2004098497-A2.
XX
PD 18-NOV-2004.
XX
PF 23-APR-2004; 2004WO-US012652.
XX
PR 28-APR-2003; 2003US-0466235P.
XX
PA (GSMV) GENENCOR INT INC.
XX
PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD;
PI Stickler M;
XX
DR WPI; 2004-813965/80.
XX
XX
PT Identifying CD4+ human papillomavirus (HPV) epitopes or determining T-
PT cell epitope of HPV strain, useful in prophylactic/therapeutic vaccines,
PT by combining dendritic cells, CD4+ and/or CD8+ T-cells with pepset of
PT peptides from HPV.
XX
PS Claim 4; SEQ ID NO 82; 56pp; English.
XX
CC This invention relates to a novel method of identifying CD4+ human
CC papillomavirus (HPV) epitopes or determining a T-cell epitope of a HPV
CC strain. The method comprises combining a solution of differentiated
CC dendritic cells and naive CD4+ and/or CD8+ T-cells with a set of peptides
CC from the HPV (which comprises the T-cell epitope) and measuring T-cell
CC proliferation. The invention may be useful for the production of
CC compounds with an antiviral or cytostatic activity. The method or the
CC modified epitopes are useful in prophylactic and/or therapeutic vaccines,
CC as means for the development of HPV vaccines for the prevention of
CC infection with high-risk HPV strains, or as means for use in the development of
CC therapeutic vaccines against high-risk HPV types for use in the
CC prevention of the development of benign and/or malignant tumors in
CC infected individuals. The present sequence is that of a Human

CC papillomavirus-derived epitope peptide which was identified using the
CC method of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 41.0%; Score 32; DB 8; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
QY 4 RDHNDVSKN 12
DB 6 RDHIDYWKH 14
XX
RESULT 14
ADV11513
ID ADV11513 standard; peptide; 15 AA.
XX
AC ADV11513;
XX
DT 24-FEB-2005 (first entry)
XX
DE HPV type 16 E2 protein CD4+ T-cell epitope, SEQ ID No:82.
XX
KM Papillomavirus infection; CD4+ T-cell; T-lymphocyte; E2;
XX immune modulation; vaccine; tumor suppressor; infection; virucide.
XX
OS Human papillomavirus type 16.
XX
PN WO2004105681-A2.
XX
PD 09-DEC-2004.
XX
PF 23-APR-2004; 2004WO-US012650.
XX
PR 28-APR-2003; 2003US-0466235P.
XX
PA (INNO-) INNOGENETICS NV.
XX
PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD;
PI Stickler M;
XX
DR WPI; 2005-021230/02.
XX
XX
PT Novel isolated human papillomavirus epitope (HPV) e.g., HPV B6.16 or HPV
PT E7.16 epitope, useful for producing medicament for inducing immune
PT response against HPV.
XX
PS Claim 1; SEQ ID NO 82; 56pp; English.
XX
XX
CC The invention relates to isolated human papillomavirus (HPV) epitopes
CC given as SEQ ID Nos 1-109 in the specification. The epitopes are CD4+ T-
CC cell epitopes in B6, E7 and E2 proteins isolated from various strains of
CC HPV. Also claimed are: a polynucleotide comprising one or more of the
CC nucleic acid sequences encoding an epitope of the invention, a vector
CC comprising the above polynucleotide, a polypeptide encoded by the above
CC polynucleotide, a cell comprising the above polynucleotide, a composition
CC comprising the above polypeptide, one or more peptide that has a HPV
CC epitope or one or more nucleic acid that encodes the HPV epitope, and a
CC vaccine composition comprising a HPV epitope or one or more nucleic acid
CC that encodes a HPV epitope. The HPV epitopes of the invention are useful
CC for producing a medicament for inducing an immune response (e.g. an
CC antibody-mediated response or cell-mediated response) directed against
CC one or more strain of HPV. The epitopes are useful in the development of
CC HPV vaccines (particularly multivalent vaccines) for the prevention of
CC infection with high-risk HPV strains. The HPV epitopes are useful in
CC prophylactic and therapeutic vaccines against HPV. The therapeutic
CC vaccines can be used to prevent the development of benign and/or
CC malignant tumors in HPV infected individuals. This sequence represents a
CC HPV epitope of the invention.
XX
SQ Sequence 15 AA;

AC AAU96325;
 XX
 DT 15-JUL-2002 (first entry)
 XX
 DE Der HMW-map polypeptide #12.
 XX
 KM Der HMW-map; American house dust mite; anti-allergic; mite; IGB;
 KM mite allergenic protein; immunoglobulin E; hypersensitivity;
 KM immunocomplex formation.
 XX
 OS Dermatophagoides farinae.
 XX
 PN WO200222807-A2.
 XX
 PD 21-MAR-2002.
 XX
 PF 14-SEP-2001; 2001WO-US028730.
 XX
 PR 14-SEP-2000; 2000US-00662293.
 XX
 PA (HESKA-) HESKA CORP.
 XX
 PI Mccall CA, Hunter SW, Weber ER;
 XX
 DR WPI; 2002-351888/38.
 XX
 PT New mite allergenic protein isolated from Dermatophagoides, designated
 PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
 XX
 PS Claim 12; Page 71; 161pp; English.
 XX
 SQ The invention relates to an isolated mite allergenic protein of
 CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
 CC acid. The Der HMW-map protein is useful for eliciting an immune response
 CC against Der HMW-map protein. The protein or a reagent comprising a non-
 CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
 CC cat) susceptible to or having an allergic response to a mite. A
 CC therapeutic composition is useful for desensitizing a host animal to an
 CC allergic response to a mite. The DNA and protein can be used in the
 CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
 CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
 CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
 CC binding of proteins to IgE, to prevent immunocomplex formation, thus
 CC reducing hypersensitivity responses to mite allergens, and as vaccines
 CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
 CC represent Der HMW-map polypeptides of the invention
 XX
 SQ Sequence 18 AA;
 Query Match 41.0%; Score 32; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 2e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 8 DYSKNP 13
 ||:||||
 1 DYAKNP 6
 Db
 RESULT 18
 AARI5551
 ID AARI5551 standard; protein; 20 AA.
 XX
 AC AARI5551;
 XX
 DT 02-MAR-1992 (first entry)
 XX
 DE Immunopeptide #2 derived from HPV16 E2 peptide.
 XX
 KM cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
 KM squamous cell carcinoma; ELISA; HPV 16.
 XX
 OS Synthetic.
 XX

PN WO9118294-A.
 XX
 PD 28-NOV-1991.
 XX
 PF 11-MAY-1990; 90SR-00001705.
 XX
 PR 11-MAY-1990; 90SR-00001705.
 XX
 PA (MEDS-) MEDSCAND AB.
 XX
 PI Dillner J, Dillner L, Cheng HW;
 XX
 DR WPI; 1991-369390/50.
 XX
 PT Diagnosis of human papilloma virus infection and PV-carrying tumours -
 PT using synthetic peptide(s) to detect virus specific antigen-antibody
 PT complexes by immunoassay.
 XX
 PS Disclosure; Page 38; 72pp; English.
 XX
 CC This is one of a large number of peptides which have been synthesised on
 CC the basis of the amino acid sequences for the E2, E4, E7, L1 or L2
 CC proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The selection of
 CC peptide sequences was based on the assumption that an immunoreactive
 CC region might be situated in the same relative region of a protein from
 CC different HPV types. The peptides were used in diagnostic immunoassays to
 CC detect HPV-infection. See AARI5523-R15601
 XX
 SQ Sequence 20 AA;
 Query Match 41.0%; Score 32; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 2.2e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 RDNDYSKN 12
 |||:||:
 12 RDHIDYWK 20
 Db
 RESULT 19
 ADK08339
 ID ADK08339 standard; peptide; 9 AA.
 XX
 AC ADK08339;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human papillomavirus peptide #394.
 XX
 KM pathogenic virus; alternative reading frame; antigenic determinant;
 KM vaccine; vaccine; therapeutic agent; infection; HPV.
 XX
 OS Human papillomavirus.
 XX
 PN WO2004011650-A2.
 XX
 PD 05-FEB-2004.
 XX
 PF 24-JUL-2003; 2003WO-EP008112.
 XX
 PR 24-JUL-2002; 2002AT-00001124.
 XX
 PR 11-JUL-2003; 2003EP-00450171.
 XX
 PA (INTB-) INTERCELL AG.
 XX
 PI Mattner F, Schmidt W, Habel A;
 XX
 DR WPI; 2004-169243/16.
 XX
 PT New polypeptide encoded by an alternative reading frame of a pathogenic
 PT virus comprising an antigenic determinant, useful for treating or
 PT preventing an infection with the pathogenic virus.
 XX

PS Claim 18; Page 177; 220pp; English.

XX This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.

XX Sequence 9 AA;

Query Match 39.7%; Score 31; DB 8; Length 9;
Best Local Similarity 75.0%; Pred. No. 2e+06; 2; Indels 0; Gaps 0;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSK 11
|||
Db 2 RDHIDYWK 9

RESULT 20

AAW35621
ID AAW35621 standard; peptide; 20 AA.

XX AAW35621;

AC 13-MAY-1998 (first entry)

XX Immunomodulatory peptide #12 of vespid antigen 5.

DE Immunomodulatory peptide; vespid antigen 5; immunogenic; allergy;

KM vespid venom; white face hornet wasp.

XX Dolichovespula maculata.

OS Synthetic.

XX WO9733910-A1.

XX 18-SEP-1997.

XX 11-MAR-1997; 97WO-US003753.

XX 11-MAR-1996; 96US-00614935.

XX (UYRQ) UNIV ROCKEFELLER.

XX Kling TP;

XX WPI; 1997-470817/43.

XX Vespid venom antigen 5 peptide fragments - useful to treat or diagnose

XX Vespid venom sensitivity.

XX Claim 2; Page 50; 73pp; English.

XX This sequence represents a specifically claimed peptide which is derived
CC from vespid venom antigen 5 (VVS) and is antigenic for T cell
CC proliferation in mice immunised with VVS. The peptide can be used to
CC treat or diagnose vespid venom sensitivity e.g. to Dolichovespula
CC maculata (white face hornet), Vespula vulgaris (yellowjacket), V.
CC maculifrons (yellowjacket), D. areolaris (yellow hornet), Polistes
CC annularis (wasp), P. exclamans (wasp), V. crabro (European hornet), V.
CC flavopilosa (yellowjacket), V. germanica (yellowjacket), V. pennsylvanica
CC (yellowjacket), V. squamosa (yellowjacket), V. vidua (yellowjacket) and
CC P. fuscatus (paperwasp)

XX Sequence 20 AA;

Query Match 39.7%; Score 31; DB 2; Length 20;

Best Local Similarity 45.5%; Pred. No. 3.3e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKRDHNDYSKN 12
| : ||| : :
Db 4 IKRDHNDYRQN 14

RESULT 21

AAW62711
ID AAW62711 standard; protein; 15 AA.

XX AAW62711;

AC 09-NOV-1998 (first entry)

XX Streptococcus pneumoniae polypeptide.

DE Polypeptide; ORF; open reading frame; infection; bacterial;

KM streptococcal; bacteremia; diagnosis; prophylaxis.

XX Streptococcus pneumoniae.

XX WO9823631-A1.

XX 04-JUN-1998.

XX 24-NOV-1997; 97WO-US021976.

XX 27-NOV-1996; 96US-0031879P.

XX (SMIK) SMITHKLINE BEECHAM CORP.

XX (SMIK) SMITHKLINE BEECHAM PLC.

XX Black MT, Hodgson JE, Knowles DJC, Lonetto MA, Nicholas RO;

XX Reid RH, Zarfos PN;

XX WPI; 1998-322654/28.

XX Streptococcus pneumoniae polynucleotides - useful for developing products

XX for diagnosis, prevention and treatment of infections e.g. pneumonia,

XX bacteremia, meningitis or endocarditis.

XX Claim 5; Page 32; 181pp; English.

XX The sequence is that of a Streptococcal polypeptide. The polypeptide can
CC potentially be used for the diagnosis and prevention of bacterial
CC infections, especially sp infection. It may be used for the treatment of
CC diseases such as otitis media, conjunctivitis, pneumonia, bacteremia,
CC meningitis, sinusitis, pleural empyema, endocarditis or infection of the
CC cerebrospinal fluid

XX Sequence 15 AA;

Query Match 38.5%; Score 30; DB 2; Length 15;

Best Local Similarity 55.6%; Pred. No. 3.5e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SIKRDHNDY 9
: ||| :
Db 2 AINRFHNDP 10

RESULT 22
ABU70887
ID ABU70887 standard; protein; 19 AA.

XX ABU70887;

XX 10-JUN-2003 (first entry)

XX Human adipocyte Selected Interacting domain, SID, #518.

KM Human; prey; adipocyte; SID; selected interacting domain; anorectic;
 KM antidiabetic; protein-protein interaction; diabetes;
 KM yeast 2-hybrid assay; metabolic disorder; obesity.
 XX
 OS Homo sapiens.
 XX
 PN WO200286122-A2.
 XX
 PD 31-OCT-2002.
 XX
 PF 14-MAR-2002; 2002WO-BP003768.
 XX
 PR 14-MAR-2001; 2001US-0275734P.
 XX
 PA (HYBR-) HYBRGENICS.
 XX
 PI Legrain P, Davlet L;
 DR WPI; 2003-103412/09.
 DR N-PSDB; ACA57431.
 XX
 PT New complex between two interacting proteins in adipocyte cells, useful
 PT for identifying selected interacting domains that modulate protein
 PT interactions, or for preventing or treating metabolic disorders such as
 PT obesity or diabetes.
 XX
 PS Claim 6, Page 279, 382pp; English.
 XX
 CC The invention relates to a complex between two interacting proteins in
 CC adipocyte cells, given in the specification. The proteins are identified
 CC by selecting a bait protein from a known adipocyte marker and then
 CC performing a yeast 2-hybrid selection to isolate prey proteins encoded by
 CC members of an adipocyte cDNA library. The proteins are designated SID
 CC (RTM) (selected interacting domains) proteins. Also included are a
 CC polynucleotide encoding a polypeptide in the adipocyte cells, a
 CC recombinant host cell expressing at least one of the interacting
 CC polypeptides of the complex, selecting a modulating compound in adipocyte
 CC cells, a SID (RTM) polypeptide comprising any of the 738 amino acid
 CC sequences given in the specification (including its fragment or variant),
 CC a SID (RTM) polynucleotide comprising any of the 738 nucleotide sequences
 CC given in the specification (including its fragment or variant), a vector
 CC comprising the SID (RTM) polynucleotide, a recombinant host cell
 CC comprising the vector, a protein chip comprising the polypeptides and a
 CC record comprising all or part of the data, listed in the specification.
 CC The complex, polypeptides, polynucleotides and compounds are useful for
 CC preventing or treating metabolic disorders such as obesity or diabetes.
 CC The polynucleotides are useful as probes or primers. The complex is
 CC particularly useful for identifying selected interacting domains (SID
 CC (RTM)) for screening drugs that modulate the protein interaction, thus
 CC exhibiting the therapeutic effect. The present sequence represents a SID
 CC (prey) protein of the invention
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 38.5%; Score 30; DB 6; Length 19;
 Best Local Similarity 55.6%; Pred. No. 4.7e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 RDHNDYSKN 12
 :|||:|:
 Db 9 RDHNDYRKS 17
 XX
 RESULT 23
 AAB33557
 ID AAB33557 standard; peptide; 20 AA.
 XX
 AC AAB33557;
 XX
 XX 12-SEP-2003 (revised)
 DT 22-JAN-2001 (first entry)
 XX
 DB 5/20 native Ara h 2 peptide #11.

XX
 KM Allergy; allergic reaction; allergen; anaphylactic antigen; peanut;
 KM Ara h 1; Ara h 2; Ara h 3; epitope; binding; immunoglobulin E; IgE;
 KM food antigen; sensitising; immune response; anti-allergic.
 XX
 OS Arachis hypogaea.
 XX
 PN WO200051647-A2.
 XX
 PD 08-SEP-2000.
 XX
 PF 03-MAR-2000; 2000WO-US005655.
 XX
 PR 03-MAR-1999; 99US-0122960P.
 PR 06-DEC-1999; 99US-00455294.
 XX
 PA (MOUN) MOUNT SINAI SCHOOL MEDICINE.
 PA
 PI Sampson HA;
 PI
 DR WPI; 2000-611341/58.
 DR
 XX
 PT Non-human animal sensitized to an antigen, useful as an animal model for
 PT studying allergic reactions to allergens, such as those in food and in
 PT the environment.
 XX
 PS Example 5, Page 62, 124pp; English.
 XX
 CC The present invention describes an animal model which can be used for
 CC studying allergic reactions to allergens. The animal is sensitized to a
 CC selected antigen by administering the antigen itself or a nucleic acid
 CC encoding the antigen, where preferably the antigen is an anaphylactic
 CC antigen. The sensitized animal can then be used to screen for compounds
 CC which may help to prevent, ameliorate, or cure allergic conditions in
 CC humans. The animal model can be used for studying allergic reactions to
 CC allergens, such as those in food (peanuts, fruit, berry, nut, bean, milk,
 CC dairy products), or in the environment (weed pollen, grass pollen, tree
 CC pollen, mite, animal, animal dander, fungal, and insect antigens).
 CC AAB33478 to AAB33601 represent sequences which are used in examples from
 CC the present invention to specifically examine the peanut allergy, and the
 CC peanut anaphylactic antigens Ara h 1 to 3. (Updated on 12-SEP-2003 to
 CC standardise OS field)
 CC
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 38.5%; Score 30; DB 3; Length 20;
 Best Local Similarity 36.4%; Pred. No. 5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 3 KRDNDSKNP 13
 :|||:|:
 Db 1 QRDSDSYERDP 11
 XX
 RESULT 24
 AAB23108
 ID AAB23108 standard; peptide; 20 AA.
 XX
 AC AAB23108;
 XX
 DT 29-JAN-2001 (first entry)
 XX
 XX Peanut wild-type Ara h 2 20 residue peptide #11.
 DE
 XX
 KM Ara h 2 protein; peanut; epitope; antigen; allergy; asthma;
 KM immunomodulation; unmethylated CpG oligonucleotide; anti-allergic.
 XX
 OS Arachis hypogaea.
 OS
 PN WO200054803-A2.
 XX
 PD 21-SEP-2000.
 XX

PF 16-MAR-2000; 2000WO-US007213.
XX
PT 16-MAR-1999; 99US-0124595P.
PR 17-MAR-1999; 99US-0125071P.
XX
XX (PANA-) PANACEA PHARM LLC.
XX
PI Sosin HB, Caplan MJ;
XX
DR WPI, 2000-628168/60.
XX
XX Immunostimulatory composition for treating or preventing an allergic
PT reaction leading to conditions such as asthma or anaphylaxis, comprises
PT oligonucleotides with unmethylated CpG sequences and antigens derived
PT from allergens.
XX
XX Example 3; Page 67; 103pp; English.
XX
XX The invention relates to an immunomodulatory composition comprising a CpG
CC oligonucleotide of the sequence 5' purine-purine-C-G-pyrimidine-
CC pyrimidine 3', where C and G are unmethylated, and at least one antigen
CC derived from an allergen that causes anaphylaxis. The composition is
CC useful for treating allergy in an individual. The composition prevents or
CC modulates an individual's immune response to an antigen which leads to
CC asthma and/or anaphylaxis. Individuals susceptible to anaphylactic shock
CC upon exposure to allergens from foods (e.g., peanut), venom or rubber may
CC be treated using the composition. Sequences AAB23098-B23125 represent a
CC series of 20-residue peptides from wild-type peanut Ara h 2 protein used
CC in an exemplification of the invention
XX
SQ Sequence 20 AA;
XX
XX
Query Match 38.5%; Score 30; DB 3; Length 20;
Best Local Similarity 36.4%; Pred. No. 5e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 KRDNDYSKNP 13
: || : | : : |
Db 1 QRDEDSYERDP 11
XX
RESULT 25
AAU04770
ID AAU04770 standard; peptide; 20 AA.
XX
XX AAU04770;
XX
XX 23-OCT-2001 (first entry)
XX
XX Native anaphylactic antigen Ara h 2 peptide #11.
DE
XX Ara h 2; anaphylactic antigen; immunoglobulin E; IgE; immunogenic;
KW allergy; mast cell; basophil; mouse; epitope.
XX
XX Mus sp.
OS
XX
XX WO200140264-A2.
PN
XX
PD 07-JUN-2001.
XX
XX 06-DEC-2000; 2000WO-US033124.
PF
XX
XX 06-DEC-1999; 99US-00455294.
PR 23-JUN-2000; 2000US-0213765P.
PR 27-SEP-2000; 2000US-0235797P.
XX
XX (PANA-) PANACEA PHARM LLC.
PA (UYAR-) UNITV ARKANSAS.
PA (MOUN) MOUNT SINAI SCHOOL MEDICINE NEW YORK.
XX
XX Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;
PT
XX WPI; 2001-381378/40.
DR

XX
XX Antigenic fragments useful for reducing anaphylactic risk and reducing
PT the severity and/or number of allergic symptoms in individuals sensitive
PT to antigens, have reduced ability to bind Immunoglobulin E.
XX
XX Claim 40; Page 52; 100pp; English.
XX
XX The sequence represents the amino acid sequence of native anaphylactic
CC antigen Ara h 2 peptide #11. Ara h 2 is an anaphylactic antigen (A) which
CC was used to design antigenic peptides having a reduced ability to bind
CC IgE as compared with the intact (A), or having a sequence substantially
CC identical to a portion of sequence of an antigen that includes at least
CC one IgE binding site, where at least one IgE binding site of the peptide
CC is altered. The antigenic peptides are used in a composition which is
CC useful for reducing risk or severity of allergic reaction to an antigen.
CC This is done by identifying an individual at risk of allergic reaction to
CC an antigen by identifying prior display of allergic symptoms when exposed
CC to the antigen, or a familial relationship with an individual who
CC previously displayed allergic symptoms when exposed to the antigen.
CC Following this an antigen-specific IgE present on one or more mast cells
CC or basophils in the individual's serum is identified. The individual is
CC then contacted with a peptide corresponding to a portion of the antigen,
CC which is selected, formulated, and delivered so that binding of the
CC peptide to antigen-specific IgE is reduced as compared with IgE binding
CC of intact antigen. The composition is also useful for treating and
XX preventing allergic reactions
XX
SQ Sequence 20 AA;
XX
XX
Query Match 38.5%; Score 30; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 5e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 3 KRDNDYSKNP 13
: || : | : : |
Db 1 QRDEDSYERDP 11
XX
RESULT 26
AAU05095
ID AAU05095 standard; peptide; 20 AA.
XX
XX AAU05095;
XX
XX 24-OCT-2001 (first entry)
XX
XX Anaphylactic peanut antigen Ara h 2, native peptide #11.
DE
XX Anaphylactic antigen; Ara h 2; peanut; desensitisation; antigen; allergy;
KW immunotherapy; rush immunotherapy; anaphylaxis; asthma; food allergen;
KW milk allergen; shellfish allergen; latex; drug; environmental allergen;
KW grass pollen; ovalbumin; insect venom; peanut oil; immunoglobulin E; IgE.
XX
XX Arachis sp.
OS
XX
XX WO200139799-A2.
PN
XX
PD 07-JUN-2001.
XX
XX 06-DEC-2000; 2000WO-US033125.
PF
XX
XX 06-DEC-1999; 99US-00455294.
PR 23-JUN-2000; 2000US-0213765P.
PR 27-SEP-2000; 2000US-0235797P.
XX
XX (PANA-) PANACEA PHARM LLC.
PA
XX
XX Caplan M;
PT
XX WPI; 2001-408258/43.
DR
XX
XX Preventing allergic response against antigens, e.g. food and
PT environmental allergens such as peanut allergen or grass pollen, latex or

PT drug, comprises administering agent, e.g. a peptide, that blocks antigen
 binding sites on offending IGE.
 XX Example 2, Page 46, 76pp, English.
 CC The sequence represents the amino acid sequence of anaphylactic peanut
 antigen Ara h 2, native peptide #11. The peptide is used in active or
 passive desensitization of an individual to an antigen, for alleviating
 or preventing allergic reactions and for decreasing the risk of allergic
 reactions during immunotherapy or rush immunotherapy, anaphylaxis and
 asthma. The antigen may be a food allergen (e.g. peanut or milk
 allergen), shellfish allergen, environmental allergen (e.g. grass pollen
 or tree pollen), latex, drug, pollen, ovalbumin, an insect venom antigen
 or predominantly linear epitopes. The protein is useful for protecting an
 individual against subsequent inadvertent or intentional exposure to
 antigen, e.g. receiving blocking agent before eating a chocolate bar
 which may inadvertently contain peanut components or before eating foods
 prepared using peanut oil. Administration of the blocking agent does not
 result in cross-linking of anti-allergenic IGE. After exposure to the
 agent, the individual's antigen sensitivity is at least temporarily
 reduced. Only those IGE molecules that bind the offending antigen and
 contribute to the risk of an allergic response are blocked
 CC
 XX Sequence 20 AA,
 SQ
 Query Match 38.5%; Score 30; DB 4; Length 20;
 Best Local Similarity 36.4%; Pred. No. 5e+02; 3; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 3 KRDNHDSKNP 13
 :||:|:|:
 Db 1 GRDEDSYERDP 11
 RESULT 27
 AA017451
 ID AA017451 standard; peptide; 20 AA.
 XX
 AC AA017451;
 XX
 DT 11-JUL-2002 (first entry)
 XX
 DE P falciparum TRAP CD4+ T cell epitope #10.
 KM Tuberculosis; TB; vaccination; vaccine; CD4+ T cell immune response;
 KM poxvirus vector; HIV; malaria; Helicobacter pylori; influenza; hepatitis;
 KM viral infection; leprosy; protozoan parasite; cancer; tuberculosis;
 KM anti-HIV; protease; antibacterial; virucide; hepatotropic;
 KM anti-inflammatory; antileptotic; cytostatic; epitope.
 XX
 OS Plasmodium falciparum.
 XX
 PN WO200224224-A2.
 XX
 PD 28-MAR-2002.
 XX
 PF 13-SEP-2001; 2001WO-GB004116.
 XX
 PR 21-SEP-2000; 2000GB-00023203.
 XX
 PA (OXO-) OXON PHARMACEUTICALS LTD.
 XX
 PI Hill AVS, Mcshane H, Gilbert S, Reece W, Schneider J;
 XX
 DR WPI, 2002-394098/42.
 XX
 PT Inducing CD4+ T-cell response against target antigen by administering a
 PT composition comprising a source of CD4+ epitopes which is a non-
 PT replicating or replicating impaired recombinant poxvirus vector.
 XX
 PS Example 2, Page 33, 50pp, English.
 XX
 CC The present invention relates to a method of inducing a CD4+ T-cell

CC response against a target antigen, by administering two different
 CC compositions comprising a source of CD4+ T-cell epitope(s) of the target
 CC antigen, where the second composition further includes an epitope which
 CC is same as the epitope of the first composition, where the source of the
 CC epitopes for the compositions is a non-replicating or replicating
 CC impaired recombinant poxvirus vector. The methods are useful for inducing
 CC CD4+ T-cell immune responses against diseases such as tuberculosis, human
 CC immunodeficiency virus (HIV) (persistent viral infection), malaria,
 CC Helicobacter pylori, influenza, hepatitis (chronic hepatitis B and C),
 CC cytomegalovirus (CMV), viral infection, herpes virus-induced disease,
 CC leprosy and diseases caused by non-malarial protozoan parasite such as
 CC toxoplasma and cancer. The present sequence is an epitope from Plasmodium
 CC falciparum useful in the method of the invention
 XX
 SQ Sequence 20 AA;
 QY 2 IKRDNDYSKN 12
 :||:|:|:
 Db 10 IIRLHSDASKN 20
 RESULT 28
 ADD12247
 ID ADD12247 standard; peptide; 20 AA.
 XX
 AC ADD12247;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE PDZ ligand (PL) peptide #9.
 XX
 KM modulator; PDZ; post-synaptic density protein 95; PSD95;
 KM Drosophila large disc protein; zonula occludin 1 protein; ZO-1;
 KM PDZ ligand; PL; anti-inflammatory; anti-allergic; antitumor; antidiabetic;
 KM antiasthmatic; dermatological; neuroprotective; virucide; antidiabetic;
 KM osteopathic; antiarthritic; immunosuppressive; antiatherosclerotic;
 KM cytostatic; anti-HIV; vasotropic; immunomodulator; neurological disease;
 KM immune response disease; muscular disease; cancer;
 KM modulating vesicular trafficking; tumor suppression;
 KM signal transduction; protein sorting; membrane polarity; apoptosis;
 KM synapse formation; multi-protein complex; leukocyte activation inhibitor.
 OS Unidentified.
 XX
 PN WO2003014303-A2.
 XX
 PD 20-FEB-2003.
 XX
 PF 02-AUG-2002; 2002WO-US024655.
 XX
 PR 03-AUG-2001; 2001US-0309841P.
 XX
 PR 25-FEB-2002; 2002US-0360061P.
 XX
 PA (ARBO-) ARBOR VITA CORP.
 XX
 PI Lu PS, Rabinowitz JD, Schweizer J, Carrick DM;
 XX
 DR WPI, 2003-268193/26.
 XX
 PT Modulator of binding between discs-large homology repeat protein, PDZ and
 PT PDZ ligand protein, is a peptide having few residues of C-terminal
 PT sequence of PDZ ligand protein.
 XX
 PS Example 7, Page 150, 172pp, English.
 XX
 CC The invention relates to a novel modulator of binding between a PDZ
 CC protein (post-synaptic density protein 95 (PSD95), Drosophila large disc
 CC protein and zonula Occludin 1 protein (ZO-1)) and a PDZ ligand (PL)
 CC protein. The modulator is a peptide having 3 residues of a C-terminal

CC sequence of a PL protein. PDZ and PL proteins are a binding pair given in
 CC specification, or a peptide mimetic of the 3 residue PL protein, or a
 CC small molecule having similar functional activity as the 3 residue PL
 CC protein. The reagents of the invention have the following activities:
 CC antiinflammatory, antiallergic, antitumor, antiparasitic, antiasthmatic,
 CC dermatological, neuroprotective, virucide, antidiabetic, osteopathic,
 CC antiarthritic, immunosuppressive, antiatherosclerotic, cystostatic, anti-
 CC HIV, vasotropic, and immunomodulator. The novel modulator is useful for
 CC treating a disease correlated with binding between a PDZ protein and PL
 CC protein. The disease can be a neurological disease, immune response
 CC disease, muscular disease or cancer. The modulator is useful for
 CC modulating vesicular trafficking, tumor suppression, signal
 CC transduction, protein sorting, establishment of membrane polarity,
 CC apoptosis, regulation of immune response and organization of synapse
 CC formation. The modulator is useful for facilitating the assembly of multi-
 CC -protein complexes, often serving as a bridge between several proteins,
 CC or regulating the function of other proteins, and to inhibit leukocyte
 CC activation. The modulator is useful for treating diseases characterised
 CC by inflammatory and humoral immune responses e.g., inflammation, allergy,
 CC inflammatory bowel diseases, ulcerative colitis, psoriasis, asthma,
 CC allergic rhinitis, atopic dermatitis, arthritis, multiple sclerosis,
 CC diabetes, osteoarthritis, graft-versus-host diseases, atherosclerosis,
 CC leukemia, infectious diseases (viral infection such as human
 CC immunodeficiency virus (HIV)), and ischemia. This sequence represents a
 CC PDZ ligand (PL) peptide of the invention.

XX
 SQ Sequence 20 AA;

Query Match 38.5%; Score 30; DB 7; Length 20;
 Best Local Similarity 57.1%; Pred. No. 5e+02;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDYSKNP 13
 DB 9 NDFTQNP 15

RESULT 29

ADW33950
 ID ADM33950 standard; peptide; 20 AA.

XX ADW33950;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #4700.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KW viral disease; cancer.

XX Unidentified.

OS WO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX
 SQ Sequence 20 AA;

Query Match 38.5%; Score 30; DB 7; Length 20;
 Best Local Similarity 63.6%; Pred. No. 5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
 DB 5 IIRLHSDASKN 15

RESULT 30

ADW35183
 ID ADM35183 standard; peptide; 20 AA.

XX ADW35183;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #5933.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KW viral disease; cancer.

XX Unidentified.

OS WO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX Claim 1; Page 52-379; 382pp; English.

XX The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The

CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW39251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 20 AA;

Query Match 38.5%; Score 30; DB 7; Length 20;
 Best Local Similarity 63.6%; Pred. No. 5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKRDHNDYSKN 12
 |||:||||
 Db 5 IIRLHSDASKN 15

RESULT 31

ADW36547
 ID ADW36547 standard; peptide; 20 AA.

XX ADW36547;

XX 10-MAR-2005 (first entry)

XX HLA binding epitope #7297.

XX Virocidic; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

XX MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

XX viral disease; cancer.

XX Unidentified.

XX WO2003040165-A2.

XX 15-MAY-2003.

XX 18-OCT-2001; 2001WO-US051650.

XX 19-OCT-2000; 2000US-0242350P.

XX 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

XX Sette A, Sidney J, Southwood S;

XX MPI; 2003-441519/41.

XX New composition comprising at least one peptide having allele-specific

XX binding motifs for HLA, useful for preventing, treating or diagnosing

XX viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or

CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW39251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 20 AA;

Query Match 38.5%; Score 30; DB 7; Length 20;
 Best Local Similarity 63.6%; Pred. No. 5e+02;
 Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKRDHNDYSKN 12
 |||:||||
 Db 5 IIRLHSDASKN 15

RESULT 32

ADK08317
 ID ADK08317 standard; peptide; 8 AA.

XX ADK08317;

XX 06-MAY-2004 (first entry)

XX Human papillomavirus peptide #372.

XX pathogenic virus; alternative reading frame; antigenic determinant;

XX virocidic; vaccine; therapeutic agent; infection; HPV.

XX Human papillomavirus.

XX WO2004011650-A2.

XX 05-FEB-2004.

XX 24-JUL-2003; 2003WO-EP008112.

XX 24-JUL-2002; 2002AT-00001124.

XX 11-JUL-2003; 2003EP-00450171.

XX (INTE-) INTERCELL AG.

XX Mattner F, Schmidt W, Habel A;

XX MPI; 2004-169243/16.

XX New polypeptide encoded by an alternative reading frame of a pathogenic

XX virus comprising an antigenic determinant, useful for treating or

XX preventing an infection with the pathogenic virus.

XX Claim 16; Page 177; 220pp; English.

CC This invention relates to a novel polypeptide encoded by an alternative
 CC reading frame of a pathogenic virus, where the polypeptide starts with a
 CC methionine amino acid residue, which comprises an antigenic determinant
 CC and more than 7 amino acid residues. The invention may be useful for the
 CC production of compounds with a virocidic activity or the development of a
 CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
 CC agent. It is also useful for the manufacture of a medicament for treating
 CC or preventing an infection with the pathogenic virus. The present
 CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
 CC invention.

XX Sequence 8 AA;

Query Match 37.2%; Score 29; DB 8; Length 8;
 Best Local Similarity 83.3%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RDHNDY 9
 |||||
 Db 2 RDHNDY 7

```

RESULT 33
AAV46600
ID AAV46600 standard; peptide; 10 AA.
XX
AC AAV46600;
XX
DT 01-DEC-1999 (first entry)
XX
DE Immunogenic peptide having a human leukocyte antigen binding motif #1211.
XX
KW Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
KW immune response; T cell activation; major histocompatibility complex;
KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
KW vaccine; immunisation.
XX
OS Synthetic.
OS Homo sapiens.
XX
PN MO945954-A1.
XX
PD 16-SEP-1999.
XX
PF 13-MAR-1998; 98WO-US005039.
XX
PR 13-MAR-1998; 98WO-US005039.
XX
PA (EPIM-) EPIMUNE INC.
XX
PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
XX
DR WPI; 1999-551214/46.
XX
PT New immunogenic peptides with HLA binding motif, useful in treatment and
PT diagnosis of cancers and viral diseases.
XX
PS Claim 1; Page 78; 150pp; English.
XX
AAV45390 to AAV48214 represent specifically claimed immunogenic peptides
CC having a human major histocompatibility complex (MHC) Class I (also known
CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
CC (CTLs) which destroy antigen-bearing cells are normally induced by an
CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
CC than the intact foreign antigen itself, and are particularly important in
CC tumour rejection and in fighting viral infections. The peptides are
CC therefore useful therapeutically to treat or prevent viral infections and
CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
CC elicit an immune response in individuals susceptible or otherwise at risk
CC of viral infection or cancer, or used to treat chronic or acute
CC conditions. They are also useful diagnostically, and can be used to
CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
CC patient. The polynucleotides encoding the immunogenic peptides are also
CC useful therapeutically and for immunisation as above
XX
SQ Sequence 10 AA;

Query Match          37.2%; Score 29; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

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ID ADR08377 standard; peptide; 10 AA.
XX
AC ADR08377;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #432.
XX
KW pathogenic virus; alternative reading frame; antigenic determinant;
KW virucide; vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.
XX
PD 05-FEB-2004.
XX
PF 24-JUL-2003; 2003WO-EP008112.
XX
PR 24-JUL-2002; 2002AT-00001124.
XX
PR 11-JUL-2003; 2003EP-00450171.
XX
PA (INTE-) INTERCELL AG.
XX
PI Mattner F, Schmidt W, Habel A;
XX
DR WPI; 2004-169243/16.
XX
PT New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
PS Claim 18; Page 178; 220pp; English.
XX
This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
SQ Sequence 10 AA;

Query Match          37.2%; Score 29; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 3.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY 4 RDHNDY 12
   |||||
DB 1 RLHSDASKN 9

RESULT 34
ADR08377

```

```

QY 4 RDHNDY 9
   |||||
DB 5 RDHNDY 10

RESULT 35
AD64049
ID AD64049 standard; peptide; 12 AA.
XX
AC AD64049;
XX
DT 18-DEC-2003 (first entry)
XX
DE Carbon black-binding peptide #11.
XX
KW polyhydroxyalkanoate-containing structure; PHA-containing structure;
KW PHA synthase; polyhydroxyalkanoate synthase; 3-hydroxyacyl coenzyme A;
KW pigment dispersant; electrophotography toner; laminated structure;
KW OHP film; microcapsule pigment ink; electrophoresis particle;
KW electrophoresis display; colour filter; enzyme;
XX carbon black-binding peptide.
XX

```

OS Unidentified.
 XX
 PN EPI275728-A1.
 XX
 PD 15-JAN-2003.
 XX
 PF 10-JUL-2002; 2002EP-00015374.
 XX
 PR 10-JUL-2001; 2001JP-00210052.
 XX
 PR 13-JUN-2002; 2002JP-00172978.
 XX
 PA (CANO) CANON KK.
 XX
 PI Nomoto T, Yano T, Kozaki S, Honma T,
 DR WPI; 2003-459566/44.
 XX
 PT Manufacturing polyhydroxyalkanoate-containing structure useful as toner
 PT for electrophotography, by immobilizing polyhydroxyalkanoate synthase on
 PT base material and synthesizing polyhydroxyalkanoate on base material.
 PS
 PS Claim 49, SEQ ID NO 48; 277pp; English.
 XX
 CC The invention comprises a method for producing a polyhydroxyalkanoate
 CC (PHA)-containing structure. The method involves immobilizing a PHA
 CC synthase enzyme on a base material surface and then synthesizing PHA
 CC using 3-hydroxyacyl coenzyme A as a substrate. The method of the
 CC invention is useful for manufacturing a PHA-containing structure. The PHA
 CC -containing structure has a wide range of applications as a variety of
 CC functional structures, such as: a pigment dispersant of excellent
 CC dispersion stability; a toner for electrophotography of excellent
 CC electrostatic property; and the laminated structure as an OHP film. The
 CC structure is also useful for microcapsule pigment ink of excellent
 CC dispersion stability, an electrophoretic particle for electrophoresis
 CC display, and colouring composition for a colour filter. The present amino
 CC acid sequence represents a carbon black-binding peptide.
 XX
 SQ Sequence 12 AA;
 XX
 Query Match 37.2%; Score 29; DB 7; Length 12;
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 HNDYSKRP 13
 Db 3 NNDMSKAP 10
 XX
 RESULT 36
 ADG01812
 ID ADG01812 standard; peptide; 12 AA.
 XX
 AC ADG01812;
 XX
 DT 26-FEB-2004 (first entry)
 XX
 DE Carbon black pigment binding peptide SEQ ID NO:25.
 XX
 KM target antibody; target antigen; carrier; assay reagent; determination;
 KM detection; clinical laboratory test; environmental analysis;
 KM food analysis.
 XX
 OS Synthetic.
 XX
 PN EPI371983-A1.
 XX
 PD 17-DEC-2003.
 XX
 PF 06-JUN-2003; 2003BP-00012945.
 XX
 PR 13-JUN-2002; 2002JP-00173027.
 XX
 PR 02-MAY-2003; 2003JP-00127099.
 XX

PA (CANO) CANON KK.
 XX
 PI Honma T, Yano T, Nomoto T, Kozaki S;
 DR WPI; 2004-073347/08.
 XX
 PT Detecting presence or amount of target antibody/antigen comprises
 PT preparing carrier having immobilized antigen/antibody corresponding to
 PT antibody/antigen in specimen, mixing carrier and specimen and assaying
 PT agglutination.
 XX
 PS Claim 11; SEQ ID NO 25; 63pp; English.
 XX
 CC The present invention describes an assay (M1) for determining the
 CC presence or an amount of a target antibody or antigen in a specimen. M1
 CC comprises: (a) preparing a carrier on which an antigen or antibody
 CC corresponding to the target antibody or antigen in the specimen
 CC respectively is immobilized; and (b) mixing the carrier with the specimen
 CC and assaying the level of the immunological agglutination reaction caused
 CC by the mixing step, where the antigen or antibody immobilized on the
 CC carrier is bound to the carrier through an amino acid sequence capable of
 CC binding to the carrier. Also described: (1) an assay reagent (I), for
 CC (M1), where an antigen or antibody corresponding to the antibody or
 CC antigen is immobilized on a carrier and the antigen or antibody
 CC immobilised on a carrier is bound to the carrier through an amino acid
 CC sequence capable of binding to the carrier; (2) producing (M2) (I)
 CC comprising immobilising an antigen or antibody corresponding to the
 CC antibody or antigen immobilised on a carrier and the antigen or antibody
 CC immobilised on a carrier is bound to the carrier through an amino acid
 CC sequence capable of binding to the carrier; (3) a peptide (II) comprising
 CC one or more amino acid sequence (SEQ ID NO:1-SEQ ID NO:40); and (4) an
 CC antigen protein or antibody protein comprising one or more sequences
 CC chosen from (SEQ ID NO:1-SEQ ID NO:40). (M1) is useful for determining
 CC the presence or an amount of a target antibody or antigen. (I) can be
 CC used as an assay reagent for clinical laboratory tests or environmental
 CC or food analysis. The present sequence is used in the exemplification of
 CC the present invention.
 XX
 SQ Sequence 12 AA;
 XX
 Query Match 37.2%; Score 29; DB 8; Length 12;
 Best Local Similarity 62.5%; Pred. No. 4.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 HNDYSKRP 13
 Db 3 NNDMSKAP 10
 XX
 RESULT 37
 ADQ90327
 ID ADQ90327 standard; peptide; 12 AA.
 XX
 AC ADQ90327;
 XX
 DT 21-OCT-2004 (first entry)
 XX
 DE Carbon black binding peptide, SEQ ID 19.
 XX
 KM Substrate; organic; carbon layer; affinity region 15a; biosensor;
 KM bioreactor; detector.
 XX
 OS Unidentified.
 XX
 PN JP2004215514-A.
 XX
 PD 05-AUG-2004.
 XX
 PF 09-JAN-2003; 2003JP-00003554.
 XX
 PR 09-JAN-2003; 2003JP-00003554.
 XX
 PA (CANO) CANON KK.

XX WPI, 2004-575105/56.

DR Substrate useful in detector, bioreactor or biosensor, has organic

XX Substrate that binds to carbon layer present on substrate.

PT Claim 9; SEQ ID NO 19; 84pp; Japanese.

XX

XX The invention relates to a novel substrate (11) which has an organic

CC substance that binds to the carbon layer (12) present on the substrate.

CC The joint domain of the organic substance binds to one or more portions

CC of the carbon layer which has an affinity region (15a). The invention

CC further comprises: a detector comprising the substrate; a method for

CC producing the substrate, which involves fixing the organic substance on

CC the carbon layer that is present on the substrate having numerous pores;

CC and a biosensor or bioreactor, comprising the substrate as a module. The

CC substrate is useful in a detector, bioreactor or biosensor. This sequence

CC represents a carbon black binding peptide of the invention.

XX

XX

XX Sequence 12 AA;

XX

XX

XX Query Match 37.2%; Score 29; DB 8; Length 12;

XX Best Local Similarity 62.5%; Pred. No. 4.1e+02;

XX Matches 5; Conservativity 2; Mismatches 1; Indels 0; Gaps 0;

XX

XX 6 HNDYSKNP 13

XX :||:|

XX Db 3 NNDWSKAP 10

XX

XX

XX RESULT 38

XX AAY94623

XX ID AAY94623 standard; peptide; 13 AA.

XX AC

XX AAY94623;

XX

XX 15-AUG-2000 (first entry)

XX

XX Peptide used to generate polyclonal antibodies directed against ELVIS.

XX

XX Epidermal growth factor-like variant in skin-1; ELVIS; cytostatic;

XX chromosome 4q12-13; antipsoriatic; vulnery; dermatological; chemotaxis;

XX antiinflammatory; antiallergic; cell proliferation; differentiation;

XX angiogenesis; psoriasis; cancer; hair loss; wound healing; gene therapy;

XX contact dermatitis; burn; bipolar affective disorder; antibody.

XX

XX Synthetic.

XX

XX WO200029438-A1.

XX

XX 25-MAY-2000.

XX

XX 19-NOV-1999; 99WO-US027576.

XX

XX 19-NOV-1998; 98US-00196269.

XX

XX (MILL-) MILLENNIUM PHARM INC.

XX

XX Bufield S, Gearing DP;

XX

XX WPI, 2000-387744/33.

XX

XX New nucleic acid molecules encoding epidermal growth factor-like variant

XX in skin proteins (ELVIS), useful for treating psoriasis and cancer.

XX

XX Disclosure; Page 15; 99pp; English.

XX

XX This sequence represents a peptide used to generate polyclonal antibodies

CC against human epidermal growth factor-like variant in skin (ELVIS)

CC proteins. The ELVIS gene is located on chromosome 4q12-13. The invention

CC relates to a family of ELVIS proteins (ELVIS-1, 2, and 3), ELVIS-1 is a

CC membrane protein, while ELVIS-2 and ELVIS-3 are secreted proteins. These

CC proteins show considerable identity to transforming growth factor alpha

CC	(TGF- α) . The nucleotide sequence encoding the ELVIS proteins of the
CC	invention have antiproliferative, cytostatic, vulnerary, dermatological,
CC	antiinflammatory, and antiallergic activity. ELVIS encoding nucleotide
CC	sequences are useful as modulating agents in regulating a variety of
CC	cellular processes such as cell proliferation, cell migration and
CC	chemotaxis, cellular differentiation and/or angiogenesis and also in
CC	screening and detection assays and as predictive medicines. Elvis
CC	nucleotide sequences are useful in gene therapy techniques and to express
CC	ELVIS proteins. The ELVIS proteins are useful for treating proliferative
CC	disorders such as psoriasis and cancer, and to promote hair growth and
CC	wound healing. Modulators of ELVIS are useful in the treatment of contact
CC	dermatitis and burns, for treating bipolar affective disorder. The
CC	proteins can also be used to modulate epithelial cell growth and in the
CC	treatment of hair loss
XX	
SQ	Sequence 13 AA;
Query Match	37.2%; Score 29; DB 3; Length 13;
Best Local Similarity	62.5%; Pred. No. 4.Se+02;
Matches 5; Conservative	0; Mismatches 3; Indels 0; Gaps 0;
Oy	5 DHNDYSKN 12
Db	5 DHNSYCTN 12
RESULT 39	
ID ABM02379	ABM02379 standard; protein; 13 AA.
XX ABM02379;	
DT 12-FEB-2004	(first entry)
XX DE	Human ELVIS peptide #1 used to generate polyclonal antibody.
KM ELVIS; epidermal growth factor-like variant in skin; wound; hair loss;	
KW burn; gene therapy; dermatological; vulnerary; human.	
XX OS	Homo sapiens.
PN US2003138912-A1.	
PD 24-JUL-2003.	
PJ 16-JAN-2003; 2003US-00345764.	
PR 19-NOV-1998; 98US-00196269.	
PR 19-NOV-1999; 99US-00443959.	
PA (MILL-) MILLENNIUM PHARM INC.	
PI Buefield SJ, Gearing DP;	
DR WPI; 2003-851733/79.	
XX	
PT New epidermal growth factor-like variant in skin (ELVIS) nucleic acid,	
PT for treating a disorder characterized by the aberrant expression/activity	
PT of the polypeptide or nucleic acid e.g. wounds, burns, hair loss or	
PT unwanted hair growth.	
PS	
XX Disclosure; SEQ ID NO 22; 50bp; English.	
CC	The present invention relates to isolated nucleic acid molecules,
CC designated ELVIS-1, ELVIS-2, ELVIS-3 (epidermal growth factor-like	
CC variant in skin-1, 2, 3). The invention is useful for treating a disorder	
CC characterised by the aberrant activity of the polypeptide or nucleic acid	
CC molecule, e.g. skin conditions such as wounds, burns, hair loss or	
CC unwanted hair growth. The invention is also useful in gene therapy. The	
CC present sequence is human ELVIS peptide used to generate polyclonal	
CC antibody	
XX Sequence 13 AA;	

Query Match 37.2%; Score 29; DB 7; Length 13;
 Best Local Similarity 62.5%; Pred. No. 4.5e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
 |||||
 DB 5 DHNGYCIN 12

RESULT 40

ADFS3453 standard; peptide; 14 AA.

XX ADFS3453;
 AC ADFS3453;
 XX 12-FEB-2004 (first entry)
 DT
 XX
 XX MCPC 603 antibody CDR2 mutant peptide amino acid sequence 14.

XX walk-through mutagenesis; prototype amino acid; prototype nucleotide;
 KW mutant polypeptide production; MCPC 603;
 KM complementarity determining region; CDR; heavy chain; CDR2; mutant;
 KM mutain.

XX Unidentified.
 OS Synthetic.

XX WO2003089671-A1.

XX 30-OCT-2003.

XX 16-APR-2003; 2003WO-US011935.

XX 17-APR-2002; 2002US-0373686P.

XX (CREA/) CREA R.

XX (CAPP/) CAPPUCCILLI G.

XX Crea R, Cappuccilli G;

XX WPI; 2003-854132/79.

XX Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
 PT for producing mutant polypeptides comprising synthesizing oligonucleotides
 PT comprising a nucleotide sequence for each target region of a prototype
 PT amino acid.

XX Example; Fig 6; 40pp; English.

XX This invention relates to a novel method of walk-through mutagenesis of a
 CC nucleic acid encoding a polypeptide which comprises synthesizing a
 CC mixture of oligonucleotides comprising a nucleotide sequence for each
 CC target region of a prototype amino acid, where each oligonucleotide
 CC contains, at each sequence position in the target region, a prototype
 CC nucleotide for synthesis of the prototype amino acid, or a predetermined
 CC nucleotide that is required for synthesis of the predetermined amino
 CC acid. The method is useful in producing mutant polypeptides in which the
 CC overall presence of the predetermined amino acid is limited to one or two
 CC positions per mutated polypeptide, leaving the remaining amino acids in
 CC the targeted region intact or as close as possible to the prototype
 CC sequence. The invention was exemplified using the three complementarity
 CC determining regions (CDRs) of the heavy chain of the monoclonal antibody
 CC MCPC 603.

XX Sequence 14 AA;

Query Match 37.2%; Score 29; DB 7; Length 14;
 Best Local Similarity 50.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
 |||||: ::

DB 7 DHNDHGH 14

RESULT 41

AAM48458 standard; peptide; 15 AA.

XX AAM48458;
 AC AAM48458;
 XX 24-MAY-2002 (first entry)
 DT
 XX
 XX Oestrogenic effect B pyridate protein 30.69 peptide fragment.

XX Oestrogenic effect B pyridate protein 30.69 peptide fragment.
 DE
 XX
 XX Oestrogenic effect B pyridate protein 30.69;
 KW female reproduction organ maldevelopment;
 KW female sexual character abnormality; female reproduction system tumour;
 KW oestrogenic related metabolism abnormality.

XX Unidentified.

XX CN1326966-A.

XX 19-DEC-2001.

XX 05-JUN-2000; 2000CN-00116340.

XX 05-JUN-2000; 2000CN-00116340.

XX (BODE-) BODE GENE DEV CO LTD SHANGHAI.

XX Mao Y, Xie Y;

XX WPI; 2002-206975/27.

XX New polypeptide-oestrogenic effect B pyridate protein 30.69 for treating
 PT female reproduction organ maldevelopment, female sexual character
 PT abnormality, female reproduction system tumor, or estrogenic related
 PT metabolism abnormality.

XX Example 5; Page 19 (Disclosure); 33pp; Chinese.

XX The present invention relates to oestrogenic effect B pyridate protein
 CC 30.69 (AAM48457). The protein and its coding sequence are useful in
 CC treating various diseases, such as female reproduction organ
 CC maldevelopment, female sexual character abnormality, female reproduction
 CC system tumour and oestrogenic related metabolism abnormality. The present
 CC sequence is an N-terminal peptide fragment of the protein, which was used
 CC in an example from the invention

XX Sequence 15 AA;

Query Match 37.2%; Score 29; DB 5; Length 15;
 Best Local Similarity 83.3%; Pred. No. 5.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
 |||||
 DB 8 DYSKEP 13

RESULT 42

AAB22995 standard; protein; 15 AA.

XX AAB22995;
 AC AAB22995;
 XX 29-AUG-2003 (revised)
 DT 21-AUG-2002 (first entry)
 DT
 XX
 XX Infectious salmon anemia virus (ISAV) 9AI antigenic peptide #3.

XX Infectious salmon anemia virus (ISAV) 9AI antigenic peptide #3.
 DE
 XX
 XX Infectious salmon anemia virus; ISAV; infectious salmon anaemia;
 KW M1 protein; M2 protein; vaccine; antigen.

QY 5 DHNDYSKN 12
 |||||: ::

```

XX OS Infectious salmon anemia virus.
XX PN MO200226784-A2.
XX PD 04-APR-2002.
XX PF 25-SEP-2001; 2001MO-BP011129.
XX PR 28-SEP-2000; 2000EP-00203358.
XX PA (ALKU) AKZO NOBEL NV.
XX PI Biering E, Krossov B;
XX DR WPI; 2002-416474/44.
XX PT New infectious salmon anemia virus polynucleotide for use in diagnostics
XX PT and vaccines to protect fish against the infectious salmon anemia caused
XX PT by the virus.
XX PS Example 2; Page 17; 33pp; English.
XX CC The invention relates to polynucleotides encoding proteins M1 and M2 of
XX CC infectious salmon anemia virus (ISAV). Sequences of the invention are
XX CC useful in diagnostics e.g. to detect the presence of ISAV or anti-ISAV
XX CC antibodies in fish, in vaccines to protect fish against the infectious
XX CC salmon anaemia caused by the virus and in a marker vaccine to distinguish
XX CC vaccination from field infections with the virus. Polynucleotides of the
XX CC invention are used for the manufacture of DNA vaccines or vector vaccines
XX CC to protect fish against the anaemia. The present sequence is an antigenic
XX CC peptide of ISAV M1 and M2 protein from clone 9A1. (Updated on 29-AUG-2003
XX CC to standardise OS field)
XX SQ Sequence 15 AA;

Query Match          37.2%; Score 29; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNND 8
   :|||:
   5 RRDHNE 10

Db

RESULT 43
ADU68122
ID ADU68122 standard; peptide; 15 AA.
XX AC ADU68122;
XX DT 10-FEB-2005 (first entry)
XX DE Human papillomavirus-derived epitope peptide SegID81.
XX KM epitope mapping; T-cell; antiviral; cytostatic; vaccine;
XX KM vaccine, antiviral; benign tumor; tumor.
XX OS Human papillomavirus.
XX PN WO2004098497-A2.
XX PD 18-NOV-2004.
XX PF 23-APR-2004; 2004MO-US012652.
XX PR 28-APR-2003; 2003US-0466235P.
XX PA (GENEV) GENENCOR INT INC.
XX PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD,
XX PI Stickler M;
XX CC

```

```

DR WPI; 2004-813965/80.
XX PT Identifying CD4+ human papillomavirus (HPV) epitopes or determining T-
XX PT cell epitope of HPV strain, useful in prophylactic/therapeutic vaccines,
XX PT by combining dendritic cells, CD4+ and/or CD8+ T-cells with pepset of
XX PT peptides from HPV.
XX PS Claim 4; SEQ ID NO 81; 56pp; English.
XX CC This invention relates to a novel method of identifying CD4+ human
XX CC papillomavirus (HPV) epitopes or determining a T-cell epitope of a HPV
XX CC strain. The method comprises combining a solution of differentiated
XX CC dendritic cells and naive CD4+ and/or CD8+ T-cells with a set of peptides
XX CC from the HPV (which comprises the T-cell epitope) and measuring T-cell
XX CC proliferation. The invention may be useful for the production of
XX CC compounds with an antiviral or cytostatic activity. The method or the
XX CC modified epitopes are useful in prophylactic and/or therapeutic vaccines,
XX CC as means for the development of HPV vaccines for the prevention of
XX CC infection with high-risk HPV strains, or as means for the development of
XX CC therapeutic vaccines against high-risk HPV types for use in the
XX CC prevention of the development of benign and/or malignant tumors in
XX CC infected individuals. The present sequence is that of a Human
XX CC papillomavirus-derived epitope peptide which was identified using the
XX CC method of the invention.
XX SQ Sequence 15 AA;

Query Match          37.2%; Score 29; DB 8; Length 15;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHNDY 9
   |||||
   9 RDHIDY 14

Db

RESULT 44
ADV11512
ID ADV11512 standard; peptide; 15 AA.
XX AC ADV11512;
XX DT 24-FEB-2005 (first entry)
XX DE HPV type 16 E2 protein CD4+ T-cell epitope, SEQ ID NO:81.
XX KM Papillomavirus infection; CD4+ T-cell; T-lymphocyte; E2;
XX KM immune modulation; vaccine; tumor suppressor; infection; virucide.
XX OS Human papillomavirus type 16.
XX PN WO2004105681-A2.
XX PD 09-DEC-2004.
XX PF 23-APR-2004; 2004MO-US012650.
XX PR 28-APR-2003; 2003US-0466235P.
XX PA (INNO-) INNOGENETICS NV.
XX PI Babe LM, De Young LM, Harding FA, Huang MTF, Power SD,
XX PI Stickler M;
XX DR WPI; 2005-021230/02.
XX PT Novel isolated human papillomavirus epitope (HPV) e.g., HPV E6.16 or HPV
XX PT E7.16 epitope, useful for producing medicament for inducing immune
XX PT response against HPV.
XX PS Claim 1; SEQ ID NO 81; 58pp; English.
XX CC The invention relates to isolated human papillomavirus (HPV) epitopes

```


CC multiple sclerosis or a disorder characterized by excessive or undesired
CC MMP-26 activity, for example periodontitis, rheumatoid arthritis or
CC osteoarthritis. The present sequence is that of a CDR peptide which was
CC used during the development of the novel MMP26-binding antibodies of the
CC invention.
XX
SQ Sequence 16 AA;

Query Match 37.2%; Score 29; DB 9; Length 16;
Best Local Similarity 55.6%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DNDYSKNP 13
|:|:|
Db 5 DSSDYFNP 13

RESULT 47
ADU79009
ID ADU79009 standard; peptide; 20 AA.
XX
AC ADU79009;
XX
DT 27-JAN-2005 (first entry)
XX
DE Human peptide fragment, SEQ ID 382.
XX
KW Neuroprotective; Antidepressant; Neuroleptic; Tranquillizer;
KW Antiparkinsonian; Nootropic; Antidiabetic; Anorectic;
KW Cardiovascular-Gen.; Antiartherosclerotic; Antilipemic;
KW Alzheimer's disease; neurological disorder; phosphatase; enzyme.
XX
OS Homo sapiens.
XX
PN US2004226056-A1.
XX
PD 11-NOV-2004.
XX
PF 09-FEB-2004; 2004US-00776013.
XX
PR 22-DEC-1998; 98US-0113534P.
PR 12-MAR-1999; 99US-0124120P.
PR 30-JUN-1999; 99US-0141243P.
PR 21-DEC-1999; 99US-00466139.
PR 17-OCT-2000; 2000US-0240790P.
PR 13-JUL-2001; 2001US-0304775P.
PR 10-SEP-2001; 2001US-00948904.
PR 12-OCT-2001; 2001US-00975072.
PR 15-JUL-2002; 2002US-00194967.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Roch J, Bartel P, Heichman K;
XX
DR MPI; 2004-794772/78.
XX
PT Selecting agents useful for treating Alzheimer's disease comprises
PT contacting focal adhesion kinase 2 with a test agent and measuring a
PT biological activity related to focal adhesion kinase 2 function with or
PT without the test agent.
XX
PS Disclosure; SEQ ID NO 382; 247pp; English.
XX
CC The present invention relates to a method for selecting agents that are
CC potentially useful for the treatment of Alzheimer's disease. The method
CC comprises contacting focal Adhesion Kinase 2 (FAK2) with a test agent and
CC measuring a biological activity related to FAK2 function in the presence
CC and absence of the test agent. The method is useful for screening
CC compounds or agents that can be used to treat neurological disorders,
CC ailments and diseases including mild cognitive impairment, depression,
CC schizophrenia, obsessive-compulsive disorder, bipolar disorder, and
CC neurodegenerative diseases and disorders and motor neuron diseases and
CC disorders such as Alzheimer's disease, Parkinson's disease, dementia with

CC Lewy bodies, amyotrophic lateral sclerosis or Lou Gehrig's disease,
CC Alpers' disease, Leigh's disease, Pelizaeus-Merzbacher disease,
CC Olivopontocerebellar atrophy, Friedreich's ataxia, leukodystrophies, Rett
CC syndrome, Ramsay Hunt syndrome type II, and Down's syndrome, as well as
CC for treating or preventing other diseases such as dislipidemia, diabetes,
CC obesity, cardiovascular diseases such as atherosclerosis and coronary
CC heart disease. Also disclosed is the coding sequence for a novel human
CC phosphatase called PN7740 (ADU78628 and ADU78629). PN7740 contains a
CC protein phosphatase 2C domain, which likely acts to dephosphorylate
CC specific phospho-serine or phospho-threonine residues on particular
CC protein substrates. Although the precise role played by protein
CC phosphatase 2Cs in Alzheimer's disease pathogenesis has yet to be
CC defined, the inventors have discovered that fragments of PN7740 interact
CC with the first phosphorylation binding domain (PTB) domain of Pe65 (also
CC known as ABBA1 (710) or amyloid beta (A4) precursor protein-binding,
CC family B, member 1, isoform B9 (710)), suggesting that PN7740 may well be
CC involved somehow. Pe65 is known to interact with the cytosolic C-terminal
CC region of Amyloid beta (A4) precursor protein (APP) and APP metabolism is
CC critical to the pathogenesis of Alzheimer's disease, because it leads to
CC the release of either toxic Abeta or trophic secreted APP (sAPP)
CC metabolites. The present sequence is a potentially useful agent for
CC Alzheimer's disease.
XX
SQ Sequence 20 AA;

Query Match 37.2%; Score 29; DB 8; Length 20;
Best Local Similarity 50.0%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKNP 13
|:|:|
Db 3 HNDYRNP 10

RESULT 48
ABW02632
ID ABW02632 standard; peptide; 17 AA.
XX
AC ABW02632;
XX
DT 12-FEB-2004 (first entry)
XX
DE Human oestrogen receptor (ER) alpha mutant peptide, ER2.
XX
KW Tamoxifen activated system; TAS; 4-hydroxytamoxifen; OHT; gene therapy;
KW oestrogen receptor; ER; fundamental research; transgenic; biomedical;
KW disease model; breast cancer; human; mutant; mutlein.
XX
OS Homo sapiens.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 16..17
FT /note= "Encoded by GAC"
XX
PN US2003199022-A1.
XX
PD 23-OCT-2003.
XX
PF 11-MAR-2002; 2002US-00095373.
XX
PR 11-MAR-2002; 2002US-00095373.
XX
PA (UNITI) UNITV ILLINOIS FOUNO.
XX
PI Mao C, Shapito DJ;
XX
DR MPI; 2003-852787/79.
XX
DR N-PSDB; AAD64541.
XX
PT New isolated polynucleotide useful for gene therapy applications (e.g. in
PT treating breast cancer), in vivo and in vitro gene expression, in
PT producing bioactive or toxic polypeptides, in research, or in producing

PT transgenic animals.
 XX
 PS Claim 12, SEQ ID NO 12, Opp; English.
 CC The invention relates to tamoxifen activated system (TAS) and 4-
 CC hydroxytamoxifen (OHT) activated system for regulated production of
 CC proteins in eukaryotic cells. TAS includes mutant oestrogen receptors
 CC (BRs) and chimeras thereof. The invention is useful in gene therapy (e.g.
 CC in treating breast cancer) or in vivo and in vitro gene expression, in
 CC producing bioactive, toxic, recombinant polypeptides in mammalian cells,
 CC in biomedical and fundamental research, or in producing transgenic
 CC animals. The transgenic animals may be used as disease models, in
 CC studying the function and/or activity of a polypeptide, or in identifying
 CC and/or evaluating modulators of a polypeptide activity. The present
 CC sequence is human ERalpha mutant peptide used in TAS
 CC
 SQ Sequence 17 AA;
 Query Match 36.5%; Score 28.5; DB 7; Length 17;
 Best Local Similarity 77.8%; Pred. No. 7.5e+02;
 Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;
 QY 1 SIKRDHNDY 9
 Db 10 SIKR-HNDY 17
 RESULT 49
 AAY55315
 ID AAY55315 standard; peptide; 10 AA.
 AC AAY55315;
 XX
 DT 07-JAN-2000 (first entry)
 XX
 DE CD34 antigen antigenic peak peptide SEQ ID NO:209.
 XX
 KM Antibody releasing peptide; CD34; hybridoma; binding; antigen;
 KM cell surface antigen; identification; haematopoietic stem cell; tumour;
 KM cancer; immune system; therapy; displacement.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN US5968753-A.
 XX
 PD 19-OCT-1999.
 XX
 PF 07-JUN-1995; 95US-00482228.
 XX
 PR 14-JUN-1994; 94US-00259427.
 XX
 PA (NEXE-) NEXELT THERAPEUTICS INC.
 XX
 PI Guillermo R. Helgersen SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX
 DR WPI, 1999-590399/50.
 XX
 PT Short peptides useful for displacing antibodies from cell surface
 PT antigens.
 XX
 PS Example 11, Col 38; 81pp; English.
 XX
 CC The present invention describes peptides of 4-17 amino acids which
 CC displace either the anti-CD34 monoclonal antibody designated 561, the
 CC anti-CD34 mouse monoclonal antibody produced by the hybridoma ATCC HB-
 CC 11646 (designated 9063), the anti-CD34 antibody produced by hybridoma
 CC ATCC HB-11885 (9079), or the anti-human breast cancer antibody produced
 CC by hybridoma ATCC HB-11884 (9187), from a cell surface antigen on a
 CC target cell. The peptides are useful for displacing antibodies bound to
 CC cell surfaces to release cells that have been positively selected by
 CC antibody-mediated binding to beads or other solid support. AAY5107 to

CC AAY55319 represent peptides used in the exemplification of the present
 CC invention
 CC
 SQ Sequence 10 AA;
 Query Match 35.3%; Score 28; DB 2; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 4 RDHNDYSK 11
 Db 1 KDHSYSQ 8
 RESULT 50
 AAY87061
 ID AAY87061 standard; peptide; 10 AA.
 XX
 AC AAY87061;
 XX
 DT 09-MAY-2000 (first entry)
 XX
 DE Human haematopoietic CD34+ cell binding peptide SEQ ID #209.
 XX
 KM Human; haematopoietic CD34+ cell; binding peptide; monoclonal antibody;
 KM non-enzymatic cell selection method; haematopoietic stem cell;
 KM haematopoietic progenitor cell; antibody 561; breast cancer cell;
 KM antibody 9187; cell surface determinant; diagnostic cell based assay.
 XX
 OS Homo sapiens.
 OS
 FN US6017719-A.
 XX
 PD 25-JAN-2000.
 XX
 PF 07-JUN-1995; 95US-00482528.
 XX
 PR 14-JUN-1994; 94US-00259427.
 XX
 PA (NEXE-) NEXELT THERAPEUTICS INC.
 XX
 PI Guillermo R. Helgersen SL, Deans RJ, Tseng-Law J, Kobori JA;
 PI Al-Abdaly FA;
 XX
 DR WPI, 2000-136676/12.
 XX
 PT Non-enzymatic method for the positive selection of target cells from a
 PT heterogeneous cell suspension, useful for selecting human breast cancer
 PT cells from a patient's blood or bone marrow.
 XX
 PS Example 11; Col 43; 82pp; English.
 XX
 CC This sequence represents a human haematopoietic CD34+ cell binding
 CC peptide, and was used to test the method of the invention. The method is
 CC a non-enzymatic method for the positive selection of one or more target
 CC cells from a heterogeneous cell suspension, by using specific peptides
 CC which effect the displacement and release of a specific target cell from
 CC a specific monoclonal antibody. The method is useful for positive
 CC selection and specific release of target human haematopoietic
 CC stem/progenitor cells bound by the monoclonal anti-CD34 antibodies and
 CC the antibody 561. The method is also useful for positive selection and
 CC specific release of target human breast cancer cells, bound by the
 CC monoclonal anti-breast cancer antibody 9187, from a patient's blood or
 CC bone marrow. Identification of peptide epitopes for antibodies which
 CC recognize cell surface determinants also allows construction of
 CC diagnostic cell based assays. The peptide mediated release is enzyme free
 CC and thus leaves the cell surface proteins intact. Moreover, peptide
 CC mediated release leaves the target cell free of bound antibody or
 CC antibody fragments. The method also produces a high yield of functional
 CC target cells and is relatively inexpensive to carry out
 CC
 SQ Sequence 10 AA;

Query Match 35.9%; Score 28; DB 3; Length 10;
 Best Local Similarity 50.0%; Pred. No. 4.9e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDYYSK 11
 :|||:
 DB 1 KDHQSYSQ 8

RESULT 51

ABJ36893
 ID ABJ36893 standard; peptide; 11 AA.

AC ABJ36893;
 XX

DT 01-MAY-2003 (first entry)
 XX

DE G protein coupled receptor related peptide SEQ ID NO 247.
 XX

XX Nootropic; cardiast; antiarteriosclerotic; hypotensive; cytoastric;
 KW antibacterial; analgesic; antiallergic; antisthmatic; antiinflammatory;
 KW osteoparactic; neuroprotective; anxiolytic; anorectic; lead compound;
 KW G protein coupled receptor signaling inhibitor; GPCR; library;
 KW high throughput screening assay; stroke; myocardial infarction;
 KW restenosis; atherosclerosis; hypotension; cancer; infection; asthma;
 KW septic shock; pain; allergic disorder; inflammatory bowel disease;
 KW osteoporosis; obesity; psychotic; neurological disorder; anxiety;
 KW schizophrenia; Alzheimer's disease.

OS Unidentified.
 XX

PN WO200272778-A2.
 XX

PD 19-SEP-2002.
 XX

PF 14-MAR-2002; 2002WO-US007561.
 XX

PR 14-MAR-2001; 2001US-0275472P.
 XX

PR 11-MAY-2001; 2001US-00852910.
 XX

PA (CUBB-) CUB BIOTECH.
 XX

PI Gilchrist A, Hamm HE;
 XX

DR WPI; 2003-247841/24.
 XX

PT Identifying G protein coupled receptor (GPCR) signaling inhibitors,
 PT useful in screening drugs for treating stroke, cancers or pain, by
 PT identifying compounds that block GPCR mediated signaling with high
 PT affinity and specificity.
 XX

PS Claim 94; Page 69; 94pp; English.
 XX

XX The invention relates to a novel method for identifying a G protein
 CC coupled receptor (GPCR) signaling inhibitor. The novel method comprises
 CC selecting or identifying a member of a library of peptides and/or
 CC candidate compounds, having binding to a GPCR of higher affinity than
 CC that of the native peptide. The peptide library is based on a native GPCR
 CC binding peptide. The method is useful for identifying inhibitors of a G
 CC protein coupled receptor (GPCR) signaling. The method is particularly
 CC useful for identifying drugs that antagonise the binding between a GPCR
 CC and its extracellular ligand(s). The method is especially useful in
 CC modern high throughput screening assays for identifying potent lead
 CC compounds. The compounds, peptides or inhibitors identified by the method
 CC are useful for preventing, ameliorating or treating diseases in which
 CC GPCR signaling is a causative factor or in which a specific class of G
 CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
 CC atherosclerosis, hypotension, cancers, infections, septic shock, pain,
 CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
 CC obesity, or psychotic and neurological disorders (e.g. anxiety, schizophrenia or Alzheimer's disease). This sequence represents a peptide
 CC relating to the G protein coupled receptors of the invention
 XX

SQ Sequence 11 AA;

Query Match 35.9%; Score 28; DB 6; Length 11;
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRDNDY 9
 :|||:
 DB 1 LQRDHYEY 8

RESULT 52

ADT51321
 ID ADT51321 standard; peptide; 11 AA.

AC ADT51321;
 XX

DT 13-JAN-2005 (first entry)
 XX

DE G protein coupled receptor signalling modifying peptide #222.
 XX

XX cerebroprotective; vasotropic; cardiast; antiarteriosclerotic;
 KW hypotensive; cytoastric; antibacterial; fungicide; virucide; analgesic;
 KW antiallergic; antisthmatic; antiinflammatory; antiparkinsonian;
 KW neuroprotective; nootropic; gene therapy; G protein coupled receptor;
 KW GPC.
 XX

OS Synthetic.
 XX

PN WO2004092199-A2.
 XX

PD 28-OCT-2004.
 XX

PF 12-APR-2004; 2004WO-US011167.
 XX

PR 11-APR-2003; 2003US-00411336.
 XX

PA (CUBB-) CUB BIOTECH INC.
 XX

PI Gilchrist A, Hamm HM;
 XX

DR WPI; 2004-766826/75.
 XX

PT Identifying modulators of G protein coupled receptor (GPCR) signaling,
 PT useful for treating diseases associated with altered GPCR signaling (e.g.
 PT stroke), comprises screening a peptide library for high affinity binding
 PT to the GPCR.
 XX

PS Disclosure; SEQ ID NO 247; 264pp; English.
 XX

XX The invention relates to a method of identifying a G protein coupled
 CC receptor (GPCR) signaling modifying peptide by providing a peptide
 CC library based on a native GPCR binding peptide, screening the peptide
 CC library for high affinity binding to the GPCR, and selecting a member of
 CC the peptide library having binding to the GPCR of higher affinity than
 CC that of the native peptide. The composition and methods are useful for
 CC identifying modulators of GPCR signaling, for modulating the activity of
 CC GPCR or for drug designing. These may be used for diagnosing, preventing
 CC or treating diseases associated with altered GPCR signaling, such as
 CC stroke, myocardial infarction, atherosclerosis, hypertension, cancer,
 CC infections (e.g. bacterial, fungal or viral), pain, allergies, asthma,
 CC inflammation, Parkinson's disease and Alzheimer's disease. This sequence
 CC corresponds to a peptide of the invention.
 XX

SQ Sequence 11 AA;

Query Match 35.9%; Score 28; DB 8; Length 11;
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IRDNDY 9
 :|||:
 DB 1 LQRDHYEY 8

RESULT 53
 AAB39702
 ID AAB39702 standard; peptide; 12 AA.
 XX
 AC AAB39702;
 XX
 DT 05-FEB-2001 (first entry)
 XX
 DE Anti-IL12 antibody L chain CDR3 related amino acid sequence SEQ ID 218.
 XX
 KM Human; neutralizing antibody; interleukin-12; IL-12; antiinflammatory;
 KM complementarity determining region; CDR; antirheumatic; antiarthritic;
 KM antileukemic; neuroprotective; antiparasitic; antiaesthetic; cardiant;
 KM antiparasitic; antibacterial; immunosuppressive; Crohn's disease;
 KM multiple sclerosis; rheumatoid arthritis.
 XX
 OS Homo sapiens.
 XX
 PN WO200056772-A1.
 XX
 PD 28-SEP-2000.
 XX
 PF 24-MAR-2000; 2000WO-US007946.
 XX
 PR 25-MAR-1999; 99US-0126603P.
 XX
 PA (BADI) BASP AG.
 PA (GEMV) GENERICS INST INC.
 XX
 PI Salfield JG, Roguska M, Paekind M, Banerjee S, Tracey DE, White M;
 PI Kaymakalan Z, Labrovsky B, Sakorafas P, Friedrich S, Myles A;
 PI Veldman GM, Venturini A, Warne NW, Widom A, Elvin JG, Duncan AR;
 PI Derbyshire EJ, Carmen S, Smith S, Holter TL, Du Fou SL;
 XX
 DR WPI; 2000-638250/61.
 XX
 PT New human antibody specific for human interleukin-12 (IL-12) used to
 PT treat disorders characterized by aberrant IL-12 expression e.g. Crohn's
 PT disease and multiple sclerosis.
 XX
 PS Example 1; Page 129; 377p; English.
 XX
 CC This invention relates to a new human antibody specific for human
 CC interleukin-12 (IL-12). The invention also includes antigen binding
 CC portions that bind to IL-12. Sequences AAB39485-B39516 represent human
 CC anti-IL-12 antibody heavy and light chain complementarity determining
 CC region (CDR) amino acid sequences, and also includes variable region
 CC amino acid sequences. Other variable region amino acid sequences are
 CC given in AAB39517-B39560 and AAB40068-B40149. Sequences AAB39561-B39771
 CC represent anti-IL-12 CDR3 related amino acid sequences, AAB39772-B40063
 CC represent other CDR sequences. Light chain CDR3 consensus sequences are
 CC given in AAB40064-B40067. Primers used in the identification and
 CC construction of the antibodies of the invention are given in AAC61062-
 CC C61071. The antibody of the invention is a neutralizing antibody and has
 CC antirheumatic; antiarthritic; antileukemic; antinflammatory;
 CC neuroprotective; antiparasitic; antiaesthetic; cardiant; antiparasitic;
 CC antibacterial and immunosuppressive activity. The antibodies or antigen-
 CC binding fragments are useful in the treatment of disorders associated
 CC with detrimental release of human IL-12, especially Crohn's disease,
 CC multiple sclerosis and rheumatoid arthritis. They can also be used in the
 CC manufacture of a pharmaceutical composition to treat human IL-12
 CC disorders
 XX
 SQ Sequence 12 AA;
 XX
 QY Query Match 35.9%; Score 28; DB 3; Length 12;
 Best Local Similarity 50.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 SIKRDHNDYS 10
 | | | | |

DB 2 SYDRGHNNPS 11
 RESULT 54
 ADF53455
 ID ADF53455 standard; peptide; 14 AA.
 XX
 AC ADF53455;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE MCP6 603 antibody CDR2 mutant peptide amino acid sequence 16.
 XX
 KM walk-through mutagenesis; prototype amino acid; prototype nucleotide;
 KM mutant polypeptide production; MCP6 603;
 KM complementarity determining region; CDR; heavy chain; CDR2; mutant;
 KM muten.
 XX
 OS Unidentified.
 OS Synthetic.
 XX
 PN WO2003089671-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 16-APR-2003; 2003WO-US011935.
 XX
 PR 17-APR-2002; 2002US-0373686P.
 XX
 PA (CREA/) CREA R.
 PA (CAPP/) CAPPUCCILLI G.
 XX
 PI Crea R, Cappuccilli G;
 XX
 DR WPI; 2003-854132/79.
 XX
 PT Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
 PT for producing mutant polypeptides comprising synthesizing oligonucleotides
 PT comprising a nucleotide sequence for each target region of a prototype
 PT amino acid.
 XX
 PS Example; Fig 6; 40pp; English.
 XX
 CC This invention relates to a novel method of walk-through mutagenesis of a
 CC nucleic acid encoding a polypeptide which comprises synthesizing a
 CC mixture of oligonucleotides comprising a nucleotide sequence for each
 CC target region of a prototype amino acid, where each oligonucleotide
 CC contains at each sequence position in the target region, a prototype
 CC nucleotide for synthesis of the prototype amino acid, or a predetermined
 CC acid. The method is useful in producing mutant polypeptides in which the
 CC overall presence of the predetermined amino acid is limited to one or two
 CC positions per mutated polypeptide, leaving the remaining amino acids in
 CC the targeted region intact or as close as possible to the prototype
 CC sequence. The invention was exemplified using the three complementarity
 CC determining regions (CDRs) of the heavy chain of the monoclonal antibody
 CC MCP6 603.
 XX
 SQ Sequence 14 AA;
 XX
 QY Query Match 35.9%; Score 28; DB 7; Length 14;
 Best Local Similarity 57.1%; Pred. No. 7.3e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 5 DHNDYSK 11
 | | | | |
 DB 7 DHDSDHK 13
 | | | | |
 RESULT 55
 ADU00097
 ID ADU00097 standard; peptide; 14 AA.
 XX

```

AC ADU00097;
XX
XX 13-JAN-2005 (first entry)
XX
XX Amino acid sequence of the Chk2 phosphorylation site of Cdc25A.
XX
XX Chk2; E2F-1; DNA damage; DNA damage signalling pathway;
XX checkpoint control; tumour suppressor; drug discovery; checkpoint kinase;
XX Cdc25A.
XX
XX Unidentified.
XX
XX WO2004092738-A2.
XX
XX 28-OCT-2004.
XX
XX
XX 15-APR-2004; 2004WO-GB001631.
XX
XX 15-APR-2003; 2003GB-00008711.
XX
XX (UNITU ) UNITV GLASGOW.
XX
XX La Thangue NB, Stevens C;
XX
XX WPI; 2004-758394/74.
XX
XX
XX Determining the activity of a Chk2 polypeptide, useful in drug discovery
XX industry, comprises contacting a Chk2 polypeptide and an E2F-1
XX polypeptide comprising residue Ser 364 and determining whether Ser 364
XX has been phosphorylated.
XX
XX Example; Fig 2b; 41pp; English.
XX
XX The specification describes a method for determining the activity of
XX checkpoint kinase Chk2. The method comprises contacting a Chk2
XX polypeptide and an E2F-1 polypeptide comprising residue Ser 364 under
XX conditions in which Chk2 is able to phosphorylate the E2F-1 polypeptide,
XX and determining whether the Ser 364 residue of E2F-1 polypeptide has been
XX phosphorylated. Chk2 functions as a key effector of E2F-1 induction
XX during DNA damage. The regulation of E2F-1 activity through the DNA
XX damage signalling pathway and specifically by Chk2 implies a role for E2F
XX -1 in checkpoint control. Such a role for E2F-1 may contribute to the
XX tumour suppressor activity of E2F-1. Antibodies which bind preferentially
XX to the phosphorylated form of E2F-1 protein are useful for prognosing
XX or determining whether Ser 364 of E2F-1 in samples obtained from patients
XX is in a phosphorylated or unphosphorylated form, thus useful for
XX determining appropriate treatments for patients. The method is useful in
XX the drug discovery industry. ADU00097-ADU00102 represent Chk2
XX phosphorylation sites, which were compared to derive a consensus
XX
XX
XX Sequence 14 AA;
XX
XX Query Match 35.9%; Score 28; DB 8; Length 14;
XX Best Local Similarity 50.0%; Pred. No. 7.3e+02;
XX Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 1 SIKRDND 8
XX :|||:|
XX 2 ALKSHSD 9
XX
XX
XX
XX RESULT 56
XX AAW95137
XX ID AAW95137 standard; peptide; 15 AA.
XX
XX AC AAW95137;
XX
XX
XX 17-OCT-2003 (revised)
XX 27-AUG-2003 (revised)
XX 24-MAY-1999 (first entry)
XX
XX Peptide X8 expressed by a modified bacteriophage library.
XX

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XX
XX Modified phage library; screening; cell-surface associated protein;
XX therapeutic; diagnostic; disease; ligand; drug; toxin; fractionation;
XX noise elimination; bacteriophage.
XX
XX Enterobacteria phage M13.
XX
XX WO9906542-A1.
XX
XX 11-FEB-1999.
XX
XX 29-JUL-1998; 98WO-GB002269.
XX
XX 30-JUL-1997; 97GB-00016094.
XX
XX (UNITU ) UNITV GLASGOW.
XX
XX Allen JM, Lavery B;
XX
XX WPI; 1999-153772/13.
XX
XX
XX Modified phage display library depleted in phage that react with native
XX cellular proteins - provides reduced noise and higher signal-to-noise
XX ratio when screened against cells transfected to express a specific
XX heterologous protein, used to identify potential therapeutic and
XX diagnostic agents.
XX
XX Example 1; Page 29; 49pp; English.
XX
XX The invention relates to a modified phage library for use with a selected
XX strain of cells that have been transformed to express a heterologous
XX protein (I) in a screening procedure, to detect specific binding between
XX individual phage and a recognition site on the heterologous protein. The
XX modified library is produced as follows. The initial phage library is
XX fractionated by contact with strain of cells that do not express (I) to
XX bind any phage that bind to cellular proteins other than the (I). Bound
XX and unbound phages are separated to produce the modified library,
XX depleted in components that bind proteins other than (I). The library is
XX used to identify phage that bind to cell-surface associated (I)
XX specifically receptors. Peptides identified by screening with the
XX modified library are potentially useful as therapeutic and diagnostic
XX agents, for diseases involving (I) or its ligands (including as carriers
XX for delivering drugs, toxins or antibodies to cells), and their amino
XX acid sequences can be used to design other agents for the same uses. The
XX initial fractionation eliminates much of the noise caused by binding to
XX other cell-surface proteins, and the use of transfected cells for
XX screening (these express a far greater number of (I) than wild-type
XX cells) improves the signal-to-noise ratio. The number of rounds of
XX screening may thus be reduced. (Updated on 27-AUG-2003 to correct OS
XX field.) (Updated on 17-OCT-2003 to standardise OS field)
XX
XX
XX Sequence 15 AA;
XX
XX Query Match 35.9%; Score 28; DB 2; Length 15;
XX Best Local Similarity 50.0%; Pred. No. 7.9e+02;
XX Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 5 DHDNYSKPM 14
XX |||||
XX 6 DHDNDQPIPL 15
XX
XX
XX
XX RESULT 57
XX ADH62398
XX ID ADH62398 standard; peptide; 15 AA.
XX
XX AC ADH62398;
XX
XX
XX 25-MAR-2004 (first entry)
XX
XX Arabidopsis thaliana EDS1 peptide.
XX
XX PAD4; resistance; microbial disease; crop improvement; ornamental;
XX

```


KM Gene therapy; plant protectant; mouse-ear crass; enzyme; mouse-ear crass.
XX
XX Arabidopsis thaliana.
XX
XX US620985-B1.
XX
XX 16-SEP-2003.
XX
XX
XX 04-NOV-1999; 99US-00434840.
XX
XX 12-NOV-1998; 98US-0183020P.
XX
XX (UYMA-) UNIV MARYLAND BIOTECHNOLOGY INST.
XX (PLAN-) PLANT BIOSCIENCE LTD.
XX
XX Glazebrook J, Jirage D, Tootle TL, Zhou N, Feys BJF;
XX WPI; 2003-895430/82.
XX
XX New PAD4 proteins and nucleic acids from Arabidopsis, useful for
PT enhancing the resistance of a plant to disease such as those caused by
PT virus, bacteria, fungi, oomycetes, nematodes or insects.
XX
XX Example 3; SEQ ID NO 81; 105bp; English.
XX
XX The present invention provides PAD4 compositions and methods for using
CC PAD4 compositions for enhancing disease resistance of a plant. The
CC invention is useful for enhancing the resistance of a plant to disease
CC such as those caused by virus, bacteria, fungi, oomycetes, nematodes and
CC insects. The invention is also useful in producing plants having enhanced
CC disease resistance and in-plant protection against diseases which
CC consequently reduces or minimizes the need for traditional chemical
CC practices, increases production efficiency, improves crop and ornamental
CC quality. The invention is also useful in gene therapy. The present
CC sequence is Arabidopsis thaliana Eds1 peptide.
XX
XX Sequence 15 AA;
SQ
Query Match 35.9%; Score 28; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.9e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 4 RDNDYSK 11
DB 8 RDHHSYEE 15
RESULT 58
ADU15281
ID ADU15281 standard; peptide; 16 AA.
XX
XX ADU15281;
AC
XX
XX 27-JAN-2005 (first entry)
DT
XX Clostridium difficile-specific human antibody CDR-H3 peptide - SEQ ID 27.
DE
XX
XX vaccine; antibody; antigen binding fragment; infection; CDR-H3.
XX
XX Homo sapiens.
OS
XX
XX WO2004094474-A1.
XX
XX 04-NOV-2004.
XX
XX 14-APR-2004; 2004WO-GB001619.
XX
XX 17-APR-2003; 2003GB-00009126.
XX
XX (NEUT-) NEUTEC PHARMA PLC.
XX
XX Burnle JP, Matthews RC;
XX
XX

DR WPI; 2004-795532/78.
XX
XX New Clostridium difficile focused antibodies for diagnosing, preventing
PT or treating infections caused by C. difficile, comprises the
PT complementarity determining region (CDR)-H3 and/or CDR-L3 sequences.
XX
XX Claim 1; SEQ ID NO 27; 91pp; English.
XX
XX The invention comprises antibodies/antigen binding fragments that target
CC Clostridium difficile. The antibodies and antigen binding fragments of
CC the invention are useful for diagnosing, preventing (vaccine), and
CC treating infections caused by Clostridium difficile. The present amino
CC acid sequence represents a Clostridium difficile-specific human antibody
CC CDR-H3 peptide of the invention.
XX
XX Sequence 16 AA;
SQ
Query Match 35.9%; Score 28; DB 8; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 DHNDYS 10
DB 6 DHHDPS 11
RESULT 59
ADU15291
ID ADU15291 standard; peptide; 16 AA.
XX
XX ADU15291;
AC
XX
XX 27-JAN-2005 (first entry)
DT
XX
XX Clostridium difficile-specific human antibody VH CDR3 peptide SEQ ID 37.
DE
XX
XX vaccine; antibody; antigen binding fragment; infection; VH CDR3.
XX
XX Homo sapiens.
OS
XX
XX WO2004094474-A1.
XX
XX 04-NOV-2004.
XX
XX 14-APR-2004; 2004WO-GB001619.
XX
XX 17-APR-2003; 2003GB-00009126.
XX
XX (NEUT-) NEUTEC PHARMA PLC.
XX
XX Burnle JP, Matthews RC;
XX
XX WPI; 2004-795532/78.
XX
XX New Clostridium difficile focused antibodies for diagnosing, preventing
PT or treating infections caused by C. difficile, comprises the
PT complementarity determining region (CDR)-H3 and/or CDR-L3 sequences.
XX
XX Disclosure; SEQ ID NO 37; 91pp; English.
XX
XX The invention comprises antibodies/antigen binding fragments that target
CC Clostridium difficile. The antibodies and antigen binding fragments of
CC the invention are useful for diagnosing, preventing (vaccine), and
CC treating infections caused by Clostridium difficile. The present amino
CC acid sequence represents a Clostridium difficile-specific human antibody
CC VH CDR3 peptide of the invention.
XX
XX Sequence 16 AA;
SQ
Query Match 35.9%; Score 28; DB 8; Length 16;
Best Local Similarity 66.7%; Pred. No. 8.5e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 DHNDYS 10
DB 6 DHHDPS 11

FT	Modified-site	2	/note= "this residue must be present, and is optionally sulphated"
FT	Modified-site	6	/note= "this residue must be present, and is optionally sulphated"
PT			
PT			
PT			
XX	WO2004072096-A2.		
PV			
PD	26-AUG-2004.		
XX			
XX	06-FEB-2004; 2004MO-US003467.		
PF			
PR	10-FEB-2003; 2003US-0445853P.		
XX			
XX	(BGHM) BRIGHAM & WOMENS HOSPITAL.		
PA			
PI	Farzan MR, Dorfman TK;		
DR	WPI; 2004-616038/59.		
XX			
PT	New peptides that bind gp120 of HIV-1, useful for blocking the entry of HIV-1 into cells, for studying or treating AIDS, or for developing new approaches to control HIV infection.		
PT			
XX	Claim 1; SEQ ID NO 2; 27pp; English.		
CC	ADRA5756-ADRA5761 represent peptides which bind to gp120 of human immunodeficiency virus type 1 (HIV-1). The peptides are derived from the region of anti-HIV-1 antibodies which bind to gp120. This region has sulphared tyrosines, which must be present in the present peptides. The affinity of the peptides for gp120 on the HIV-1 viral surface may be increased by sulphating tyrosine residues. The peptides are useful for preventing the binding of gp120 to CCR5 receptors on the surface of immune cells, thus blocking the entry of HIV-1 into cells. They may be used for studying or treating AIDS and for developing new approaches to control HIV infection.		
CC			
XX	Sequence 18 AA;		
SQ			
Query Match	35.9%; Score 28; DB 8; Length 18;		
Best Local Similarity	66.7%; Pred. No. 9.8e+02;		
Matches	4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;		
OY	5 DANDYS 10		
: : :			
Db	5 DYNDYA 10		
RESULT 63			
AEA89657			
ID	AEA89657 standard; peptide; 19 AA.		
XX			
AC	AEA89657;		
XX			
DT	25-AUG-2005 (first entry)		
XX			
DE	Tumor metastases treatment-related protein region #45.		
XX			
KM	metastasis; therapeutic; gene expression; cytostatic; tumor;		
KM	breast tumor; sarcoma; nervous system tumor; prostate tumor;		
KM	pancreas tumor; colon tumor; rectal tumor; medulloblastoma;		
KV	b-cell lymphoma; c-cell lymphoma; multiple myeloma; lung tumor; cancer.		
OS	Unidentified.		
XX			
PN	WO2005056043-A2.		
XX			
PD	23-JUN-2005.		
XX			
PP	10-DEC-2004; 2004WO-IT000689.		
XX			
PK	11-DEC-2003; 2003IT-RM000572.		

XX	(ZOLLI/) ZOLLO M.
PA	
XX	Zollo M,
PI	
XX	WPI, 2005-445065/45.
DR	
XX	
PT	Use of inhibitors of human-PRUNE cyclic nucleotide phosphodiesterase for
PT	preparation of medicament in the treatment of tumor metastases associated
PT	with overexpression of human-PRUNE.
XX	
PS	Example 1; Fig 1; 89pp; English.
XX	
CC	This invention relates to a novel method for preparing a medicament for
CC	the treatment of tumor metastases associated with overexpression of human
CC	-PRUNE. The method comprises using inhibitors of human-PRUNE cyclic
CC	nucleotide phosphodiesterase. The invention may be useful for the
CC	development of compounds with a cytostatic activity acting as human-PRUNE
CC	overexpression inhibitors. The invention is useful for preparation of
CC	medicaments in the treatment of tumor metastases, for example breast
CC	carcinoma, sarcoma, neuroblastoma, prostate tumor, pancreatic tumor,
CC	colonic tumor, rectal tumor, medulloblastoma, epithelioma, epatocarcinoma,
CC	cell T or cell B lymphomas, myeloma and melanoma and pulmonary tumor. As
CC	the h-PRUNE poses cyclic nucleotide phosphodiesterase activity with
CC	preferential activity for camp over cGMP, the h-PRUNE overexpression can
CC	be effectively suppressed by certain PDE inhibitors thus the PDE
CC	inhibitor provides an effective alternative therapy for cancer treatment.
CC	The present sequence is that of a protein motif which was used during the
CC	development of the novel method of the invention.
XX	
SQ	Sequence 19 AA;
XX	
Query Match	35.9%; Score 28; DB 9; Length 19;
Best Local Similarity	36.4%; Pred. No. 1e+03;
Matches	4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy	2 IKRDNDYSKN 12
Db	5 ILTDHNEFOGS 15
XX	
RESULT 64	
ARI5556	
ID	ARI5556 standard; protein; 20 AA.
XX	
AC	ARI5556;
XX	
DT	02-MAR-1992 (first entry)
XX	
DB	Immunopeptide #7 derived from HPV16 E2 peptide.
XX	
KW	cervical cancer; cervical intraepithelial neoplasia; CIN; wart;
XX	squamous cell carcinoma; ELISA; HPV 16.
XX	
OS	Synthetic.
XX	
PN	WO9118294-A.
XX	
PD	28-NOV-1991.
XX	
PF	11-MAY-1990; 90SE-00001705.
XX	
PR	11-MAY-1990; 90SE-00001705.
XX	
PA	(MEDS-) MEDSCAND AB.
XX	
PI	Dillner J, Dillner L, Cheng HW;
XX	
DR	WPI; 1991-369390/50.
XX	
PT	Diagnosis of human papilloma virus infection and PV-carrying tumours -
PT	using synthetic peptide(s) to detect virus specific antigen-antibody
PT	complexes by immunoassay.

XX Disclosure; Page 38; 72pp; English.
 PS
 XX
 CC This is one of a large number of peptides which have been synthesised on
 CC the basis of the amino acid sequences for the E2, E4, E7, L1 or L2
 CC proteins of HPV 1, 5, 6, 8, 11, 16, 18, 31 and 33. The selection of
 CC peptide sequences was based on the assumption that an immunoreactive
 CC region might be situated in the same relative region of a protein from
 CC different HPV types. The peptides were used in diagnostic immunoassays to
 CC detect HPV-infection. See AAR15523-R15601
 CC
 SQ Sequence 20 AA;
 QY
 DB 3 KRDNDSKN 12
 7 KDDAEKYSKN 16
 RESULT 65
 AAR45558
 ID AAR45558 standard; protein; 20 AA.
 XX
 AC AAR45558;
 XX
 DT 25-MAR-2003 (revised)
 DT 13-JUL-1994 (first entry)
 XX
 DE Cry j I pollen allergen peptide CJI-17.
 XX
 KM Japanese cedar; detection; allergy; treatment; diagnosis; T cell epitope;
 KM sensitivity.
 OS Crypomeria japonica.
 XX
 PN WO9401560-A1.
 PD 20-JAN-1994.
 XX
 PF 15-JAN-1993; 93WO-US000139.
 XX
 PR 10-JUL-1992; 92WO-US005661.
 PR 01-SEP-1992; 92US-00938990.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Griffith ID, Pollock J, Bond JF, Garman RD, Kuo M;
 XX
 DR WPI, 1994-035066/04.
 XX
 PT Antigens derived from Japanese cedar pollen allergen Cry j I - contain at
 PT least two T cell epitope(s), used to treat or diagnose allergy.
 XX
 PS Claim 1; Fig 13; 137pp; English.
 XX
 CC The sequence is that of an isolated peptide of the Japanese cedar pollen
 CC allergen Cry j I (amino acids 161-180). The peptide, CJI-17, can be used
 CC for the treatment and diagnosis of allergies associated with Japanese
 CC cedar pollen. It has enhanced therapeutic properties but reduced side
 CC effects compared to naturally occurring allergens. (Updated on 25-MAR-
 CC 2003 to correct PN field.)
 CC
 SQ Sequence 20 AA;
 QY
 DB Query Match 35.9%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 DHNDYSKN 12
 ||| : | :

DB 4 DHNSFSNS 11
 RESULT 66
 AAR82507
 ID AAR82507 standard; protein; 20 AA.
 XX
 AC AAR82507;
 XX
 DT 27-AUG-2003 (revised)
 DT 15-APR-1996 (first entry)
 XX
 DE Cry j I Japanese Cedar pollen allergen peptide fragment (CJI-17).
 XX
 KM Cry j I; Japanese cedar pollen allergen; modified; drug production;
 KM allergy; Crypomeria japonica.
 XX
 OS Crypomeria japonica.
 XX
 PN WO9527786-A1.
 PD 19-OCT-1995.
 XX
 PF 06-APR-1995; 95WO-US004249.
 XX
 PR 08-APR-1994; 94US-00226248.
 PR 06-DEC-1994; 94US-00350225.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 PI Franzen HM, Powers SP, Kuo M, Evans S, Shaked Z, Chen X;
 XX
 DR WPI, 1995-366391/47.
 XX
 PT Modified Crypomeria japonica (Cry j) I peptide(s) - useful for treating
 PT allergy to Japanese cedar pollen allergen or immunologically cross
 PT reactive allergens.
 XX
 PS Disclosure; Fig 2; 60pp; English.
 XX
 CC Novel peptides of cry j I have been modified as a part of a
 CC preformulation scheme to develop an optimised drug product for
 CC therapeutic treatment of humans suffering from allergy to Japanese cedar
 CC pollen allergen or an allergen which is immunologically cross reactive
 CC with Japanese cedar pollen allergen. Such modified peptides possess
 CC certain characteristics which render them particularly suitable for drug
 CC product formulation. Peptide fragments of Cry j I, modified and
 CC unmodified, are given in AAR82491-R82525. This peptide fragment
 CC corresponds to amino acids 161-180 of the allergen mature protein.
 CC (Updated on 27-AUG-2003 to correct OS field.)
 CC
 SQ Sequence 20 AA;
 QY
 DB Query Match 35.9%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 DHNDYSKN 12
 ||| : | :
 DB 4 DHNSFSNS 11
 RESULT 67
 ADD93865
 ID ADD93865 standard; peptide; 20 AA.
 XX
 AC ADD93865;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Japanese cedar pollen allergen Cry j I peptide, SEQ ID NO:17.
 XX
 KM Japanese cedar; pollen allergen; Cry j I; dog; Canis familiaris;

KM allergic dermatitis; veterinary; DNA vaccine; dermatological;
 KM antiinflammatory; vaccine; gene therapy.
 OS Cryptomeria japonica.
 XX JP2003116556-A.
 XX
 PD 22-Apr-2003.
 XX
 XX 09-Oct-2001, 2001JP-00311433.
 XX
 XX 09-Oct-2001; 2001JP-00311433.
 XX
 XX (NIPZ) NIPPON ZENYAKU KOGYO KK.
 PA WPI; 2003-771273/73.
 DR
 XX
 PT New cedar pollinosis antigen T-cell epitope in a dog useful for preparing
 PT a DNA vaccine that can be used to prevent allergic dermatitis.
 XX
 PS Example 7; SEQ ID NO 17; 20pp; Japanese.
 CC The invention relates to T-cell epitopes of the Japanese cedar
 CC (Cryptomeria japonica) pollen allergen Cry j 1 which stimulate an immune
 CC response in dogs. The invention also encompasses DNA encoding the Cry j 1
 CC T-cell epitopes, a vector comprising a Cry j 1 T-cell epitope-encoding
 CC DNA, and DNA vaccine containing a vector of the invention for the
 CC treatment of allergic dermatitis. The Cry j 1 T-cell epitopes and their
 CC encoding nucleic acids are useful in the preparation of vaccines,
 CC especially DNA vaccines, for the treatment of allergic dermatitis in
 CC dogs. The DNA vaccine of the invention can be prepared inexpensively with
 CC easier manufacturing and purification processes. The present sequence
 CC represents a Cry j 1 peptide used in an example of the invention.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 35.9%; Score 28; DB 7; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 DHNDYSKN 12
 ||| :| :
 Db 4 DHNSFSNS 11
 RESULT 68
 AEB24275
 ID AEB24275 standard; peptide; 20 AA.
 XX
 AC AEB24275;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Japanese cedar pollen allergen T-cell epitope, SEQ ID 203.
 XX
 KW pollen; allergen; transformation; antiallergic; pollinosis.
 XX
 OS Cryptomeria japonica.
 OS
 PN US2005152927-A1.
 XX
 PD 14-JUL-2005.
 XX
 XX 30-AUG-2004; 2004US-00931260.
 XX
 PR 12-JUL-1991; 91US-00729134.
 PR 15-JUL-1991; 91US-00730452.
 PR 01-SEP-1992; 92US-00938990.
 PR 12-NOV-1992; 92US-00975179.
 PR 15-JAN-1993; 93WO-US000139.
 PR 08-APR-1994; 94US-00226248.
 PR 29-JAN-1999; 99US-00240203.
 XX

PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 XX Griffith J, Pollock J, Bond JF, Garman RD, Kuo M, Powers SP;
 PI Exley MA, Chen X, Shaked Z;
 XX
 DR WPI; 2005-496786/50.
 XX
 XX
 PT New Japanese cedar pollen allergen produced in a host cell, useful in
 PT preparing a composition for diagnosing, treating or preventing Japanese
 PT cedar pollinosis.
 XX
 PS Disclosure; SEQ ID NO 203; 189pp; English.
 XX
 CC The invention relates to a novel isolated Japanese cedar pollen allergen.
 CC The allergen is produced in a host cell transformed with a nucleic acid,
 CC comprising any of the fully defined sequences having 1337 or 1726 bp
 CC (AEB24081 or AEB24213). The invention further comprises: an isolated
 CC peptide of a Japanese cedar pollen allergen, comprising any of the fully
 CC defined sequences having 374 or 514 amino acids (AEB24082 or AEB24214),
 CC where the peptide has at least one epitope of the pollen allergen, and
 CC where the epitope does not consist of amino acid residues 1-20 or 325-340
 CC of the 374-amino acid sequence. The isolated Japanese cedar pollen
 CC allergen has an antiallergic activity as it is useful in preparing a
 CC composition for diagnosing, treating or preventing Japanese cedar
 CC pollinosis. This sequence represents a Japanese cedar pollen allergen
 CC epitope polypeptide of the invention.
 XX
 XX Sequence 20 AA;
 SQ
 Query Match 35.9%; Score 28; DB 9; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.1e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 5 DHNDYSKN 12
 ||| :| :
 Db 10 DHNSFSNS 17
 RESULT 69
 AEB24122
 ID AEB24122 standard; peptide; 20 AA.
 XX
 AC AEB24122;
 XX
 DT 22-SEP-2005 (first entry)
 XX
 DE Japanese cedar pollen allergen T-cell epitope, SEQ ID 42.
 XX
 KW pollen; allergen; transformation; antiallergic; pollinosis.
 XX
 OS Cryptomeria japonica.
 OS
 PN US2005152927-A1.
 XX
 PD 14-JUL-2005.
 XX
 XX 30-AUG-2004; 2004US-00931260.
 XX
 PR 12-JUL-1991; 91US-00729134.
 PR 15-JUL-1991; 91US-00730452.
 PR 01-SEP-1992; 92US-00938990.
 PR 12-NOV-1992; 92US-00975179.
 PR 15-JAN-1993; 93WO-US000139.
 PR 08-APR-1994; 94US-00226248.
 PR 29-JAN-1999; 99US-00240203.
 XX
 PA (IMMU-) IMMUNOLOGIC PHARM CORP.
 XX
 XX Griffith J, Pollock J, Bond JF, Garman RD, Kuo M, Powers SP;
 PI Exley MA, Chen X, Shaked Z;
 XX
 DR WPI; 2005-496786/50.
 XX

PT New Japanese cedar pollen allergen produced in a host cell, useful in
PT preparing a composition for diagnosing, treating or preventing Japanese
PT cedar pollinosis.
XX
PS Example 6; SEQ ID NO 42; 189pp; English.
CC The invention relates to a novel isolated Japanese cedar pollen allergen.
CC The allergen is produced in a host cell transformed with a nucleic acid,
CC comprising any of the fully defined sequences having 1337 or 1726 bp
CC (AEB24081 or AEB24213). The invention further comprises: an isolated
CC peptide of a Japanese cedar pollen allergen, comprising any of the fully
CC defined sequences having 374 or 514 amino acids (AEB24082 or AEB24214),
CC where the peptide has at least one epitope of the pollen allergen, and
CC where the epitope does not consist of amino acid residues 1-20 or 325-340
CC of the 374-amino acid sequence. The isolated Japanese cedar pollen
CC allergen has an anti-allergic activity as it is useful in preparing a
CC composition for diagnosing, treating or preventing Japanese cedar
CC pollinosis. This sequence represents a Japanese cedar pollen allergen
CC epitope polypeptide of the invention.
XX
SQ Sequence 20 AA;
Query Match 35.3%; Score 28; DB 9; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 5 DHDVYSKN 12
DB 4 DHNSPSSNS 11
RESULT 70
ID ADR84038
ID ADR84038 standard; peptide; 19 AA.
XX ADR84038;
XX
DT 02-DEC-2004 (first entry)
XX
DE S. pyogenes hyperimmune system reactive antigen SPA1316.1.
XX
KM hyperimmune serum reactive antigen; vaccine; anticaline.
XX
OS Streptococcus pyogenes.
XX
PN MO2004078907-AA.
XX
PD 16-SEP-2004.
XX
PF 02-MAR-2004; 2004MO-EP002087.
XX
PR 04-MAR-2003; 2003EP-00450061.
XX
PA (INTE-) INTERCELL AG.
XX
PI Meinke A, Nagy E, Winkler B, Gelbmann D;
XX
DR WPI; 2004-653698/63.
XX
PT New isolated nucleic acid molecules encoding hyperimmune serum-reactive
PT antigens from Streptococcus pyogenes, useful for diagnosing, preventing
PT and treating S. pyogenes infections.
XX
XX
PS Claim 14; Page 69; 145pp; English.
CC This invention describes a novel nucleic acid molecule encoding a
CC hyperimmune serum reactive antigen or its fragment from Streptococcus
CC pyogenes. The nucleic acid molecule or hyperimmune serum-reactive antigen
CC or its fragment are useful for the manufacture of a pharmaceutical
CC preparation, especially a vaccine, against S. pyogenes infection. In
CC addition, the hyperimmune serum reactive antigen or fragment is used for
CC the isolation and/or purification and/or identification of an interaction
CC partner of the hyperimmune serum reactive antigen or its fragment, for

CC the generation of a peptide (e.g. anticaline) binding to the antigen or
CC fragment, or for the manufacture of a functional nucleic acid selected
CC from aptamers and Spiegelmers. The nucleic acid molecule may also be used
CC for the manufacture of functional ribonucleic acids, such as ribozymes,
CC antisense nucleic acids and siRNA. ADR83733-ADR84189 represent S.
CC pyogenes hyperimmune serum reactive antigens, fragments and the encoding
CC polynucleotide described in the invention.
XX
SQ Sequence 19 AA;
Query Match 35.3%; Score 27.5; DB 8; Length 19;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 2; Indels 1; Gaps 1;
QY 3 KRDH-NDVYSKN 12
DB 4 RHDHVCYSRN 14
RESULT 71
ID AAE14547
ID AAE14547 standard; peptide; 7 AA.
XX AAE14547;
XX
DT 17-MAY-2002 (first entry)
XX
DE Human alpha-synuclein aggregation inhibitor #2.
XX
KM Alpha-synuclein; inhibitor; neurodegenerative disease; Lewy body;
KM Parkinson's disease; Alzheimer's disease; diffuse Lewy body disease;
KM multiple system atrophy; Hallervorden-Spatz disease; human.
XX
OS Homo sapiens.
XX
PN WO200204482-A1.
XX
PD 17-JAN-2002.
XX
PF 06-JUL-2001; 2001WO-US021379.
XX
PR 07-JUL-2000; 2000US-0217319P.
PR 28-MAR-2001; 2001US-0279199P.
XX
PA (PANA-) PANACERA PHARM INC.
XX
PI Wolozin B, Ostretova-Golts N, Lebowitz MS;
XX
DR WPI; 2002-179695/23.
XX
PT Determination of an agent capable of inhibiting aggregation of alpha
PT synuclein useful for treating a neurodegenerative disease involves
PT determining aggregation of alpha synuclein in the presence of exogenous
PT iron or copper.
XX
PS Claim 40; Page 37; 52pp; English.
XX
XX
CC The invention relates to screening of inhibitors of alpha-synuclein
CC aggregation in the presence of exogenous iron or copper. The inhibitors
CC are magnesium and alpha-synuclein binding peptides, which are useful for
CC treating neurodegenerative disease that involves the formation of Lewy
CC bodies e.g. Parkinson's disease (PD), Alzheimer's disease (AD), diffuse
CC Lewy body disease, mixed AD-PD, multiple system atrophy and Hallervorden-
CC Spatz disease. The present sequence is a peptide that binds to C-terminal
CC portion of human alpha-synuclein and inhibits its aggregation
XX
SQ Sequence 7 AA;
Query Match 34.6%; Score 27; DB 5; Length 7;
Best Local Similarity 66.7%; Pred. No. 2e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 9 YSKNPM 14

Db 2 YAKMPI 7

RESULT 72
ADSL4010
ID ADSL4010 standard; peptide; 7 AA.
XX
AC ADSL4010,
XX
DT 02-DEC-2004 (first entry)
XX
DE Thrombin peptide inhibitor segment - SEQ ID 61.
XX
KM thrombin inhibitor; fibrinogen recognition exosite; anticoagulant.
XX
OS Synthetic.
XX
PN WO2004076484-A1.
XX
PD 10-SEP-2004.
XX
PF 27-FEB-2004; 2004WO-CA000301.
XX
PR 27-FEB-2003; 2003US-0449878P.
XX
PA (CANADA) NAT RES COUNCIL CANADA.
XX
PI N1 P, Su Z, Tolkatchev D, Natapova A, Koutychenko A;
XX
DR WPI; 2004-653369/63.
XX
PT New isolated or purified multivalent polypeptide inhibitors of thrombin
PT containing only genetically encodable natural amino acids, useful as
PT potent anticoagulants.
XX
PS Claim 5; SEQ ID NO 61; 158bp; English.
XX
CC The invention comprises peptide inhibitors of thrombin. The peptide
CC inhibitors of the invention consist of the general formula: SBM-PBM-SBM;
CC SBM is a sequence moiety comprising P-substrate residues of the thrombin
CC inhibitor. PBM is a sequence moiety comprising P'-substrate residues of the
CC thrombin inhibitor, and SBM is a peptide sequence moiety that binds to
CC the fibrinogen recognition exosite of thrombin. The peptide inhibitors of
CC the invention are useful for inhibiting thrombin or as anticoagulants.
CC The present amino acid sequence represents a PBM segment of a thrombin
CC inhibitor peptide of the invention.
XX
SQ Sequence 7 AA;
XX

Query Match 34.6%; Score 27; DB 8; Length 7;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDND 8
DB 2 QDND 6

RESULT 73
AAM96968
ID AAM96968 standard; peptide; 8 AA.
XX
AC AAM96968;
XX
DT 24-JAN-2002 (first entry)
XX
DE Human peptide #243 encoded by a SNP oligonucleotide.
XX
KM immunosuppressive; immunostimulatory; antiinflammatory; cyostatic;
KM neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
KM amyloid protein; angiotensin; apoptosis related protein; cadherin;
KM cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;

KM complement related protein; cytochrome; kinesin; cytokine; interferon;
KM interleukin; G-protein coupled receptor; thioesterase; inflammation;
KM multifactorial disease; autoimmune disease; infection;
KM nervous system disease.
XX
OS Homo sapiens.
XX
PN WO200147944-A2.
XX
PD 05-JUL-2001.
XX
PE 28-DEC-2000; 2000WO-US035498.
XX
PR 28-DEC-1999; 99US-0173419P.
PR 27-DEC-2000; 2000US-00173419.
XX
PA (CURA-) CURAGEN CORP.
XX
PI Shinkets RA, Leach M;
XX
DR WPI; 2001-465210/50.
XX
PT Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
PT oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
PT autoimmune diseases and infections.
XX
PS Disclosure; Page 3721; 4143pp; English.
XX
CC The present invention relates to oligonucleotides (see AYL26793-AYL34659)
CC encoding polymorphic variants of proteins related to amylases, amyloid
CC proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
CC polymerase, oncogenes, histones, kinases, colony stimulating factors,
CC complement related proteins, cytochromes, kinesins, cytokines,
CC interferons, interleukins, G-protein coupled receptors and thioesterases.
CC The present sequence is a peptide encoded by one such oligonucleotide.
CC The oligonucleotides and the peptides encoded by them may be used in the
CC prevention, diagnosis and treatment of diseases associated with
CC inappropriate expression of the proteins listed above. Disorders that may
CC be prevented, diagnosed and/or treated include multifactorial diseases
CC with a genetic component, such as autoimmune diseases (e.g. rheumatoid
CC arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
CC and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
CC brain, breast, colon and kidney, leukaemia), diseases of the nervous
CC system and an infection of pathogenic organisms
XX
SQ Sequence 8 AA;
XX

Query Match 34.6%; Score 27; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRND 8
DB 1 KRND 6

RESULT 74
ADK08340
ID ADK08340 standard; peptide; 9 AA.
XX
AC ADK08340;
XX
DT 06-MAY-2004 (first entry)
XX
DE Human papillomavirus peptide #395.
XX
KM pathogenic virus; alternative reading frame; antigenic determinant;
KM vaccine; therapeutic agent; infection; HPV.
XX
OS Human papillomavirus.
XX
PN WO2004011650-A2.

PD 05-FEB-2004.
XX
PI 24-JUL-2003; 2003MO-BF0089112.
XX
XX 24-JUL-2002; 2002AT-00001124.
PR 11-JUL-2003; 2003EP-00450171.
XX
XX (INTE-) INTERCELL AG.
XX
PI Matner F, Schmidt W, Habel A;
XX
XX WPI; 2004-169243/16.
XX
XX New polypeptide encoded by an alternative reading frame of a pathogenic
PT virus comprising an antigenic determinant, useful for treating or
PT preventing an infection with the pathogenic virus.
XX
XX Claim 18; Page 177; 220pp; English.
XX
XX This invention relates to a novel polypeptide encoded by an alternative
CC reading frame of a pathogenic virus, where the polypeptide starts with a
CC methionine amino acid residue, which comprises an antigenic determinant
CC and more than 7 amino acid residues. The invention may be useful for the
CC production of compounds with a virucide activity or the development of a
CC vaccine. The polypeptide or its fragments may be useful as a therapeutic
CC agent. It is also useful for the manufacture of a medicament for treating
CC or preventing an infection with the pathogenic virus. The present
CC sequence is that of a human papillomavirus (HPV) epitope peptide of the
CC invention.
XX
XX Sequence 9 AA;
SQ

Query Match 34.6%; Score 27; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06; 2; Indels 0; Gaps 0;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 DHNDYSKN 12
Db 1 DHIDYWKH 8

RESULT 75
ABJ36831
ID ABJ36831 standard; peptide; 11 AA.
XX
AC ABJ36831;
XX
DT 01-MAY-2003 (first entry)
XX
DE G protein coupled receptor related peptide SEQ ID No 185.
XX
XX Nootropic; cardiant; antiarteriosclerotic; hypotensive; cyrostatic;
KM antiatherial; analgesic; antiallergic; antiaslamic; antiinflammatory;
KM osteopathic; neuroprotective; anxiolytic; anorectic; lead compound;
KM G protein coupled receptor signaling inhibitor; GPCR; library;
KM high throughput screening assay; stroke; myocardial infarction;
KM restenosis; atherosclerosis; hypotension; cancer; infection; asthma;
KM septic shock; pain; allergic disorder; inflammatory bowel disease;
KM osteoporosis; obesity; psychotic; neurological disorder; anxiety;
KM schizophrenia; Alzheimer's disease.
XX
XX Unidentified.
OS
XX
XX WO200272778-A2.
PN
XX
PD 19-SEP-2002.
XX
XX 14-MAR-2002; 2002MO-US007561.
PF
XX
PR 14-MAR-2001; 2001US-0275472P.
PR 11-MAY-2001; 2001US-00852910.
XX
XX (CUB-) CUB BIOTECH.

XX
PI Gilchrist A, Hamm HE;
XX
XX WPI; 2003-247841/24.
DR
XX
XX Identifying G protein coupled receptor (GPCR) signalling inhibitors,
PT useful in screening drugs for treating stroke, cancers or pain, by
PT identifying compounds that block GPCR mediated signalling with high
PT affinity and specificity.
XX
XX Claim 94; Page 65; 94pp; English.
PS
XX
XX The invention relates to a novel method for identifying a G protein
CC coupled receptor (GPCR) signalling inhibitor. The novel method comprises
CC selecting or identifying a member of a library of peptides and/or
CC candidate compounds, having binding to a GPCR of higher affinity than
CC that of the native peptide. The peptide library is based on a native GPCR
CC binding peptide. The method is useful for identifying inhibitors of a G
CC protein coupled receptor (GPCR) signalling. The method is particularly
CC useful for identifying drugs that antagonise the binding between a GPCR
CC and its extracellular ligand(s). The method is especially useful in
CC modern high throughput screening assays for identifying potent lead
CC compounds. The compounds, peptides or inhibitors identified by the method
CC are useful for preventing, ameliorating or treating diseases in which
CC GPCR signalling is a causative factor or in which a specific class of G
CC protein is relevant, e.g. stroke, myocardial infarction, restenosis,
CC atherosclerosis, hypotension, cancer, infections, septic shock, pain,
CC allergic disorders, asthma, inflammatory bowel disease, osteoporosis,
CC obesity, or psychotic and neurological disorders (e.g. anxiety,
CC schizophrenia or Alzheimer's disease). This sequence represents a peptide
CC relating to the G protein coupled receptors of the invention
XX
XX Sequence 11 AA;
SQ

Query Match 34.6%; Score 27; DB 6; Length 11;
Best Local Similarity 33.3%; Pred. No. 8.2e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 2 IKRDNDYS 10
Db 1 LQNNHNEYN 9

RESULT 76
ADTS1259
ID ADTS1259 standard; peptide; 11 AA.
XX
AC ADTS1259;
XX
DT 13-JAN-2005 (first entry)
XX
DE G protein coupled receptor signalling modifying peptide #160.
XX
XX cerebroprotective; vasotropic; cardiant; antiarteriosclerotic;
KM hypotensive; cyrostatic; antibacterial; fungicide; virucide; analgesic;
KM antiallergic; antiaslamic; antiinflammatory; antiparkinsonian;
KM neuroprotective; nootropic; gene therapy; G protein coupled receptor;
KM GPC.
XX
XX Synthetic.
OS
XX
XX WO2004092199-A2.
PN
XX
PD 28-OCT-2004.
XX
XX 12-APR-2004; 2004MO-US011167.
PF
XX
PR 11-APR-2003; 2003US-00411336.
XX
XX (CUB-) CUB BIOTECH INC.
XX
XX Gilchrist A, Hamm HM;
XX
XX

DR WPI; 2004-766826/75.
XX
XX Identifying modulators of G protein coupled receptor (GPCR) signaling.
PT useful for treating diseases associated with altered GPCR signaling (e.g.
PT stroke), comprises screening a peptide library for high affinity binding
PT to the GPCR.
XX
PS Disclosure; SEQ ID NO 185; 264bp; English.
XX
XX The invention relates to a method of identifying a G protein coupled
CC receptor (GPCR) signaling modifying peptide by providing a peptide
CC library based on a native GPCR binding peptide, screening the peptide
CC library for high affinity binding to the GPCR, and selecting a member of
CC the peptide library having binding to the GPCR of higher affinity than
CC that of the native peptide. The composition and methods are useful for
CC identifying modulators of GPCR signaling, for modulating the activity of
CC GPCR or for drug designing. These may be used for diagnosing, preventing
CC or treating diseases associated with altered GPCR signaling, such as
CC stroke, myocardial infarction, atherosclerosis, hypertension, cancer,
CC inflammation, Parkinson's disease and Alzheimer's disease. This sequence
CC corresponds to a peptide of the invention.
XX
SQ Sequence 11 AA;

Query Match 34.6%; Score 27; DB 8; Length 11;
Best Local Similarity 33.3%; Pred. No. 8.2e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDHNDYS 10
:::|::|:
Db 1 LQMHNEYN 9

RESULT 77
ID AAR83314 standard; peptide; 12 AA.
XX
AC AAR83314;
XX
DT 24-MAY-1996 (first entry)
XX
DE Kb-binding random peptide, B2.
XX
KM MHC; Kb; major histocompatibility complex; terminal; identification;
KW investigation; random.
XX
OS Synthetic.
XX
PN WO9527901-A1.
XX
PD 19-OCT-1995.
XX
PF 10-APR-1995; 95WO-US004509.
XX
PR 11-APR-1994; 94US-00227101.
XX
PA (IXSY-) IXSYS INC.
XX
PI Gay DA;
XX
DR WPI; 1995-366462/47.
XX
XX Identifying peptide(s) which bind MHC molecules - using a library of
PT random peptide(s) expressed as fusion proteins and obtaining terminal
PT octamers or nonamers.
XX
XX
PS Disclosure; Fig 5; 46bp; English.
XX
XX AAR83313-R83350 are random MHC binding peptides which are identified from
CC a library of random peptides expressed as fusion proteins on the surface
CC of a cell or virus. These peptides are isolated using the murine MHC
CC molecule Kb. The identification method rapidly identifies MHC binding

CC motif, provides sequence information on neighbouring amino acids and
CC relationships between amino acids within the peptides and reveals a
CC preference for several amino acids at peptide positions previously
CC thought to be indiscriminate
XX
SQ Sequence 12 AA;

Query Match 34.6%; Score 27; DB 2; Length 12;
Best Local Similarity 83.3%; Pred. No. 9.1e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
||| |
Db 4 DYSNMP 9

RESULT 78
ID AAY88130 standard; peptide; 12 AA.
XX
AC AAY88130;
XX
DT 17-OCT-2000 (first entry)
XX
DE Fluorescein binding peptide fluorette #7.
XX
KW Fluorette; fluorophore dye; fluorescent; detection; diagnostic.
XX
OS Synthetic.
XX
PN WO200023463-A2.
XX
PD 27-APR-2000.
XX
PF 15-OCT-1999; 99WO-US024266.
XX
PR 16-OCT-1998; 98US-0104465P.
XX
PA (STRD) UNIV LEIAND STANFORD JUNIOR.
XX
PI Nolan GP, Rozinov MN;
XX
DR WPI; 2000-339647/29.
XX
XX Novel fluorette peptides which bind with high specificity to fluorophore
PT dyes, useful for detecting biological materials, molecules, target
PT analytes, and intra- and inter-molecular interactions.
XX
PS Claim 11; Page 19; 64bp; English.
XX
XX This invention describes a novel peptide (I) termed a fluorette which
CC comprises a sequence of at least 8 amino acids and which binds to a
CC fluorophore dye. The fluorettes maybe used in detecting biological
CC materials, molecules or target analytes, intracellular events, and intra-
CC and inter-molecular interactions, as well as discovering effective
CC inhibitors. They may also be used for in vitro assays using a large set
CC of fluorophore dyes, e.g. in detection of viral and delivery systems,
CC diagnostics and high throughput assays. The new peptides, due to their
CC small size, are not intrusive to the systems being studied hence, permit
CC detection and analysis of a target moiety or molecule while minimizing
CC target modification. Unlike conventional techniques such as the light-
CC emitting technique, the use of fluorettes minimize or avoid substantial
CC genetic manipulations which may disrupt, interfere, or alter the process
CC being measured. This sequence represents a peptide fluorette capable of
CC binding to Fluorescein which is described in the method of the invention
XX
SQ Sequence 12 AA;

Query Match 34.6%; Score 27; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9

```
Db          |||||
            2 HNDY 5

RESULT 79
AAV88188
XX AAV88188 standard; peptide; 12 AA.
AC
XX
XX
XX
XX 17-OCT-2000 (first entry)
DE Fluorescein binding peptide fluorette from phage clone Flus315.
XX
XX Fluorette; fluorophore dye; fluorescent; detection; diagnostic.
KM
XX
XX Synthetic.
OS
XX WO200023463-A2.
XX
XX 27-APR-2000.
XX
XX 15-OCT-1999; 99WO-US024266.
XX
XX 16-OCT-1998; 98US-0104465P.
XX
XX (STRD ) UNIV LELAND STANFORD JUNIOR.
XX
XX Nolan GP, Rozinov MN;
XX
XX WPI; 2000-339647/29.
XX
XX Novel fluorette peptides which bind with high specificity to fluorophore
XX PT dyes, useful for detecting biological materials, molecules, target
XX PT analytes, and intra- and inter-molecular interactions.
XX
XX Example 3; Page 41; 64pp; English.
XX
XX This invention describes a novel peptide (I) termed a fluorette which
XX CC comprises a sequence of at least 8 amino acids and which binds to a
XX CC fluorophore dye. The fluorettes may be used in detecting biological
XX CC materials, molecules or target analytes, intracellular events, and intra-
XX CC and inter-molecular interactions, as well as discovering effective
XX CC inhibitors. They may also be used for in vitro assays using a large set
XX CC of fluorophore dyes, e.g. in detection of viral and delivery systems,
XX CC diagnostics and high throughput assays. The new peptides, due to their
XX CC small size, are not intrusive to the systems being studied hence, permit
XX CC detection and analysis of a target moiety or molecule while minimizing
XX CC target modification. Unlike conventional techniques such as the light-
XX CC emitting technique, the use of fluorettes minimize or avoid substantial
XX CC genetic manipulations which may disrupt, interfere, or alter the process
XX CC being measured. This sequence represents a peptide fluorette capable of
XX CC binding to Fluorescein which is described in the method of the invention
XX
XX Sequence 12 AA;
SQ

Query Match          34.6%; Score 27; DB 3; Length 12;
Best Local Similarity 100.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HNDY 9
        |||||
Db      2 HNDY 5

RESULT 80
AAW53909
ID AAW53909 standard; peptide; 14 AA.
XX
XX
XX
XX AAW53909,
AC
XX
XX 17-AUG-1998 (first entry)
XX
```

```
DE Interleukin-1 receptor accessory molecule epitope P248-E261.
XX
XX Interleukin-1 receptor accessory molecule; IL-1R AcM; human;
XX KM signal transduction; agonist; antagonist; antibody; infection;
XX KM septic shock; inflammation; rheumatoid arthritis; therapy; epitope;
XX KM antigen.
XX
XX Homo sapiens.
XX
XX WO9808969-A1.
XX
XX 05-MAR-1998.
XX
XX 26-AUG-1996; 96WO-US013954.
XX
XX 26-AUG-1996; 96WO-US013954.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Bednarik DP, Olsen HS, Rosen CA;
XX
XX WPI; 1998-230267/20.
XX
XX Nucleic acid encoding interleukin-1 receptor accessory protein - used for
XX PT therapeutic modulation of IL-1 activity.
XX
XX Claim 17; Page 83; 95pp; English.
XX
XX This peptide corresponds to amino acids 248-261 of novel human
XX CC Interleukin-1 receptor accessory molecule (IL-1R AcM) (see AAW53897), a
XX CC new member of the immunoglobulin superfamily that forms a complex with
XX CC type 1 IL-1R. It comprises an epitope-bearing portion of IL-1R AcM. 18
XX CC Antigenic peptides comprising epitope-bearing portions of human IL-1R AcM
XX CC are claimed (see AAW53898-915). These can be used to generate soluble IL-
XX CC 1R AcM-specific antibodies, and may be produced by chemical synthesis or
XX CC by recombinant means using nucleic acid molecules (see AAV23659) of the
XX CC invention. The antibodies are useful as immunoassay reagents for
XX CC detecting IL-1R AcM, for affinity purification of IL-1R AcM and for
XX CC identifying cells that express IL-1R AcM
XX
XX Sequence 14 AA;
SQ

Query Match          34.6%; Score 27; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY      5 DENDYSKNP 13
        |||||
Db      3 DHVVEKEP 11

RESULT 81
ADN94288
ID ADN94288 standard; peptide; 15 AA.
XX
XX
XX ADN94288;
AC
XX
XX 01-JUL-2004 (first entry)
XX
XX Human 202P5A5v.1 protein epitope #4524.
XX
XX 202P5A5; human; cancer; tumour; epitope.
XX
XX Homo sapiens.
XX
XX WO2004016736-A2.
XX
XX 26-FEB-2004.
XX
XX 16-JUN-2003; 2003WO-US018906.
XX
XX 16-AUG-2002; 2002US-0404306P.
XX
XX 01-NOV-2002; 2002US-0423290P.
XX
```

XX (AGEN-) AGENSYS INC.
 XX Raitano AB, Paris M, Challita-Bid PM, Jakobovits A, Ge W,
 XX WPI; 2004-203774/19.
 XX
 PT New compositions having the 202PSA5 gene and encoded protein, useful for
 PT diagnosing, preventing, prognosticating or treating cancer of the
 PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
 PT bone and/or skin.
 XX
 XX Claim 1; Fig 2A; 266pp; English.
 XX
 CC The invention relates to a composition comprising 202PSA5 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VIII-XLIX.
 CC
 SO Sequence 15 AA;
 SQ
 QY Query Match 34.6%; Score 27; DB 8; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DB 1 SIKRDHNDYSK 11
 3 SLNQDHLNSK 13
 DB
 RESULT 82
 ADN94725
 ID ADN94725 standard; peptide; 15 AA.
 XX
 AC ADN94725;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human 202PSA5v.1 protein epitope #4961.
 KM 202PSA5; human; cancer; tumour; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016736-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 16-JUN-2003; 2003WO-US018906.
 XX
 PR 16-AUG-2002; 2002US-0404306P.
 PR 01-NOV-2002; 2002US-0423290P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Paris M, Challita-Bid PM, Jakobovits A, Ge W;
 XX WPI; 2004-203774/19.
 XX
 PT New compositions having the 202PSA5 gene and encoded protein, useful for
 PT diagnosing, preventing, prognosticating or treating cancer of the
 PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
 PT bone and/or skin.
 XX
 XX Claim 1; Fig 2A; 266pp; English.
 XX
 CC The invention relates to a composition comprising 202PSA5 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VIII-XLIX.
 CC

SO Sequence 15 AA;
 SQ
 QY Query Match 34.6%; Score 27; DB 8; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DB 1 SIKRDHNDYSK 11
 3 SLNQDHLNSK 13
 DB
 RESULT 83
 ADN94151
 ID ADN94151 standard; peptide; 15 AA.
 XX
 AC ADN94151;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human 202PSA5v.1 protein epitope #4387.
 KM 202PSA5; human; cancer; tumour; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO2004016736-A2.
 XX
 PD 26-FEB-2004.
 XX
 PF 16-JUN-2003; 2003WO-US018906.
 XX
 PR 16-AUG-2002; 2002US-0404306P.
 PR 01-NOV-2002; 2002US-0423290P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Raitano AB, Paris M, Challita-Bid PM, Jakobovits A, Ge W;
 XX WPI; 2004-203774/19.
 XX
 PT New compositions having the 202PSA5 gene and encoded protein, useful for
 PT diagnosing, preventing, prognosticating or treating cancer of the
 PT prostate, bladder, colon, lung, ovary, breast, stomach, cervix, lymphoma,
 PT bone and/or skin.
 XX
 XX Claim 1; Fig 2A; 266pp; English.
 XX
 CC The invention relates to a composition comprising 202PSA5 proteins. The
 CC composition and proteins are useful for detecting and treating cancer by
 CC inhibiting the growth or viability of cancer cells. The present sequence
 CC represents the amino acid sequence of a human 202PSA5v.1 protein epitope.
 CC Note the epitope sequences are displayed in tables VIII-XLIX.
 CC
 SO Sequence 15 AA;
 SQ
 QY Query Match 34.6%; Score 27; DB 8; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.2e+03;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DB 1 SIKRDHNDYSK 11
 3 SLNQDHLNSK 13
 DB
 RESULT 84
 ADN94437
 ID ADN94437 standard; peptide; 15 AA.
 XX
 AC ADN94437;
 XX
 DT 01-JUL-2004 (first entry)
 XX
 DE Human 202PSA5v.1 protein epitope #4673.
 XX

XX Example; SEQ ID NO 1406; 200bp; English.

PS The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The present invention also relates to novel
CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
CC methods for detecting the presence of a N- or S-gene of the hSARS virus
CC or of the protein in a biological sample and identifying a subject
CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein
CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADT40120 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADT40601 are the peptides from the
CC first reading frame protein. ADT40602 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT40603-
CC ADT40976 are the peptides from the second reading frame protein. ADT40977
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT40978-ADT41482 are the peptides from the
CC third reading frame protein.

SO Sequence 15 AA;

Query Match 34.6%; Score 27; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 DHNDYSKN 12
|:|:|:|
Db 7 DYNDNSHN 14

RESULT 87
ADST9835
ID ADST9835 standard; protein; 15 AA.

AC ADST9835;
XX
DT 30-DEC-2004 (first entry)
XX
DE SARS virus complementary DNA strand reading frame 1 protein #298.
XX
KM virucide; vaccine; detection; severe acute respiratory syndrome;
KM real-time quantitative polymerase chain reaction; SARS.
XX
OS SARS coronavirus.
XX
PN WO2004085455-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-CN000247.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-045931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464866P.
PR 05-MAY-2003; 2003US-0468139P.
PR 16-MAY-2003; 2003US-0471200P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
XX WPI; 2004-737292/72.
XX

PT New isolated nucleic acid molecule useful for detecting, treating,
PT ameliorating, or preventing the virus causing severe acute respiratory
PT syndrome in humans using a real-time quantitative polymerase chain
PT reaction assay.

PS Example; SEQ ID NO 1406; 183bp; English.

XX The invention relates to an isolated nucleic acid molecule consisting
CC essentially of, and/or hybridizes under stringent conditions to a fully
CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-
CC 2476), or its complement. The methods and compositions of the present
CC invention are useful for the detection of the virus causing Severe Acute
CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
CC polymerase chain reaction (PCR) assay. They can also be used in treating,
CC ameliorating, managing or preventing SARS. This sequence corresponds to a
CC partial SARS protein sequence from the complementary reading frame 1.

SO Sequence 15 AA;

Query Match 34.6%; Score 27; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 5 DHNDYSKN 12
|:|:|:|
Db 7 DYNDNSHN 14

RESULT 88
ADT37948
ID ADT37948 standard; peptide; 15 AA.

AC ADT37948;
XX
DT 30-DEC-2004 (first entry)
XX
DE hSARS virus peptide, SEQ ID 1406.
XX
KM virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
OS SARS coronavirus.
XX
PN WO2004085633-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-CN000248.
XX
PR 24-MAR-2003; 2003US-0457031P.
PR 26-MAR-2003; 2003US-0457730P.
PR 02-APR-2003; 2003US-045931P.
PR 03-APR-2003; 2003US-0460357P.
PR 08-APR-2003; 2003US-0461265P.
PR 14-APR-2003; 2003US-0462805P.
PR 23-APR-2003; 2003US-0464866P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
XX Leung FC;
XX WPI; 2004-728736/71.
XX
DR New isolated human severe acute respiratory syndrome (hSARS) virus,
PT useful as vaccine for diagnosing or treating SARS or in clinical and
PT scientific research applications.

PS Example; SEQ ID NO 1406; 176bp; English.

XX The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
CC hSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein

CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hSARS virus genome (ADP36557) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADP3650 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADP3651-ADP3813 are the peptides from the
CC first reading frame protein. ADP38132 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADP38133-
CC ADP38506 are the peptides from the second reading frame protein. ADP38507
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADP38508-ADP39012 are the peptides from the
CC third reading frame protein.

XX Sequence 15 AA;

Query Match 34.6%; Score 27; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
|:|:|:|:
Db 7 DYDNDSHN 14

RESULT 89
ADC97706
ID ADC97706 standard; peptide; 17 AA.
XX
AC ADC97706;
XX
DT 01-JAN-2004 (first entry)
XX
DE Mouse monoclonal antibody LL2 VH CDR2.

XX
XX Mouse; monoclonal antibody; LL2; heavy chain variable region; VH;
KW cytotoxic; complementarity determining region; CDR; B-lymphoma;
KW leukaemia; humanised antibody.

OS Mus sp.

PN US2003103979-A1.

PD 05-JUN-2003.

PF 16-NOV-2001; 2001US-00988013.

PR 16-NOV-2001; 2001US-00988013.

XX (LEUNG/) LEUNG S.
PA (HANS/) HANSEN H.

XX Leung S, Hansen H;

PI WPI; 2003-801218/75.

XX Novel LL2 monoclonal antibody useful for diagnosing and treating B-cell
PT lymphoma or leukemia.

XX Claim 10; Page 11; 30pp; English.

XX The invention relates to an isolated polynucleotide comprising a DNA
CC sequence encoding the amino acid sequence of light chain (kappa) variable
CC (VK) region or heavy chain variable (VH) region of LL2 monoclonal
CC antibody (mAb), and LL2 VH domain or LL2 VH domain. Also included are a
CC protein encoded by the DNAs listed above, an isolated complementarity
CC determining region-1 (CDR1, CDR2 or CDR3) polypeptide of the VK or VH
CC region of the LL2 mAb, a LL2 mAb (comprising the light chain and heavy
CC chains of the LL2 mAb linked to the human kappa and human Igg 1 constant
CC regions, respectively), an LL2 mAb (comprising a light chain and a heavy
CC chain CDR of a LL2 mAb joined to a framework sequence of a human VK and
CC human VH region, respectively, linked to human kappa and Igg 1 constant
CC region domains, respectively, such that the LL2 mAb retains
CC substantially the B-lymphoma cell and leukaemia cell targeting cell

CC internalisation characteristics of the parent mAb2 antibody) and a
CC conjugate comprising a LL2 or LL2 antibody or its fragment covalently
CC bound to a diagnostic or therapeutic reagent. The conjugate is useful for
CC treating and diagnosing a B-cell lymphoma or leukaemia in a subject. The
CC present sequence represents mouse LL2 VH CDR2.

XX Sequence 17 AA;

Query Match 34.6%; Score 27; DB 7; Length 17;
Best Local Similarity 30.0%; Pred. No. 1.4e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRNDYSKN 12
|:|:|:|:
Db 5 RNDYTEYNON 14

RESULT 90
AEA89661
ID AEA89661 standard; peptide; 19 AA.

XX AEA89661;

DT 25-AUG-2005 (first entry)

DE Tumor metastases treatment-related protein region #49.

XX metastasis; therapeutic; gene expression; cytotoxic; tumor;
KW breast tumor; sarcoma; nervous system tumor; prostate tumor;
KW pancreas tumor; colon tumor; rectal tumor; medulloblastoma;
KW b-cell lymphoma; t-cell lymphoma; multiple myeloma; lung tumor; cancer.

OS Unidentified.

PN WO2005056043-A2.

PD 23-JUN-2005.

PF 10-DEC-2004; 2004WO-IT000689.

PR 11-DEC-2003; 2003IT-RM000572.

XX (ZOLLI/) ZOLLO M.

PI Zollo M;

DR WPI; 2005-445065/45.

XX Use of inhibitors of human-PRUNE cyclic nucleotide phosphodiesterase for
PT preparation of medicament in the treatment of tumor metastases associated
PT with overexpression of human-PRUNE.

XX Example 1; Fig 1; 89pp; English.

XX This invention relates to a novel method for preparing a medicament for
CC the treatment of tumor metastases associated with overexpression of human
CC -PRUNE. The method comprise using inhibitors of human-PRUNE cyclic
CC nucleotide phosphodiesterase. The invention may be useful for the
CC development of compounds with a cytotoxic activity acting as human-PRUNE
CC overexpression inhibitors. The invention is useful for preparation of
CC medicaments in the treatment of tumor metastases, for example breast
CC carcinoma, sarcoma, neuroblastoma, prostate tumor, pancreatic tumor,
CC colonic tumor, rectal tumor, medulloblastoma, epiteloma, epatocarcinoma,
CC cell T or cell B lymphomas, myeloma and melanoma and pulmonary tumor. As
CC the h-PRUNE poses cyclic nucleotide phosphodiesterase activity with
CC preferential activity for camp over cGMP, the h-PRUNE overexpression can
CC be effectively suppressed by certain PDE inhibitors thus the PDE
CC inhibitor provides an effective alternative therapy for cancer treatment.
CC The present sequence is that of a protein motif which was used during the
CC development of the novel method of the invention.

XX Sequence 19 AA;

Query Match 34.6%; Score 27; DB 9; Length 19;
 Best Local Similarity 62.5%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DHNDYSK 12
 |||
 Db 8 DNDTPK 15

RESULT 91

AAR45557
 ID AAR45557 standard; protein; 20 AA.

AC AAR45557;

DT 25-MAR-2003 (revised)
 DT 13-JUL-1994 (first entry)

XX Cry j I pollen allergen peptide CJI-16.

KM Japanese cedar; detection; allergy; treatment; diagnosis; T cell epitope;
 KM sensitivity.

OS Cryptomeria japonica.

PN WO9401560-A1.

PD 20-JAN-1994.

PF 15-JAN-1993; 93WO-US000139.

PR 10-JUL-1992; 92WO-US0005661.

PR 01-SEP-1992; 92US-00938990.

PA (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Griffith IJ, Pollock J, Bond JF, Garman RD, Kuo M;

DR WPI; 1994-035066/04.

PT Antigens derived from Japanese cedar pollen allergen Cry j I - contain at
 least two T cell epitope(s), used to treat or diagnose allergy.

PS Claim 1; Fig 13; 137bp; English.

XX The sequence is that of an isolated peptide of the Japanese cedar pollen
 CC allergen Cry j I (amino acids 151-170). The peptide, CJI-16, can be used
 CC for the treatment and diagnosis of allergies associated with Japanese
 CC cedar pollen. It has enhanced therapeutic properties but reduced side
 CC effects compared to naturally occurring allergens. (Updated on 25-MAR-
 CC 2003 to correct PN field.)

XX Sequence 20 AA;

Query Match 34.6%; Score 27; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYS 10
 |||
 Db 14 DHNSFS 19

RESULT 92

AAR82506
 ID AAR82506 standard; protein; 20 AA.

AC AAR82506;

DT 27-AUG-2003 (revised)
 DT 15-APR-1996 (first entry)

XX Cry j I Japanese Cedar pollen allergen peptide fragment (CJI-16).

XX Cry j I; Japanese cedar pollen allergen; modified; drug production;
 KM allergy; Cryptomeria japonica.

OS Cryptomeria japonica.

PN WO9527786-A1.

PD 19-OCT-1995.

PF 06-APR-1995; 95WO-US004249.

PR 08-APR-1994; 94US-00226248.

PR 06-DEC-1994; 94US-00350225.

PA (IMMU-) IMMUNOLOGIC PHARM CORP.

PI Franzen HM, Powers SP, Kuo M, Evans S, Shaked Z, Chen X;

DR WPI; 1995-366391/47.

PT Modified Cryptomeria japonica (Cry j) I peptide(s) - useful for treating
 PT allergy to Japanese cedar pollen allergen or immunologically cross
 PT reactive allergens.

PS Disclosure; Fig 2; 60bp; English.

XX Novel peptides of cry j I have been modified as a part of a
 CC preformulation scheme to develop an optimised drug product for
 CC therapeutic treatment of humans suffering from allergy to Japanese cedar
 CC pollen allergen or an allergen which is immunologically cross reactive
 CC with Japanese cedar pollen allergen. Such modified peptides possess
 CC certain characteristics which render them particularly suitable for drug
 CC product formulation. Peptide fragments of Cry j I, modified and
 CC unmodified, are given in AAR82491-R82525. This peptide fragment
 CC corresponds to amino acids 151-170 of the allergen mature protein.
 CC (Updated on 27-AUG-2003 to correct OS field.)

XX Sequence 20 AA;

Query Match 34.6%; Score 27; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYS 10
 |||
 Db 14 DHNSFS 19

RESULT 93

AAB33555
 ID AAB33555 standard; peptide; 20 AA.

AC AAB33555;

DT 12-SEP-2003 (revised)

DT 22-JAN-2001 (first entry)

XX 5/20 native Ara h 2 peptide #9.

KM Allergy; allergic reaction; allergen; anaphylactic antigen; peanut;
 KM Ara h 1; Ara h 2; Ara h 3; epitope; binding; immunoglobulin E; IgE;
 KM food antigen; sensitising; immune response; anti-allergic.

OS Arachis hypogaea.

PN WO200051647-A2.

PD 08-SEP-2000.

PF 03-MAR-2000; 2000WO-US005655.

PR 03-MAR-1999; 99US-0122960P.

[illegible]

CC useful in grading and/or staging of diseases of the cervix, notably
 CC cervical cancer. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDHNDYS 10
 : : : : :
 : : : : :
 Db 11 TPKKRNNDYT 20

RESULT 96
 AAY72517
 ID AAY72517 standard; peptide; 20 AA.

XX AAY72517;

XX 02-MAY-2001 (first entry)

DE MBD-2-TQIF peptide derived from Escherichia coli FimH protein.

XX FimH, adhesin protein; type 1 pilus; mannose binding domain; MBD, COL;
 KW collagen binding domain; prophylaxis; therapy; urinary tract infection;
 KM UTI; immunogen; passive immunotherapy; vaccine; antibacterial;
 KM MBD-2-TQIF.

XX Escherichia coli.

XX WO200105978-A1.

XX 25-JAN-2001.

XX 14-JUL-2000; 2000WO-US019402.

XX 15-JUL-1999; 99US-0144016P.

XX (MBDI-) MEDIMUNE INC.

XX Hultgren SJ, Langermann S;

XX WPI; 2001-159539/16.

XX Polypeptides useful as vaccines for prevention and/or treatment of
 PT diseases such as urinary tract infections, caused by Enterobacteriaceae,
 PT comprises mannose-binding domains derived from adhesin molecules.

XX Example; Page 26; 53pp; English.

XX The present sequence is MBD-2 (mannose-binding domain-2)-TQIF peptide
 CC derived from Escherichia coli FimH protein. This sequence was tested for
 CC its immunogenicity in mouse, rabbit and primates. FimH is an adhesin
 CC protein found in type 1 pili of bacteria of the family
 CC Enterobacteriaceae, especially E. coli. The FimH protein comprises
 CC mannose-binding domains (MBDs) and collagen-binding domains (COL). The
 CC present invention relates to engineered polypeptides comprising one or
 CC more domains derived from FimH protein. These polypeptides are used to
 CC produce prophylactic vaccines which are useful for the prevention and/or
 CC treatment of diseases, such as urinary tract infection (UTI) caused by a
 CC bacterium of the family Enterobacteriaceae, especially E. coli in
 CC animals, in particular humans. They are useful as immunogens to stimulate
 CC the production of antibodies for use in passive immuno-therapy, as a
 CC diagnostic reagent and as a reagent in other processes such as affinity
 CC chromatography. The antibodies of the novel poly-peptides are also
 CC useful for research purposes for studying protein-lectin or collagen
 CC binding interactions

XX Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;
 Best Local Similarity 100.0%; Pred. No. 1.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9
 : : : : :
 : : : : :
 Db 6 HNDY 9

RESULT 97
 ABB39771
 ID ABB39771 standard; peptide; 20 AA.

XX ABB39771;

XX 04-FEB-2002 (first entry)

DE Peptide #7277 encoded by human foetal liver single exon probe.

XX Human; foetal liver; gene expression; single exon nucleic acid probe.

XX Homo sapiens.

XX WO200157277-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000669.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-463447/52.

XX Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human fetal liver.

XX Claim 27; SEQ ID NO 32406; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human foetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 XX
 SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;
 Best Local Similarity 40.0%; Pred. No. 1.7e+03;

Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDHNDYS 10
 : : : : :
 : : : : :
 Db 11 TPKKRNNDYT 20

RESULT 98
 AAM33354
 ID AAM33354 standard; protein; 20 AA.

XX AAM33354;

```

XX 17-OCT-2001 (first entry)
DT Peptide #7391 encoded by probe for measuring placental gene expression.
XX
DE Probe; microarray; human; placenta; antenatal diagnosis;
XX genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200157272-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US0000663.
XX
PR 04-FEB-2000; 2000US-0180312P.
XX
PR 26-MAY-2000; 2000US-0207456P.
XX
PR 30-JUN-2000; 2000US-00608408.
XX
PR 03-AUG-2000; 2000US-00632366.
XX
PR 21-SEP-2000; 2000US-02344687P.
XX
PR 27-SEP-2000; 2000US-0236359P.
XX
PR 04-OCT-2000; 2000GB-00024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488897/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX
PS Claim 27; SEQ ID NO 33623; 654bp; English.
XX
CC The present invention relates to single exon nucleic acid probes (SENP:
XX see A131315-A157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders
XX
SQ Sequence 20 AA;
XX
Query Match 34.6%; Score 27; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
QY 1 SIRKDHNDYS 10
:|:|:|:|:
Db 11 TPKKRNNDYT 20

```

```

XX 06-DEC-1999; 99US-00455294.
XX
PR 23-JUN-2000; 2000US-0213765P.
XX
PR 27-SEP-2000; 2000US-0235797P.
XX
PA (PANA-) PANACEA PHARM LLC.
XX
PA (UYAR-) UNIV ARKANSAS.
XX
PA (MOUN ) MOUNT SINAI SCHOOL MEDICINE NEW YORK.
XX
PI Bannon GA, Burks WA, Caplan MJ, Sampson H, Sosin H;
XX
DR WPI; 2001-381378/40.
XX
PT Antigenic fragments useful for reducing anaphylactic risk and reducing
XX the severity and/or number of allergic symptoms in individuals sensitive
XX to antigens, have reduced ability to bind Immunoglobulin E.
XX
PS Claim 40; Page 52; 100pp; English.
XX
CC The sequence represents the amino acid sequence of native anaphylactic
XX antigen Ara h 2 peptide #9. Ara h 2 is an anaphylactic antigen (A), which
XX was used to design antigenic peptides having a reduced ability to bind
XX IGE as compared with the intact (A), or having a sequence substantially
XX identical to a portion of sequence of an antigen that includes at least
XX one IGE binding site, where at least one IGE binding site of the peptide
XX is altered. The antigenic peptides are used in a composition which is
XX useful for reducing risk or severity of allergic reaction to an antigen.
XX This is done by identifying an individual at risk of allergic reaction to
XX an antigen by identifying prior display of allergic symptoms when exposed
XX to the antigen, or a familial relationship with an individual who
XX previously displayed allergic symptoms when exposed to the antigen.
XX Following this an antigen-specific IGE present on one or more mast cells
XX or basophils in the individual's serum is identified. The individual is
XX then contacted with a peptide corresponding to a portion of the antigen,
XX which is selected, formulated, and delivered so that binding of the
XX CC peptide to antigen-specific IGE is reduced as compared with IGE binding
XX of intact antigen. The composition is also useful for treating and
XX preventing allergic reactions
XX
SQ Sequence 20 AA;
XX
Query Match 34.6%; Score 27; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 2 IRKDHNDYSKN 12
:|:|:|:|:
Db 10 IQRDEDSYERD 20

```

```

RESULT 99
AAU04768
ID AAU04768 standard; peptide; 20 AA.
XX
AC AAU04768;
XX
DT 23-OCT-2001 (first entry)
XX
DE Native anaphylactic antigen Ara h 2 peptide #9.
XX
XX
KW Ara h 2; anaphylactic antigen; immunoglobulin E; IGE; immunogenic;
XX allergy; mast cell; basophil; mouse; epitope.
XX
OS Mus sp.
XX
PN WO200140264-A2.
XX
PD 07-JUN-2001.
XX
PR 06-DEC-2000; 2000WO-US033124.

```

```

RESULT 100
ABB24400
ID ABB24400 standard; protein; 20 AA.
XX
AC ABB24400;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #6399 encoded by probe for measuring heart cell gene expression.
XX
XX
KW Human; gene expression; heart; microarray; vascular system;
XX cardiovascular disease; hypertension; cardiac arrhythmia;
XX congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PR 30-JAN-2001; 2001WO-US000666.
XX
PR 04-FEB-2000; 2000US-0180312P.

```

PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632266.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX

PA (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488899/53.

PT Single exon nucleic acid probes for analyzing gene expression in human hearts.
XX

PS Claim 15; SEQ ID NO 26170; 530bp; English.

XX
CC The present invention relates to single exon nucleic acid probes for measuring human gene expression in a sample derived from human heart (see ABA21535-ABA41305). The present sequence is a protein encoded by one such probe. The probes may be used for predicting, measuring and displaying gene expression in samples derived from the human heart via microarrays. CC By measuring gene expression, the probes are useful for predicting, diagnosing, grading, staging, monitoring and prognosing diseases of the human heart and vascular system e.g. cardiovascular disease, hypertension, cardiac arrhythmias and congenital heart disease. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
CC
XX

SQ Sequence 20 AA;

Query Match 34.6%; Score 27; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDHNDYS 10
: : : : :
DB 11 TPKRRNNDYT 20

Search completed: January 20, 2006, 19:05:06
Job time : 57.9038 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 ; Search time 14.6731 Seconds
(without alignments)
78.883 Million cell updates/sec

Title: US-09-662-293-1
Perfect score: 78
Sequence: 1 SIRKDHNDYSKPM 14

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA: *
1: /cgn2_6/prodata/1/1aa/5_COMB.pep: *
2: /cgn2_6/prodata/1/1aa/6_COMB.pep: *
3: /cgn2_6/prodata/1/1aa/H_COMB.pep: *
4: /cgn2_6/prodata/1/1aa/PCFUS_COMB.pep: *
5: /cgn2_6/prodata/1/1aa/RB_COMB.pep: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	14	2	US-09-292-225-1
2	33	42.3	12	1	US-08-434-355-15
3	33	42.3	12	1	US-08-459-567-15
4	33	42.3	12	1	US-08-460-327-15
5	33	42.3	12	1	US-08-459-871-15
6	32	41.0	11	1	US-08-237-418-10
7	32	41.0	11	1	US-08-616-855-10
8	32	41.0	11	2	US-08-616-854-10
9	32	41.0	11	2	US-08-468-337-10
10	32	41.0	11	2	US-09-758-318-10
11	32	41.0	11	2	US-10-340-783-10
12	32	41.0	18	2	US-09-292-225-12
13	32	41.0	20	1	US-08-934-915-29
14	31	39.7	20	1	US-08-614-935-12
15	31	39.7	20	2	US-09-130-287-12
16	29	37.2	12	2	US-10-191-540-18
17	28	35.9	10	2	US-08-482-228-209
18	28	35.9	10	2	US-08-482-528-209
19	28	35.9	12	2	US-09-534-717-218
20	28	35.9	15	2	US-09-434-840-81
21	28	35.9	15	2	US-09-142-524D-47
22	28	35.9	20	1	US-08-934-915-34
23	28	35.9	20	2	US-08-467-023-42
24	28	35.9	20	2	US-08-467-023-203
25	27.5	35.3	16	2	US-09-456-399-11
26	27	34.6	7	2	US-09-901-187C-2
27	27	34.6	12	2	US-09-419-381-33

28	27	34.6	13	2	US-08-980-326-9	Sequence 9, App1
29	27	34.6	13	2	US-08-980-326-10	Sequence 10, App1
30	27	34.6	13	2	US-08-980-326-11	Sequence 11, App1
31	27	34.6	13	2	US-08-980-326-12	Sequence 12, App1
32	27	34.6	13	2	US-08-980-326-13	Sequence 13, App1
33	27	34.6	13	2	US-08-980-326-14	Sequence 14, App1
34	27	34.6	15	2	US-09-142-524D-46	Sequence 46, App1
35	27	34.6	19	2	US-09-938-901A-36	Sequence 36, App1
36	27	34.6	20	2	US-08-467-023-41	Sequence 41, App1
37	26	33.3	11	2	US-09-311-784A-441	Sequence 441, App
38	26	33.3	12	1	US-09-611-829-6	Sequence 6, App1
39	26	33.3	12	1	US-08-260-582-18	Sequence 18, App1
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41	26	33.3	15	2	US-09-391-104-15	Sequence 15, App1
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43	26	33.3	18	1	US-08-616-844-50	Sequence 50, App1
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45	26	33.3	18	2	US-08-944-868A-50	Sequence 50, App1
46	26	33.3	18	2	US-08-944-823A-50	Sequence 50, App1
47	26	33.3	18	2	US-08-944-896-50	Sequence 50, App1
48	26	33.3	18	2	US-09-383-062-6	Sequence 6, App1
49	26	33.3	18	2	US-09-839-884-6	Sequence 6, App1
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51	25	32.1	11	1	US-08-408-604A-152	Sequence 152, App
52	25	32.1	11	2	US-08-974-549A-145	Sequence 145, App
53	25	32.1	11	2	US-09-402-181B-145	Sequence 145, App
54	25	32.1	12	2	US-09-721-456-145	Sequence 145, App
55	25	32.1	12	2	US-10-185-815A-11	Sequence 11, App1
56	25	32.1	13	2	US-08-837-226-3	Sequence 3, App1
57	25	32.1	13	2	US-08-811-583-13	Sequence 13, App1
58	25	32.1	13	2	US-09-484-114B-14	Sequence 14, App1
59	25	32.1	13	2	US-09-484-114A-15	Sequence 15, App1
60	25	32.1	13	2	US-09-537-226-3	Sequence 3, App1
61	25	32.1	13	2	US-09-981-194-15	Sequence 15, App1
62	25	32.1	13	2	US-09-981-194-15	Sequence 15, App1
63	25	32.1	14	2	US-09-765-111A-47	Sequence 47, App1
64	25	32.1	15	1	US-08-967-101-167	Sequence 167, App
65	25	32.1	15	1	US-08-592-541-167	Sequence 167, App
66	25	32.1	15	2	US-09-124-698-167	Sequence 167, App
67	25	32.1	15	2	US-09-127-480-167	Sequence 167, App
68	25	32.1	15	2	US-08-496-841C-164	Sequence 164, App
69	25	32.1	15	2	US-09-124-523-167	Sequence 167, App
70	25	32.1	15	2	US-09-636-796A-167	Sequence 167, App
71	25	32.1	16	1	US-08-480-190-188	Sequence 188, App
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73	25	32.1	16	2	US-08-837-226-7	Sequence 7, App1
74	25	32.1	16	2	US-09-025-769B-238	Sequence 238, App
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76	25	32.1	16	2	US-08-475-595A-188	Sequence 188, App
77	25	32.1	16	2	US-08-077-555A-188	Sequence 188, App
78	25	32.1	16	2	US-09-490-070A-238	Sequence 238, App
79	25	32.1	16	2	US-09-490-153-238	Sequence 238, App
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82	25	32.1	17	4	US-09-177-449-281	Sequence 281, App
83	25	32.1	17	2	US-09-066-330-1	Sequence 1, App1
84	25	32.1	17	2	US-09-812-283-281	Sequence 281, App
85	25	32.1	18	2	US-08-406-142A-10	Sequence 10, App1
86	25	32.1	18	2	US-08-406-142A-10	Sequence 10, App1
87	25	32.1	20	1	US-08-934-915-139	Sequence 139, App
88	25	32.1	20	1	US-08-602-995A-126	Sequence 126, App
89	25	32.1	20	2	US-09-500-124-126	Sequence 126, App
90	25	32.1	20	2	US-09-605-703B-2436	Sequence 2436, App
91	24.5	31.4	8	1	US-08-180-209B-24	Sequence 24, App1
92	24.5	31.4	8	1	US-08-385-245-24	Sequence 24, App1
93	24.5	31.4	8	2	US-08-485-388-24	Sequence 24, App1
94	24.5	31.4	8	2	US-08-474-853-24	Sequence 24, App1
95	24.5	31.4	8	2	US-09-166-005B-24	Sequence 24, App1
96	24.5	31.4	8	4	PCT-US94-02629-24	Sequence 24, App1
97	24	30.8	7	1	US-08-724-354D-29	Sequence 29, App1
98	24	30.8	7	2	US-09-270-984A-29	Sequence 29, App1
99	24	30.8	9	2	US-08-574-899-15	Sequence 15, App1
100	24	30.8	9	2	US-09-336-447A-40	Sequence 40, App1

ALIGNMENTS

RESULT 1
US-09-292-225-1
Sequence 1, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOCIDES NUCLEIC ACID MOLECULES, PROTEINS
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
NUMBER OF SEQ ID NOS: 49
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1
LENGTH: 14
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-09-292-225-1

Query Match
Best Local Similarity 100.0%; Score 78; DB 2; Length 14;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKNPM 14
DB 1 SIKRDNDYSKNPM 14

RESULT 2
US-08-434-255-15
Sequence 15, Application US/08434255
Patent No. 5621089
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 56210890 No. 5621089disk of No. 5621089th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/434,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Agis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-255-15

REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-434-255-15

Query Match
Best Local Similarity 42.3%; Score 33; DB 1; Length 12;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14
DB 2 DFIDYDNNPM 11

RESULT 3
US-08-459-967-15
Sequence 15, Application US/08459967
Patent No. 5622841
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: No. 56228410 No. 5622841disk of No. 5622841th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459,967
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764,400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-459-967-15

Query Match
Best Local Similarity 42.3%; Score 33; DB 1; Length 12;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14
DB 2 DFIDYDNNPM 11

RESULT 4
US-08-460-327-15
Sequence 15, Application US/08460327
Patent No. 5622850
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56228500 of No. 5622850th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/460.327
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agilis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-460-327-15
Query Match 42.3%; Score 33; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 DHNDYSKNPM 14
DB 2 DFDYDNNPM 11
RESULT 5
US-08-459-871-15
Sequence 15, Application US/08459871
Patent No. 5650326
GENERAL INFORMATION:
APPLICANT: Sloma, Alan P.
APPLICANT: Outtrup, Helle
APPLICANT: Dambmann, Claus
APPLICANT: Aaslyng, Dorrit
TITLE OF INVENTION: ALKALINE PROTEASE
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 56503260 of No. 5650326th America, Inc.
STREET: 405 Lexington Avenue, 64th Floor
CITY: New York
STATE: New York
COUNTRY: USA

Zip: 10174-6401
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/459.871
FILING DATE: 02-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/434,255
FILING DATE: 03-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Agilis Dr., Cheryl H.
REGISTRATION NUMBER: 34,086
REFERENCE/DOCKET NUMBER: 3764.400-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-867-0123
TELEFAX: 212-878-9655
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-459-871-15
Query Match 42.3%; Score 33; DB 1; Length 12;
Best Local Similarity 60.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 5 DHNDYSKNPM 14
DB 2 DFDYDNNPM 11
RESULT 6
US-08-237-418-10
Sequence 10, Application US/08237418
Patent No. 5601973
GENERAL INFORMATION:
APPLICANT: Mueller, Martin
APPLICANT: Gissmann, Lutz
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
TITLE OF INVENTION: E1 and E2
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/237.418
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/913,613
FILING DATE: 16-JUL-1992
APPLICATION NUMBER: DB P 41 23 760.9
FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 02481-1199-00000

TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-237-418-10

Query Match 41.0%; Score 32; DB 1; Length 11;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12
DB 3 RDHDYWKH 11

RESULT 7
US-08-616-855-10
Sequence 10, Application US/08616855

GENERAL INFORMATION:
APPLICANT: Douvas, Angelina
TITLE OF INVENTION: Method of Diagnosing Caprine
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,855
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-SI 1988
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-616-855-10

Query Match 41.0%; Score 32; DB 1; Length 11;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12
DB 1 KRINKYKNKN 10

RESULT 8
US-08-616-854-10
Sequence 10, Application US/08616854

Patent No. 6033672
GENERAL INFORMATION:
APPLICANT: Douvas, Angelina
TITLE OF INVENTION: Caprine Arthritis-Encephalitis Virus
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell and Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,854
FILING DATE:
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-SI 1905
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-616-854-10

Query Match 41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 25;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12
DB 1 KRINKYKNKN 10

RESULT 9
US-08-468-337-10
Sequence 10, Application US/08468337
Patent No. 6221577
GENERAL INFORMATION:
APPLICANT: Muller, Martin
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Finnegan, Henderson, Farabow, Garrett &
ADDRESS: Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,337
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE P 41 23 760.9
FILING DATE: 18-JUL-1991
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 05552-1199-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-337-10

Query Match 41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12
Db 3 RDHIDYWKH 11

RESULT 10
US-09-758-318-10
Sequence 10, Application US/09758318
Patent No. 6531127
GENERAL INFORMATION:
APPLICANT: Muller, Martin
APPLICANT: Giesmann, Lutz
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
TITLE OF INVENTION: E1 and E2
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Flinnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/758,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/468,337
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 05552-1199-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-758-318-10

Query Match 41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 4 RDHNDYSKN 12
Db 3 RDHIDYWKH 11

RESULT 11
US-10-340-783-10
Sequence 10, Application US/10340783
Patent No. 6723317
GENERAL INFORMATION:
APPLICANT: Muller, Martin
APPLICANT: Giesmann, Lutz
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
TITLE OF INVENTION: E1 and E2
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSER: Flinnegan, Henderson, Farabow, Garrett &
ADDRESSER: Dunner
STREET: 1300 I Street, N.W., Suite 700
City: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,783
FILING DATE: 13-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,318
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/468,337
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Einaudi, Carol P.
REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 05552-1199-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4000
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-340-783-10

Query Match 41.0%; Score 32; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12
Db 3 RDHIDYWKH 11

RESULT 12
US-09-292-225-12
Sequence 12, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.
 TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
 FILE REFERENCE: AL-2-C3
 CURRENT APPLICATION NUMBER: US/09/292,225
 EARLIER FILING DATE: 1999-04-15
 EARLIER APPLICATION NUMBER: 60/098,909
 EARLIER FILING DATE: 1998-09-02
 EARLIER APPLICATION NUMBER: 60/085,295
 EARLIER FILING DATE: 1998-05-13
 EARLIER APPLICATION NUMBER: 60/098,565
 EARLIER FILING DATE: 1998-04-17
 EARLIER APPLICATION NUMBER: 09/062,013
 EARLIER FILING DATE: 1998-04-17
 NUMBER OF SEQ ID NOS: 49
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 12
 LENGTH: 18
 TYPE: PRT
 ORGANISM: Dermatophagoides fariniae
 US-09-292-225-12

Query Match 41.0%; Score 32; DB 2; Length 18;
 Best Local Similarity 83.3%; Pred. No. 42;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYSKIP 13
 Db 1 DYAKNP 6

RESULT 13
 US-08-934-915-29
 Sequence 29, Application US/08934915
 Patent No. 5932412

GENERAL INFORMATION:
 APPLICANT: DILLNER, JOAKIM
 APPLICANT: DILLNER, LENA
 APPLICANT: CHENG, HWEI-MING
 TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
 TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,
 TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,
 TITLE OF INVENTION: USEFUL IN IMMUNOSSAY FOR
 TITLE OF INVENTION: DIAGNOSTIC PURPOSES
 NUMBER OF SEQUENCES: 193
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: MASON & ASSOCIATES, P.A.
 STREET: 1757 U.S. HWY. 19 NORTH, SUITE 500
 CITY: CLEARWATER
 STATE: FLORIDA
 COUNTRY: U.S.A.

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: Windows 3.0
 SOFTWARE: Microsoft Word 6.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/934,915
 FILING DATE: 22-SEP-1997
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/949,836
 FILING DATE:
 ATTORNEY/AGENT INFORMATION:
 NAME: LOUISE A. FOUTCH
 REGISTRATION NUMBER: 37,133
 REFERENCE/DOCKET NUMBER: 1946.6
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 813-538-3800
 TELEFAX: 813-538-3820
 TELEX:
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-934-915-29

Query Match 41.0%; Score 32; DB 1; Length 20;
 Best Local Similarity 66.7%; Pred. No. 48;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSKN 12
 Db 12 RDHIDYWKH 20

RESULT 14
 US-08-614-935-12
 Sequence 12, Application US/08614935
 Patent No. 5804201

GENERAL INFORMATION:
 APPLICANT: King, Te P.
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
 TITLE OF INVENTION: ANTIGEN 5
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/614,935
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-156
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 12:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: Internal
 US-08-614-935-12

Query Match 39.7%; Score 31; DB 1; Length 20;
 Best Local Similarity 45.5%; Pred. No. 78;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNDYSKN 12
 Db 4 IKRHRNDPRON 14

RESULT 15
 US-09-130-287-12
 Sequence 12, Application US/09130287
 Patent No. 6106844


```
/ GENERAL INFORMATION:
/ APPLICANT: Tseng-Law, Janet
/ APPLICANT: Kobori, Joan A.
/ APPLICANT: Al-Abdaly, Fahad A.
/ APPLICANT: Guillermo, Roy
/ APPLICANT: Helgeson, Sam L.
/ APPLICANT: Deans, Robert J.
/ TITLE OF INVENTION: POSITIVE AND POSITIVE/NEGATIVE CELL
/ TITLE OF INVENTION: SELECTION MEDIATED BY PEPTIDE RELEASE
/ NUMBER OF SEQUENCES: 215
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Janice Guthrie, Ph.D.
/ STREET: P.O. Box 15210
/ CITY: Irvine
/ STATE: California
/ COUNTRY: USA
/ ZIP: 92713-5210
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/482,528
/ FILING DATE: 07-JUN-1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Guthrie, Janice
/ REGISTRATION NUMBER: 35,170
/ REFERENCE/DOCKET NUMBER: IT-4630CIP4
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (714) 440-5353
/ TELEFAX: (714) 553-1952
/ INFORMATION FOR SEQ ID NO: 209:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/
US-08-482-528-209

Query Match          35.9%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 RDNDYSK 11
       :|||:
       1 KDHQYSQ 8

RESULT 19
US-09-534-717-218
/ Sequence 218, Application US/09534717
/ Patent No. 6914128
/ GENERAL INFORMATION:
/ APPLICANT: Jochen, Salfeld et al.
/ TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
/ FILE REFERENCE: BBI-093CP
/ CURRENT APPLICATION NUMBER: US/09/534,717
/ EARLIER FILING DATE: 2000-03-24
/ EARLIER APPLICATION NUMBER: 60/126,603
/ EARLIER FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 218
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/
US-09-534-717-218

Query Match          35.9%; Score 28; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 SIKRDNDYS 10
       :|||:
       2 SYDRGHNFS 11

RESULT 20
US-09-434-840-81
/ Sequence 81, Application US/09434840
/ Patent No. 6620985
/ GENERAL INFORMATION:
/ APPLICANT: Glazebrook, Jane
/ APPLICANT: Jirage, Dayadevi
/ APPLICANT: Tootle, Tina L
/ APPLICANT: Zhou, Nan
/ APPLICANT: Fays, Bart
/ TITLE OF INVENTION: PAD4 COMPOSITIONS AND METHODS THEREFOR
/ FILE REFERENCE: 043503.0009
/ CURRENT APPLICATION NUMBER: US/09/434,840
/ EARLIER FILING DATE: 1999-11-04
/ EARLIER APPLICATION NUMBER: 09/190,733
/ EARLIER FILING DATE: 1998-11-12
/ NUMBER OF SEQ ID NOS: 85
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 81
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Arabidopsis thaliana
/
US-09-434-840-81

Query Match          35.9%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      4 RDNDYSK 11
       :|||:
       8 RDHSYEE 15

RESULT 21
US-09-142-524D-47
/ Sequence 47, Application US/09142524D
/ Patent No. 6719976
/ GENERAL INFORMATION:
/ APPLICANT: Sone, Toshio
/ APPLICANT: Kume, Akinori
/ APPLICANT: Dairiki, Kazuo
/ APPLICANT: Iwama, Akiyo
/ APPLICANT: Kino, Kohsuke
/ TITLE OF INVENTION: Peptide-based Immunotherapeutic Agent for Treating Allergic Disease
/ FILE REFERENCE: SPO-103
/ CURRENT APPLICATION NUMBER: US/09/142,524D
/ EARLIER FILING DATE: 1998-09-09
/ PRIOR APPLICATION NUMBER: PCT/JP97/00740
/ PRIOR FILING DATE: 1997-03-10
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 47
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Crytomera japonica
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(15)
/ OTHER INFORMATION: Cryj1 peptide, Figure 1, Row 33
/
US-09-142-524D-47

Query Match          35.9%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.8e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 DHNDYSKN 12
       :|||:
       :
```

Db 4 DHNSFSNS 11

RESULT 22

US-08-934-915-34

Sequence 34, Application US/08934915

Patent No. 5932412

GENERAL INFORMATION:

APPLICANT: DILNER, JOAKIM

APPLICANT: DILNER, LENA

APPLICANT: CHENG, HWEI-MING

TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN

TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8

TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 56,

TITLE OF INVENTION: USEFUL IN IMMUNOASSAY FOR

TITLE OF INVENTION: DIAGNOSTIC PURPOSES

NUMBER OF SEQUENCES: 193

CORRESPONDENCE ADDRESS:

ADDRESSEE: MASON & ASSOCIATES, P. A.

STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500

CITY: CLEARWATER

STATE: FLORIDA

COUNTRY: U.S.A.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: Windows 3.0

SOFTWARE: Microsoft Word 6.0

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/934,915

FILING DATE: 22-SEP-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/949,836

FILING DATE:

ATTORNEY/AGENT INFORMATION:

NAME: LOUISE A. Foulch

REGISTRATION NUMBER: 37,133

REFERENCE/DOCKET NUMBER: 1946.6

TELECOMMUNICATION INFORMATION:

TELEPHONE: 813-538-3800

TELEFAX: 813-538-3820

TELEX:

INFORMATION FOR SEQ ID NO: 34:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-934-915-34

Query Match 35.9%; Score 28; DB 1; Length 20;

Best Local Similarity 60.0%; Pred. No. 2.4e+02;

Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRHDNSKN 12

Db 7 KDDAEKYSKN 16

RESULT 23

US-08-467-023-42

Sequence 42, Application US/08467023

Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

APPLICANT: Pollock, Joanne;

APPLICANT: Bond, Julian F.;

APPLICANT: Garman, Richard D.;

APPLICANT: Kuo, Mei-Chang;

APPLICANT: Yeung, Siu-mei H.;

APPLICANT: Brauer, Andrew;

APPLICANT: Exley, Mark A.;

APPLICANT: Powers, Steven P.

TITLE OF INVENTION: Allergenic Proteins And Peptides From

TITLE OF INVENTION: Japanese Cedar Pollen

NUMBER OF SEQUENCES: 261

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.

STREET: 610 Lincoln St

CITY: Waltham

STATE: MA

COUNTRY: USA

ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/467,023

FILING DATE: June 6, 1995

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/350,225

FILING DATE: December 6, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jane E. Remillard

REGISTRATION NUMBER: 38,872

REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 227-7400

TELEFAX: (617) 227-5941

INFORMATION FOR SEQ ID NO: 42:

SEQUENCE CHARACTERISTICS:

LENGTH: 20 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

FRAGMENT TYPE: internal

US-08-467-023-42

Query Match 35.9%; Score 28; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 2.4e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 DRHDYSKN 12

Db 4 DHNSFSNS 11

RESULT 24

US-08-467-023-203

Sequence 203, Application US/08467023

Patent No. 6090386

GENERAL INFORMATION:

APPLICANT: Griffith, Irwin J.;

APPLICANT: Pollock, Joanne;

APPLICANT: Bond, Julian F.;

APPLICANT: Garman, Richard D.;

APPLICANT: Kuo, Mei-Chang;

APPLICANT: Yeung, Siu-mei H.;

APPLICANT: Brauer, Andrew;

APPLICANT: Exley, Mark A.;

APPLICANT: Powers, Steven P.

TITLE OF INVENTION: Allergenic Proteins And Peptides From

TITLE OF INVENTION: Japanese Cedar Pollen

NUMBER OF SEQUENCES: 261

CORRESPONDENCE ADDRESS:

ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.

STREET: 610 Lincoln St

CITY: Waltham

STATE: MA

COUNTRY: USA

ZIP: 02154

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 203:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-203

Query Match 35.9%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
Db 10 DHNSFSNS 17

RESULT 25
US-09-456-399-11
Sequence 11, Application US/09456399
Patent No. 6444801
GENERAL INFORMATION:
APPLICANT: Institute of CytoSignal Research, Inc.
TITLE OF INVENTION: Transcriptional Inhibitor
FILE REFERENCE: SI-802PCT-US
CURRENT APPLICATION NUMBER: US/09/456,399
CURRENT FILING DATE: 1999-12-08
PRIOR APPLICATION NUMBER: JP 1996-305043
PRIOR FILING DATE: 1996-11-15
PRIOR APPLICATION NUMBER: PCT/JP97/04127
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: US 09/308,160
PRIOR FILING DATE: 1999-05-14
NUMBER OF SEQ ID NOS: 15
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: an artificially
OTHER INFORMATION: Synthesized partial peptide sequence of SI-15
US-09-456-399-11

Query Match 35.3%; Score 27.5; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 1; Gaps 1;

QY 2 IKRD-HNDYSKN 12
Db 1 LORDPNNPYDKN 12

RESULT 26

US-09-901-187C-2
Sequence 2, Application US/09901187C
Patent No. 6780971
GENERAL INFORMATION:
APPLICANT: WOLOZIN, BENJAMIN
APPLICANT: OSTRETOVA-GOLTS, NATALIE
APPLICANT: LEBOWITZ, MICHAEL
TITLE OF INVENTION: METHODS FOR PREVENTING NEURAL TISSUE DAMAGE AND FOR THE
TREATMENT OF ALPHA-SYNUCLEIN DISEASES
FILE REFERENCE: 58729 (48933)
CURRENT APPLICATION NUMBER: US/09/901,187C
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: 60/279,199
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: 60/217,319
PRIOR FILING DATE: 2000-07-07
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-09-901-187C-2

Query Match 34.6%; Score 27; DB 2; Length 7;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSKNPM 14
Db 2 YAKNPI 7

RESULT 27
US-09-419-381-33
Sequence 33, Application US/09419381
Patent No. 6747135
GENERAL INFORMATION:
APPLICANT: No. 6747135an, Garry P.
APPLICANT: Rozhnov, Michael N.
TITLE OF INVENTION: Fluorescent Dye Binding Peptides
FILE REFERENCE: A65681-1/DJB/RMS/DSS
CURRENT APPLICATION NUMBER: US/09/419,381
CURRENT FILING DATE: 1999-10-15
PRIOR APPLICATION NUMBER: 60/104,465
PRIOR FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 33
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-419-381-33

Query Match 34.6%; Score 27; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9
Db 2 HNDY 5

RESULT 28
US-08-980-326-9
Sequence 9, Application US/08980326
Patent No. 6703197
GENERAL INFORMATION:
APPLICANT: Gravel, Roy A.
APPLICANT: Rozen, Rima
APPLICANT: Leclerc, Daniel

```
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 9
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-08-980-326-9
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
        :|:|:|:|
DB      2 TVKGDVHDIGKN 13
```

```
RESULT 29
US-08-980-326-10
/ Sequence 10, Application US/08980326
/ Patent No. 6703197
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 10
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Cyanobacterium synechocystis
US-08-980-326-10
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
        :|:|:|:|
DB      2 TVKGDVHDIGKN 13
```

```
RESULT 30
US-08-980-326-11
/ Sequence 11, Application US/08980326
/ Patent No. 6703197
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
```

```
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 11
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Mycobacterium leprae
US-08-980-326-11
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
        :|:|:|:|
DB      2 TVKGDVHDIGKN 13
```

```
RESULT 31
US-08-980-326-12
/ Sequence 12, Application US/08980326
/ Patent No. 6703197
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 12
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Hemophilus influenzae
US-08-980-326-12
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
        :|:|:|:|
DB      2 TVKGDVHDIGKN 13
```

```
RESULT 32
US-08-980-326-13
/ Sequence 13, Application US/08980326
/ Patent No. 6703197
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
```

```
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PasteSeq for Windows Version 3.0
/ SEQ ID NO 13
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-08-980-326-13
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 33
US-08-980-326-14
/ Sequence 14, Application US/08980326
/ Patent No. 6703197
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002003
/ CURRENT APPLICATION NUMBER: US/08/980,326
/ CURRENT FILING DATE: 1997-11-26
/ EARLIER APPLICATION NUMBER: 60/050,310
/ EARLIER FILING DATE: 1997-06-20
/ EARLIER APPLICATION NUMBER: 60/031,964
/ EARLIER FILING DATE: 1996-11-27
/ NUMBER OF SEQ ID NOS: 75
/ SOFTWARE: PasteSeq for Windows Version 3.0
/ SEQ ID NO 14
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-08-980-326-14
```

```
Query Match          34.6%; Score 27; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 2.3e+02;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 34
US-09-142-524D-46
/ Sequence 46, Application US/09142524D
/ Patent No. 6719976
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Sone, Toshio
/ APPLICANT: Kume, Akinori
/ APPLICANT: Daijiki, Kazuo
/ APPLICANT: Iwama, Akiko
/ APPLICANT: Kuno, Kohsuke
/ TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Dise.
/ FILE REFERENCE: SPO-103
/ CURRENT APPLICATION NUMBER: US/09/142,524D
/ CURRENT FILING DATE: 1998-09-09
/ PRIOR APPLICATION NUMBER: PCT/JP97/00740
/ PRIOR FILING DATE: 1997-03-10
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 46
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Cryptosporidia japonica
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)-(15)
/ OTHER INFORMATION: Cryj1 peptide, Figure 1, Row 32
US-09-142-524D-46
```

```
Query Match          34.6%; Score 27; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDYS 10
Db      9 DHNSFS 14
```

```
RESULT 35
US-09-938-901A-36
/ Sequence 36, Application US/09938901A
/ Patent No. 6939949
/ GENERAL INFORMATION:
/ APPLICANT: Kuramitsu, Seiki
/ APPLICANT: Yokoyama, Shigeoyuki
/ TITLE OF INVENTION: No. 6939999e1 DNA Repair Enzymes, Nucleic Acids Encoding DNA Repa
/ FILE REFERENCE: 11283-013001/PH1261 US
/ CURRENT APPLICATION NUMBER: US/09/938,901A
/ CURRENT FILING DATE: 2001-08-24
/ PRIOR APPLICATION NUMBER: JP 47762/2001
/ PRIOR FILING DATE: 2001-02-23
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 36
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-09-938-901A-36
```

```
Query Match          34.6%; Score 27; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
Db      8 DNDTPPKN 15
```

```
RESULT 36
US-08-467-023-41
/ Sequence 41, Application US/08467023
/ Patent No. 6090386
/ GENERAL INFORMATION:
/ APPLICANT: Griffith, Irwin J.;
/ APPLICANT: Pollock, Joanne;
/ APPLICANT: Bond, Julian F.;
/ APPLICANT: Garman, Richard D;
/ APPLICANT: Kuo, Mei-Chang;
```


APPLICANT: Yeung, Shu-mei H.;
APPLICANT: Brauer, Andrew;
APPLICANT: Exley, Mark A.;
APPLICANT: Powers, Steven P.
TITLE OF INVENTION: Allergenic Proteins And Peptides From
TITLE OF INVENTION: Japanese Cedar Pollen
NUMBER OF SEQUENCES: 261
CORRESPONDENCE ADDRESS:
ADDRESSEE: Immunologic Pharmaceutical Corporation, Inc.
STREET: 610 Lincoln St
CITY: Waltham
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,023
FILING DATE: June 6, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/350,225
FILING DATE: December 6, 1994
ATTORNEY/AGENT INFORMATION:
NAME: Jane E. Remillard
REGISTRATION NUMBER: 38,872
REFERENCE/DOCKET NUMBER: 025.6 USD2 (IMI-028CPD2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 227-5941
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-467-023-41

Query Match 34.6%; Score 27; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10
DB 14 DHNSPS 19

RESULT 37
US-09-311-784A-441
Sequence 441, Application US/09311784A
Patent No. 6534482
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Hermanson, Gary G.
APPLICANT: Sette, Alessandro
APPLICANT: Ishioka, Glenn Y.
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert W.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Expression Vectors for Stimulating an
TITLE OF INVENTION: Immune Response and Methods of Using the Same
FILE REFERENCE: 39963-20022.01
CURRENT APPLICATION NUMBER: US/09/311,784A
CURRENT FILING DATE: 1999-05-13
PRIOR APPLICATION NUMBER: US 60/085,751
PRIOR FILING DATE: 1998-05-15
NUMBER OF SEQ ID NOS: 463
SOFTWARE: PaeSeq for Windows Version 3.0
SEQ ID NO 441

LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: PE LSA1 59 (peptide 1167.47)
US-09-311-784A-441

Query Match 33.3%; Score 26; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HDYSK 11
DB 5 HNSYK 10

RESULT 38
US-09-611-829-6
Sequence 6, Application US/09611829
Patent No. 6713066
GENERAL INFORMATION:
APPLICANT: COLLINS, Peter L.
APPLICANT: MURPHY, Brian R.
APPLICANT: BERMINGHAM, Alison
TITLE OF INVENTION: PRODUCTION OF ATTENUATED RESPIRATORY SYNCYTIAL VIRUS
TITLE OF INVENTION: VACCINES INVOLVING MODIFICATION OF M ORF2
FILE REFERENCE: 15280-4031005
CURRENT APPLICATION NUMBER: US/09/611,829
CURRENT FILING DATE: 2000-07-07
PRIOR APPLICATION NUMBER: 60/143,097
PRIOR FILING DATE: 1999-07-09
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 6
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Amino acid
OTHER INFORMATION: sequence corresponding to nucleotide sequence
OTHER INFORMATION: spanning M2 ORF1 and M2 ORF2
US-09-611-829-6

Query Match 33.3%; Score 26; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.8e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDYSK 12
DB 2 NDPAK 7

RESULT 39
US-08-260-582-18
Sequence 18, Application US/08260582
Patent No. 5635182
GENERAL INFORMATION:
APPLICANT: McCoy, John M.
APPLICANT: Lu, Zhijian
TITLE OF INVENTION: METHOD OF DETECTING LIGAND
TITLE OF INVENTION: INTERACTIONS
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridgepark Drive
CITY: Cambridge
STATE: Massachusetts
COUNTRY: U.S.
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

```
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/260,582
/ FILING DATE: 16-JUN-1994
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Meinerdt, M. C.
/ REGISTRATION NUMBER: 31,544
/ REFERENCE/DOCKET NUMBER: GI 5236
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 876-1170
/ TELEFAX: (617) 876-5851
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
US-08-260-582-18
```

```
Query Match 33.3%; Score 26; DB 1; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 RDHNDYS 10
Db 3 RDHDKFS 9
```

```
RESULT 40
PCT-US95-05471-18
/ Sequence 18, Application PC/TUS9505471
/ GENERAL INFORMATION:
/ APPLICANT:
/ TITLE OF INVENTION: METHOD OF DETECTING LIGAND INTERACTIONS
/ NUMBER OF SEQUENCES: 76
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25 (SPO)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US95/05471
/ INFORMATION FOR SEQ ID NO: 18:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 12 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ HYPOTHEICAL: NO
/ ANTI-SENSE: NO
PCT-US95-05471-18
```

```
Query Match 33.3%; Score 26; DB 4; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 4 RDHNDYS 10
Db 3 RDHDKFS 9
```

```
RESULT 41
US-09-391-104-15
/ Sequence 15, Application US/09391104
/ Patent No. 6399371
/ GENERAL INFORMATION:
/ APPLICANT: Abbott Laboratories
/ APPLICANT: Falduto, Michael T.
```

```
/ APPLICANT: Magnuson, Scott R.
/ APPLICANT: Morgan, Douglas W.
/ TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEASE GENE,
/ TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
/ TITLE OF INVENTION: OF USING SAME
/ FILE REFERENCE: 6073.US.P1
/ CURRENT APPLICATION NUMBER: US/09/391,104
/ CURRENT FILING DATE: 1999-09-07
/ PRIOR APPLICATION NUMBER: US 08/814,394
/ PRIOR FILING DATE: 1997-03-11
/ NUMBER OF SEQ ID NOS: 35
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 15
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptides
US-09-391-104-15
```

```
Query Match 33.3%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 DHND 8
Db 4 DHND 7
```

```
RESULT 42
US-09-671-089-53
/ Sequence 53, Application US/09671089
/ Patent No. 6780846
/ GENERAL INFORMATION:
/ APPLICANT: O'Mahony, Daniel J.
/ APPLICANT: Lambkin, Imelda J.
/ TITLE OF INVENTION: MEMBRANE TRANSLLOCATING PEPTIDE DRUG DELIVERY SYSTEM
/ FILE REFERENCE: E1067/20018
/ CURRENT APPLICATION NUMBER: US/09/671,089
/ CURRENT FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: 60/156,246
/ PRIOR FILING DATE: 1999-09-27
/ NUMBER OF SEQ ID NOS: 59
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 53
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: D form retroinversion peptide
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: danylated
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (2)~(16)
/ OTHER INFORMATION: D form amino acid
US-09-671-089-53
```

```
Query Match 33.3%; Score 26; DB 2; Length 16;
Best Local Similarity 27.3%; Pred. No. 4.3e+02;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 IKRDHNDYSKN 12
Db 5 LRRNHSKRN 15
```

```
RESULT 43
US-08-616-844-50
/ Sequence 50, Application US/08616844
/ Patent No. 5849578
```

GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITION AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/616,844
FILING DATE: 15-MAR-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-053
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-616-844-50

Query Match 33.3%; Score 26; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
DB 5 EYKNP 10

RESULT 44
US-08-599-654-50
Sequence 50, Application US/08599654
Patent No. 5883925
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,654
FILING DATE: 09-FEB-1996
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-599-654-50

Query Match 33.3%; Score 26; DB 1; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
DB 5 EYKNP 10

RESULT 45
US-08-944-868A-50
Sequence 50, Application US/08944868A
Patent No. 6018025
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,868A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/599,654
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A.

REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-041
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 780-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-944-868A-50

Query Match 33.3%; Score 26; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
: ||||
Db 5 EYKNP 10

RESULT 46
US-08-944-423A-50
Sequence 50, Application US/08944423A
Patent No. 6020463
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: WINDOWS 95
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,423A
FILING DATE: 06-OCT-1997
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: JUN-07-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide

US-08-944-423A-50

Query Match 33.3%; Score 26; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
: ||||
Db 5 EYKNP 10

RESULT 47
US-08-944-496-50
Sequence 50, Application US/08944496
Patent No. 6124433
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/944,496
FILING DATE: 06-OCT-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-944-496-50

Query Match 33.3%; Score 26; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 4.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
: ||||
Db 5 EYKNP 10

RESULT 48
US-09-383-062-6

/ Sequence 6, Application US/09383062
/ Patent No. 6670194
/ GENERAL INFORMATION:
/ APPLICANT: Aebereold, Rudolf H.
/ APPLICANT: Gelb, Michael H
/ APPLICANT: Gyg1, Steven
/ APPLICANT: Scott, C R
/ APPLICANT: Turecek, Prantisek
/ APPLICANT: Garber, Scott A
/ APPLICANT: Rist, Beate
/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
/ FILE REFERENCE: 64-98
/ CURRENT APPLICATION NUMBER: US/09/383,062
/ PRIOR APPLICATION NUMBER: 1999-08-25
/ PRIOR FILING DATE: 1999-08-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Test peptide
US-09-383-062-6

Query Match 33.3%; Score 26; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12
| | | | |
Db 1 KDDQNPSSN 10

RESULT 49
US-09-839-884-6
/ Sequence 6, Application US/0983884
/ Patent No. 6852544
/ GENERAL INFORMATION:
/ APPLICANT: Aebereold, Rudolf H.
/ APPLICANT: Gelb, Michael H
/ APPLICANT: Gyg1, Steven
/ APPLICANT: Scott, C R
/ APPLICANT: Turecek, Prantisek
/ APPLICANT: Garber, Scott A
/ APPLICANT: Rist, Beate
/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
/ FILE REFERENCE: 64-98A
/ CURRENT APPLICATION NUMBER: US/09/839,884
/ PRIOR APPLICATION NUMBER: 2001-04-20
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 60/097,788
/ PRIOR FILING DATE: 1998-08-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Test peptide
US-09-839-884-6

Query Match 33.3%; Score 26; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 4.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12
| | | | |

Db 1 KDDQNPSSN 10

RESULT 50
US-07-931-931A-5
/ Sequence 5, Application US/07931931A
/ Patent No. 5521097
/ GENERAL INFORMATION:
/ APPLICANT: Uchida, Toyooki
/ APPLICANT: Taugita, Akira
/ APPLICANT: Takamoto, Keiji
/ APPLICANT: Sarake, Kazuo
/ TITLE OF INVENTION: Method of Determining Amino Acid
/ TITLE OF INVENTION: Sequence of Protein or Peptide
/ Patent No. 5521097
/ NUMBER OF SEQUENCES: 6
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Adams & Wilks
/ STREET: 500 Fifth Avenue Suite 3200
/ CITY: New York
/ STATE: New York
/ COUNTRY: United States of America
/ ZIP: 10110
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb storage
/ COMPUTER: IBM PS/2, Model 30
/ OPERATING SYSTEM: PC-DOS 3.30
/ SOFTWARE: Wordperfect 5.1
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/931,931A
/ FILING DATE: 19920818
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 03-217437
/ FILING DATE: 28 AUG 1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 03-300818
/ FILING DATE: 15 NOV 1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Adams, Bruce L.
/ REGISTRATION NUMBER: 25,386
/ REFERENCE/DOCKET NUMBER: S004-2354
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 575-2600
/ TELEFAX: (212) 575-2604
/ INFORMATION FOR SEQ ID NO: 5:
/ LENGTH: 8
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear chain
US-07-931-931A-5

Query Match 32.1%; Score 25; DB 1; Length 8;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNNDY 9
| | | | |
Db 1 KKKHPDY 7

RESULT 51
US-08-408-604A-152
/ Sequence 152, Application US/08408604A
/ Patent No. 5801149
/ GENERAL INFORMATION:
/ APPLICANT: Shoelson, Steven
/ TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
/ NUMBER OF SEQUENCES: 211
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: LAHIVE & COCKFIELD
/ STREET: 60 State Street, Suite 510

CITY: Boston
STATE: Massachusetts
COUNTRY: USA
ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/408,604A
FILING DATE: 21-MAR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/134,558
FILING DATE: 08-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/959,949
FILING DATE: 09-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/722,359
FILING DATE: 19-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Myers, Louis
REGISTRATION NUMBER: 35,965
REFERENCE/DOCKET NUMBER: JDP-014CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 152:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-408-604A-152

Query Match 32.1%; Score 25; DB 1; Length 11;
Best Local Similarity 44.4%; Pred. No. 4.2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKNP 13
|||:
Db 1 DHQXYNDMP 9

RESULT 52
US-08-974-549A-145
Sequence 145, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-145

Query Match 32.1%; Score 25; DB 2; Length 11;
Best Local Similarity 55.6%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYS 10
|||:
Db 1 IKSGNDYS 9

RESULT 53
US-09-402-181B-145
Sequence 145, Application US/09402181B
Patent No. 6610839
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/402,1818
FILING DATE: 29-Sep-1997
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Augenhue, Scott L.
REGISTRATION NUMBER: 42,271
REFERENCE/DOCKET NUMBER: 015389-002620US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-09-402-181B-145
Query Match 32.1% Score 25; DB 2; Length 11;
Best Local Similarity 55.6% Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IKRDHNDYS 10
DB 1 IKSGNEDYS 9
RESULT 54
US-09-721-456-145
Sequence 145, Application US/09721456
Patent No. 6617110
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Morin, Gregg B.
Harley, Calvin B.
Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESS: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/721,456
FILING DATE: 22-No. 6617110-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 145:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 145:
US-09-721-456-145
Query Match 32.1% Score 25; DB 2; Length 11;
Best Local Similarity 55.6% Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IKRDHNDYS 10
DB 1 IKSGNEDYS 9
RESULT 55
US-10-185-815A-11
Sequence 11, Application US/10185815A
Patent No. 6916789
GENERAL INFORMATION:
APPLICANT: Elan Corporation, plc

APPLICANT: O'Mahony, Daniel
APPLICANT: Lambkin, Imelda
APPLICANT: Higgins, Lisa
TITLE OF INVENTION: Peyer's Patch And/Or M-Cell Targeting Ligands
FILE REFERENCE: P26,480-A USA
CURRENT APPLICATION NUMBER: US/10/185,815A
CURRENT FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/302,591
PRIOR FILING DATE: 2001-07-02
NUMBER OF SEQ ID NOS: 100
SOFTWARE: Patentin version 3.1
SEQ ID NO 11
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: polypeptide ligand
US-10-185-815A-11

Query Match 32.1%; Score 25; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 4.6e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSRNPM 14
:||||:
Db 3 HSKNPV 8

RESULT 56
US-08-837-226-3
Sequence 3, Application US/08837226
Patent No. 6043216
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Lieske, John C.
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING
AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF
TITLE OF INVENTION: CRYSTALS TO KIDNEY CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOPER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Cityfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,226
FILING DATE: 08-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,005
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide

US-08-837-226-3

Query Match 32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11
:||||:
Db 2 NNDYSQ 7

RESULT 57
US-08-811-583-13
Sequence 13, Application US/08811583
Patent No. 6218142
GENERAL INFORMATION:
APPLICANT: Massenegger, Michael
APPLICANT: Riedel, Leonhard
APPLICANT: Schiebel, Winfried
APPLICANT: Sanger, Heinz
TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
POLYPEPTIDES HAVING THE ENZYMATIC ACTIVITY OF AN
TITLE OF INVENTION: RNA-DIRECTED RNA POLYMERASE (RDRP)
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: FISH & NEAVE
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10020
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/811,583
FILING DATE: 05-MAR-1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Haley, James F.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MPG-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-596-9000
TELEFAX: 212-596-9090
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-811-583-13

Query Match 32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.1e+02; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRDRND 8
:||||:
Db 7 KRPHNE 12

RESULT 58
US-09-484-114B-14
Sequence 14, Application US/09484114B
Patent No. 6329178
GENERAL INFORMATION:
APPLICANT: Patel, Premal H.
APPLICANT: Loeb, Lawrence A.
TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE


```

: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/484,114B
: CURRENT FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-484-114B-14

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12

RESULT 59
US-09-484-114B-15
: Sequence 15, Application US/09484114B
: Patent No. 6329178
: GENERAL INFORMATION:
: APPLICANT: Patel, Premal H.
: TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/484,114B
: CURRENT FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 15
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-484-114B-15

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12

RESULT 60
US-09-537-226-3
: Sequence 3, Application US/09537226
: Patent No. 6482934
: GENERAL INFORMATION:
: APPLICANT: TOBACK, P. GARY
: APPLICANT: LIESKE, JOHN C.
: TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
: TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO
: TITLE OF INVENTION: KIDNEY CELLS
: FILE REFERENCE: 21459/90606
: CURRENT APPLICATION NUMBER: US/09/537,226
: CURRENT FILING DATE: 2000-03-28
: PRIOR APPLICATION NUMBER: 08/389,005
: NUMBER OF SEQ ID NOS: 23
: SOFTWARE: PatentIn Ver. 2.1
: SEQ ID NO 3
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: Description of Artificial Sequence: Synthetic
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: OTHER INFORMATION: peptide
US-09-537-226-3

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      6 HNDYSK 11
      :|||:
Db      2 NNDYSQ 7

RESULT 61
US-09-981-194-14
: Sequence 14, Application US/09981194
: Patent No. 6602695
: GENERAL INFORMATION:
: APPLICANT: Patel, Premal H.
: TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/981,194
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: US/09/484,114
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 14
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-981-194-14

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12

RESULT 62
US-09-981-194-15
: Sequence 15, Application US/09981194
: Patent No. 6602695
: GENERAL INFORMATION:
: APPLICANT: Patel, Premal H.
: APPLICANT: Loeb, Lawrence A.
: TITLE OF INVENTION: DNA POLYMERASE MUTANT HAVING ONE OR MORE
: TITLE OF INVENTION: MUTATIONS IN THE ACTIVE SITE
: FILE REFERENCE: 74890002US00
: CURRENT APPLICATION NUMBER: US/09/981,194
: CURRENT FILING DATE: 2001-10-16
: PRIOR APPLICATION NUMBER: US/09/484,114
: PRIOR FILING DATE: 2000-01-14
: NUMBER OF SEQ ID NOS: 40
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 15
: LENGTH: 13
: TYPE: PRT
: ORGANISM: Escherichia coli
US-09-981-194-15

Query Match      32.1%; Score 25; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 5.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      8 DYSKNPM 14
      |||:|:
Db      6 DYSQNEL 12
```

RESULT 63
US-09-765-111A-47
Sequence 47, Application US/09765111A
Patent No. 6723506
GENERAL INFORMATION:
APPLICANT: Fletcher, Jonathan A.
APPLICANT: Kroll, Todd G.
TITLE OF INVENTION: PAX6-PPARGAMMA NUCLEIC ACID MOLECULES
FILE REFERENCE: B0801/7196/ERP/MAT
CURRENT APPLICATION NUMBER: US/09/765,111A
PRIORITY FILING DATE: 2001-01-18
PRIORITY APPLICATION NUMBER: US 60/177,109
PRIORITY FILING DATE: 2000-01-20
PRIORITY APPLICATION NUMBER: US 60/225,079
PRIORITY FILING DATE: 2000-08-14
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 14
TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: Unknown
LOCATION: (8)...(8)
OTHER INFORMATION: Xaa = any amino acid
US-09-765-111A-47

Query Match 32.1%; Score 25; DB 2; Length 14;
Best Local Similarity 33.3%; Pred. No. 5.5e+02;
Matches 4; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDYKKN 12
: : : : :
DB 3 NISQKSEYSGN 14

RESULT 64
US-08-967-101-167
Sequence 167, Application US/08967101
Patent No. 5840540
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/967,101
FILING DATE: 10-NOV-1997
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100

INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-967-101-167

Query Match 32.1%; Score 25; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDND 8
: : : : :
DB 6 ROEHD 11

RESULT 65
US-08-592-541-167
Sequence 167, Application US/08592541
Patent No. 5986054
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Pitcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-592-541-167

Query Match 32.1%; Score 25; DB 1; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDND 8
: : : : :
DB 6 ROEHD 11

RESULT 66
US-09-124-698-167
Sequence 167, Application US/09124698
Patent No. 6117978
GENERAL INFORMATION:

APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,698
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-124-698-167

Query Match 32.1%; Score 25; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNH 8
Db 6 ROEHD 11

RESULT 67
US-09-127-480-167
Sequence 167, Application US/09127480
Patent No. 6194153
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/127,480

FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-127-480-167

Query Match 32.1%; Score 25; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNH 8
Db 6 ROEHD 11

RESULT 68
US-08-496-841C-164
Sequence 164, Application US/08496841C
Patent No. 6210919
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROMMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 175
CORRESPONDENCE ADDRESS:
ADDRESSEE: Darby & Darby, PC
STREET: 805 Third Avenue
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10022
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/496,841C
FILING DATE: 28-Jun-1995
CLASSIFICATION: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Paul F. Fehner, Ph.D.
REGISTRATION NUMBER: 35,135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 527-7700
TELEFAX: (212) 753-6237
INFORMATION FOR SEQ ID NO: 164:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 164:
US-08-496-841C-164

Query Match 32.1%; Score 25; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;

Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 3 KRDNH 8
Db 6 RQEHND 11

RESULT 69
US-09-124-523-167
Sequence 167, Application US/09124523
Patent No. 6395960
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
TITLE OF INVENTION: TO ALZHEIMER'S DISEASE
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT
STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/124,523
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-124-523-167

Query Match 32.1%; Score 25; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNH 8
Db 6 RQEHND 11

RESULT 70
US-09-636-796A-167
Sequence 167, Application US/09636796A
Patent No. 6485911
GENERAL INFORMATION:
APPLICANT: ST. GEORGE-HYSLOP, PETER H
APPLICANT: ROWMENS, JOHANNA M
APPLICANT: FRASER, PAUL E
TITLE OF INVENTION: GENETIC SEQUENCES AND PROTEINS RELATED
TO ALZHEIMER'S DISEASE
NUMBER OF SEQUENCES: 183
CORRESPONDENCE ADDRESS:
ADDRESSEE: TESTA, HURWITZ & THIBEAULT

STREET: High Street Tower - 125 High Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/636,796A
FILING DATE: 11-Aug-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/592,541
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Pletcher, Edmund R.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 248-7000
TELEFAX: (617) 248-7100
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 167:
US-09-636-796A-167

Query Match 32.1%; Score 25; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 5.9e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDNH 8
Db 6 RQEHND 11

RESULT 71
US-08-480-190-188
Sequence 188, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignall
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993

APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-188

Query Match 32.1%; Score 25; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9
| | | |
| | | |
Db 8 RGHNY 13

RESULT 72
US-08-488-379-188
Sequence 188, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignal
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid

STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-188

Query Match 32.1%; Score 25; DB 1; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9
| | | |
| | | |
Db 8 RGHNY 13

RESULT 73
US-08-837-226-7
Sequence 7, Application US/08837226
Patent No. 6043216
GENERAL INFORMATION:
APPLICANT: Toback, F. Gary
APPLICANT: Lieske, John C.
TITLE OF INVENTION: METHODS AND COMPOSITION FOR DETECTING
TITLE OF INVENTION: AND TREATING KIDNEY DISEASES ASSOCIATED WITH ADHESION OF
TITLE OF INVENTION: CRYSTALS TO KIDNEY CELLS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BRINKS, HOFER, GILSON & LIONE
STREET: NBC Tower - Suite 3600, 455 N. Clevfront
STREET: Plaza Drive
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60611-5599
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/837,226
FILING DATE: 08-APR-1997
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/389,005
FILING DATE: 15-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Martin, Alice O.
REGISTRATION NUMBER: 35,601
REFERENCE/DOCKET NUMBER: 7814/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-321-4200
TELEFAX: 312-321-4299
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-837-226-7

Query Match 32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11
: | | | |
: | | | |
Db 5 NNDYSQ 10

RESULT 74
US-09-025-769B-238
Sequence 238, Application US/09025769B
Patent No. 630064

GENERAL INFORMATION:
APPLICANT: Knappik, Achim
APPLICANT: Pack, Peter
APPLICANT: Ilag, Vic
APPLICANT: Ge, Laming
APPLICANT: Moroney, Simon
APPLICANT: Plueckhuhn, Andreas
TITLE OF INVENTION: Protein/(Poly) peptide libraries
NUMBER OF SEQUENCES: 373
CORRESPONDENCE ADDRESS:
ADDRESSEE: James P. Haley, Jr., Esq. c/o Fish & Neave
STREET: 1251 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10021
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/025,769B
FILING DATE: 18-FEB-1998
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James P. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9090
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-025-769B-238

Query Match 32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 RDNDYSKNPM 14
DB 5 RDNFSY--DPM 13

RESULT 75
US-09-537-226-21
Sequence 21, Application US/09537226
Patent No. 6482934
GENERAL INFORMATION:
APPLICANT: TOBACK, F. GARY
APPLICANT: LIESKE, JOHN C.
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
TITLE OF INVENTION: KIDNEY DISEASES ASSOCIATED WITH ADHESION OF CRYSTALS TO
FILE REFERENCE: 21459/90606
CURRENT APPLICATION NUMBER: US/09/537,226
CURRENT FILING DATE: 2000-03-28
PRIOR APPLICATION NUMBER: 08/389,005
PRIOR FILING DATE: 1995-02-15
NUMBER OF SEQ ID NOS: 23
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 21
LENGTH: 16
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-537-226-21

Query Match 32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11
DB 5 NNDYSQ 10

RESULT 76
US-08-475-399A-188
Sequence 188, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-188

Query Match 32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9
DB 8 RGNQY 13

RESULT 77

```

US-08-077-255A-188
; Sequence 188, Application US/08077255A
; Patent No. 6696061
; GENERAL INFORMATION:
; APPLICANT: Robert G. Urban
; APPLICANT: Roman M. Chicz
; APPLICANT: Mario A. A. Vignali
; APPLICANT: Mary L. Hedley
; APPLICANT: Lawrence J. Stern
; APPLICANT: Jack L. Strominger
; TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
; NUMBER OF SEQUENCES: 274
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: U.S.A.
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
; COMPUTER: IBM PS/2 Model 502 or 55SX
; OPERATING SYSTEM: MS-DOS (Version 5.0)
; SOFTWARE: WordPerfect (Version 5.1)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/077,255A
; FILING DATE: June 15, 1993
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/925,460
; FILING DATE: August 11, 1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 00246/168001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 542-5070
; TELEFAX: (617) 542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16
; TYPE: amino acid
; STRANDEDNESS: linear
; TOPOLOGY: linear
; US-08-077-255A-188

Query Match      32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      4 RDHNDY 9
      |||||
      8 RGNHNY 13

RESULT 78
US-09-490-070A-238
; Sequence 238, Application US/09490070A
; Patent No. 6696248
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Colin G. Sandercock, Esq. c/o Heller Ehrman
; WHITE & McAlliff
; STREET: 1666 K Street, N.W., Suite 300

```

```

; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20006
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,070A
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: EP 95 11 3021.0
; FILING DATE: 18-AUG-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Colin G. Sandercock, Esq.
; REGISTRATION NUMBER: 31,298
; REFERENCE/DOCKET NUMBER: 37629-0005
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 912-2000
; TELEFAX: (202) 912-2020
; INFORMATION FOR SEQ ID NO: 238:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 16 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
; SEQUENCE DESCRIPTION: SEQ ID NO: 238:

US-09-490-070A-238

Query Match      32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY      4 RDHNDYSKNPM 14
      |||||
      5 RDNHNSY-DEW 13

RESULT 79
US-09-490-153-238
; Sequence 238, Application US/09490153
; Patent No. 6706484
; GENERAL INFORMATION:
; APPLICANT: Knappik, Achim
; APPLICANT: Pack, Peter
; APPLICANT: Ilag, Vic
; APPLICANT: Ge, Liming
; APPLICANT: Moroney, Simon
; APPLICANT: Plueckhuhn, Andreas
; TITLE OF INVENTION: Protein/(Poly)peptide libraries
; NUMBER OF SEQUENCES: 373
; CORRESPONDENCE ADDRESS:
; ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave
; STREET: 1251 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10021
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/490,153
; FILING DATE: 24-Jan-2000
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,769B
; FILING DATE: 18-FEB-1998

```

APPLICATION NUMBER: EP 95 11 3021.0
FILING DATE: 18-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: James F. Haley, Jr., Esq.
REGISTRATION NUMBER: 27,794
REFERENCE/DOCKET NUMBER: MORPHO/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)596-9000
TELEFAX: (212)596-9090
INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 238:
US-09-490-153-238

Query Match 32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 RDNDYSKNPM 14
DB 5 RDNFSY--DPM 13

RESULT 80
US-09-490-324-238

Sequence 238, Application US/09490324
Patent No. 6828422

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

Ge, Peter

Ilag, Vic

Plueckhuhn, Andreas

TITLE OF INVENTION: Protein(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSEE: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 238:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid

STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 238:
US-09-490-324-238

Query Match 32.1%; Score 25; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 6.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

QY 4 RDNDYSKNPM 14
DB 5 RDNFSY--DPM 13

RESULT 81
PCT-US93-07545-188

Sequence 188, Application PC/TUS9307545

GENERAL INFORMATION:

APPLICANT: Robert G. Urban

APPLICANT: Roman M. Chicz

APPLICANT: Dario A. A. Vignall

APPLICANT: Mary L. Hedley

APPLICANT: Lawrence J. Stern

TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES

NUMBER OF SEQUENCES: 273

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: Wordperfect (Version 5.1)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07545

FILING DATE: 19930811

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 188:

SEQUENCE CHARACTERISTICS:

LENGTH: 16

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US93-07545-188

Query Match 32.1%; Score 25; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 6.4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDNDY 9
DB 8 RGNRY 13

RESULT 82

US-09-177-249-281
; Sequence 281, Application US/09177249
; Patent No. 6229064
; GENERAL INFORMATION:
; APPLICANT: Fiecher, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramon
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/177,249
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; EARLIER FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-177-249-281

Query Match 32.1%; Score 25; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKNPM 14
DB 1 DTSANPM 7

RESULT 83
US-09-066-330-1
; Sequence 1, Application US/09066330A
; Patent No. 6511666
; GENERAL INFORMATION:
; APPLICANT: Reynolds, Eric C.
; APPLICANT: Bhogal, Peter S.
; APPLICANT: Stakek, Nada
; TITLE OF INVENTION: DIAGNOSTICS AND TREATMENTS OF PERIODONTAL DISEASE
; FILE REFERENCE: Reynolds
; CURRENT APPLICATION NUMBER: US/09/066,330A
; CURRENT FILING DATE: 1998-09-15
; EARLIER APPLICATION NUMBER: PN 6275
; EARLIER FILING DATE: 1995-10-30
; EARLIER APPLICATION NUMBER: PCT/AU96/00673
; EARLIER FILING DATE: 1996-10-30
; NUMBER OF SEQ ID NOS: 15
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Organism: Porphyromonas gingivalis
US-09-066-330-1

Query Match 32.1%; Score 25; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14
DB 5 DHGDLVNTPV 14

RESULT 84
US-09-812-283-281
; Sequence 281, Application US/09812283
; Patent No. 6826477

; GENERAL INFORMATION:
; APPLICANT: Fiecher, Robert L.
; APPLICANT: Ohad, Nir
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramon
; APPLICANT: Margossian, Linda
; APPLICANT: Harada, John
; APPLICANT: Goldberg, Robert B.
; TITLE OF INVENTION: The Regents of the University of California
; TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
; FILE REFERENCE: 023070-086120US
; CURRENT APPLICATION NUMBER: US/09/812,283
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/177,249
; PRIOR FILING DATE: 1998-10-22
; PRIOR APPLICATION NUMBER: US 09/071,838
; PRIOR FILING DATE: 1998-05-01
; NUMBER OF SEQ ID NOS: 324
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 281
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Arabidopsis sp.
US-09-812-283-281

Query Match 32.1%; Score 25; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 6.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKNPM 14
DB 1 DTSANPM 7

RESULT 85
US-08-406-142A-10
; Sequence 10, Application US/08406142A
; Patent No. 6060451
; GENERAL INFORMATION:
; APPLICANT: Dimailo, John
; APPLICANT: Ni, Feng
; APPLICANT: Konishi, Yasuo
; APPLICANT: Steinmetzer, Torsten
; TITLE OF INVENTION: Thrombin Inhibitors Based on the Amino
; TITLE OF INVENTION: Acid Sequence of Hirudin
; Patent No. 6060451
; NUMBER OF SEQUENCES: 33
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley & Lardner
; STREET: 3000 K St. N.W., Suite 500
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/406,142A
; FILING DATE: 20-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/302,245
; FILING DATE: 08-SEP-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/960,425
; FILING DATE: 10-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/CA91/00213
; FILING DATE: 14-JUN-1991

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,322
FILING DATE: 15-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 47998/109/BIPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-672-5300
TELEFAX: 202-672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Acetyl-D-Cha
OTHER INFORMATION: /note= "Acetyl group is attached to the N-terminal
OTHER INFORMATION: of Cyclohexylalanine which is in the
OTHER INFORMATION: D-configuration. D-Cha is attached to the first
FEATURE:
NAME/KEY: Modified-site
LOCATION: 2..3
OTHER INFORMATION: /label= Linker
OTHER INFORMATION: /note= "Portion of the linker is (CH2)2(CO)- and
OTHER INFORMATION: is used to link the second residue Arginine to the
OTHER INFORMATION: third residue Glutamine. "
FEATURE:
NAME/KEY: Modified-site
LOCATION: 17..18
OTHER INFORMATION: /label= Cha
OTHER INFORMATION: /note= "Cyclohexylalanine is included within the
OTHER INFORMATION: peptide chain between the 17th residue Tyrosine and
OTHER INFORMATION: the 18th residue Glutamine by peptide linkage. "
US-08-406-142A-10

Query Match 32.1%; Score 25; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 7.3e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KRDNHYSKNPM 14
DB 2 RQSHNDGDEPFI 13

RESULT 86
US-08-406-142A-26
Sequence 26, Application US/08406142A
Patent No. 6060451
GENERAL INFORMATION:
APPLICANT: DiMalo, John
APPLICANT: Ni, Feng
APPLICANT: Konishi, Yasuo
APPLICANT: Steinmetzer, Torsten
TITLE OF INVENTION: Thrombin Inhibitors Based on the Amino
TITLE OF INVENTION: Acid Sequence of Hirudin
Patent No. 6060451
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESSES:
ADDRESSER: Foley & Lardner
STREET: 3000 K St. N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/406,142A
FILING DATE: 20-MAR-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/302,245
FILING DATE: 08-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/960,425
FILING DATE: 10-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/CA91/00213
FILING DATE: 14-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/538,322
FILING DATE: 15-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 47998/109/BIPH
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-672-5300
TELEFAX: 202-672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /label= Acetyl-D-config
OTHER INFORMATION: /note= "An acetyl group is attached to the
OTHER INFORMATION: N-terminal of the first residue Phenylalanine
OTHER INFORMATION: which is in the D-configuration. "
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3..4
OTHER INFORMATION: /label= Linker
OTHER INFORMATION: /note= "Portion of the linker is -(CH2)2CO- and is
OTHER INFORMATION: used to link the third residue Arginine to the
OTHER INFORMATION: fourth residue Glutamine. "
FEATURE:
NAME/KEY: Modified-site
LOCATION: 18..19
OTHER INFORMATION: /label= Cha
OTHER INFORMATION: /note= "Cyclohexylalanine is included within the
OTHER INFORMATION: peptide chain between the 18th residue Tyrosine
OTHER INFORMATION: and 19th residue Glutamine and is attached by
US-08-406-142A-26

Query Match 32.1%; Score 25; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 7.7e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 KRDNHYSKNPM 14
DB 3 RQSHNDGDEPFI 14

RESULT 87
US-08-934-915-139
Sequence 139, Application US/08934915
Patent No. 5932412
GENERAL INFORMATION:
APPLICANT: DILLNER, JOAKIM
APPLICANT: DILLNER, LENA
APPLICANT: CHENG, HWEE-MING
TITLE OF INVENTION: SYNTHETIC PEPTIDES OF HUMAN
TITLE OF INVENTION: PAPILLOMAVIRUS 1, 5, 6, 8,

;; TITLE OF INVENTION: 11, 16, 18, 31, 33 AND 55
;; TITLE OF INVENTION: USEFUL IN IMMUNODIAGNOSIS FOR
;; TITLE OF INVENTION: DIAGNOSTIC PURPOSES
;; NUMBER OF SEQUENCES: 193
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: MASON & ASSOCIATES, P.A.
;; STREET: 17757 U.S. HWY. 19 NORTH, SUITE 500
;; CITY: CLEARWATER
;; STATE: FLORIDA
;; COUNTRY: U.S.A.
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY disk
;; OPERATING SYSTEM: Windows 3.0
;; SOFTWARE: Microsoft Word 6.0
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/934,915
;; FILING DATE: 22-SEP-1997
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/949,836
;; FILING DATE:
;; ATTORNEY/AGENT INFORMATION:
;; NAME: LOUISE A. FOUTCH
;; REGISTRATION NUMBER: 37,133
;; REFERENCE/DOCKET NUMBER: 1946.6
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 813-538-3800
;; TELEFAX: 813-538-3820
;; TELEX:
;; INFORMATION FOR SEQ ID NO: 139:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-934-915-139

Query Match 32.1%; Score 25; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 8.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12
DB 7 KNAEKYSKN 16

RESULT 89
US-08-602-999A-126
;; Sequence 126, Application US/08602999A
;; Patent No. 6184205
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLES, Dana M.
;; APPLICANT: RIDER, James B.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS

;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/602,999A
;; FILING DATE: 16-FEB-1996
;; CLASSIFICATION: 435
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mierock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 126:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 20 amino acids
;; TYPE: amino acid
;; TOPOLOGY: unknown
;; MOLECULE TYPE: peptide
US-08-602-999A-126

Query Match 32.1%; Score 25; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKNP 13
DB 4 SDYSRPP 10

RESULT 89
US-09-500-124-126
;; Sequence 126, Application US/09500124
;; Patent No. 6432920
;; GENERAL INFORMATION:
;; APPLICANT: SPARKS, Andrew B.
;; APPLICANT: KAY, Brian K.
;; APPLICANT: THORN, Judith M.
;; APPLICANT: QUILIAM, Lawrence A.
;; APPLICANT: DER, Channing J.
;; APPLICANT: FOWLES, Dana M.
;; APPLICANT: RIDER, James B.
;; TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
;; TITLE OF INVENTION: ISOLATING AND USING SAME
;; NUMBER OF SEQUENCES: 467
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Pennie & Edmonds
;; STREET: 1155 Avenue of the Americas
;; CITY: New York
;; STATE: New York
;; COUNTRY: U.S.A.
;; ZIP: 10036-2711
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: FLOPPY disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/500,124
;; FILING DATE:
;; CLASSIFICATION:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/602,999
;; FILING DATE: 16-FEB-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Mierock, S. Leslie
;; REGISTRATION NUMBER: 18,872
;; REFERENCE/DOCKET NUMBER: 1101-202
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (212) 790-9090
;; TELEFAX: (212) 869-9741/8864
;; TELEX: 66141 PENNIE
;; INFORMATION FOR SEQ ID NO: 126:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-126

Query Match 32.1%; Score 25; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 8.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKND 13
:||||:
Db 4 SDYSRPP 10

RESULT 90
US-09-605-703B-2436
Sequence 2436, Application US/09605703B
Patent No. 6962989
GENERAL INFORMATION:
APPLICANT: Pompejus, Markus
APPLICANT: Kroger, Burkhard
APPLICANT: Schroder, Hartwig
APPLICANT: Zelder, Oskar
APPLICANT: Habertauer, Gregor
TITLE OF INVENTION: CORYNEBACTERIUM GLUTAMICUM GENES ENCODING NOVEL
FILE REFERENCE: BGI-129CP
CURRENT APPLICATION NUMBER: US/09/605,703B
CURRENT FILING DATE: 2000-06-27
PRIOR APPLICATION NUMBER: 60/142,764
PRIOR FILING DATE: 1999-07-08
PRIOR APPLICATION NUMBER: 60/152,318
PRIOR FILING DATE: 1999-09-03
NUMBER OF SEQ ID NOS: 2534
SEQ ID NO 2436
LENGTH: 20
TYPE: PRT
ORGANISM: Corynebacterium glutamicum
US-09-605-703B-2436

Query Match 32.1%; Score 25; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 8.2e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDMNDYSKN 12
|||:|:
Db 8 RDMDDYGED 16

RESULT 91
US-08-180-209B-24
Sequence 24, Application US/08180209B
Patent No. 5593877
GENERAL INFORMATION:
APPLICANT: King, Te-Piao
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/180,209B
FILING DATE: 11-JAN-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-180-209B-24

Query Match 31.4%; Score 24.5; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IRDNDNDY 9
:||||:
Db 1 LKR-HNDF 7

RESULT 92
US-08-385-745-24
Sequence 24, Application US/08385745
Patent No. 561209
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,745
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/031,400
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 3288-020
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8664/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-385-745-24

Query Match 31.4%; Score 24.5; DB 1; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9
: || ||| :
Db 1 LKR-HNDF 7

RESULT 93
US-08-485-388-24
Sequence 24, Application US/08485388
Patent No. 6270763
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: Cloning and Recombinant Production of
TITLE OF INVENTION: Vespid Venom Phospholipases, and Immunological Therapies
TITLE OF INVENTION: Based Thereon
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,388
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,745
FILING DATE: 08-FEB-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,400
FILING DATE: 11-MAR-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 FWCA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-388-24

Query Match 31.4%; Score 24.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;
QY 2 IKRDNDY 9
: || ||| :

Db 1 LKR-HNDF 7

RESULT 94
US-08-474-853-24
Sequence 24, Application US/08474853
Patent No. 6287559
GENERAL INFORMATION:
APPLICANT: King, Te Piao
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,853
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 CIPB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-474-853-24

Query Match 31.4%; Score 24.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9
: || ||| :
Db 1 LKR-HNDF 7

RESULT 95
US-09-166-205B-24
Sequence 24, Application US/09166205B
Patent No. 6372471
GENERAL INFORMATION:
APPLICANT: Te Piao King
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF VESPID VENOM ENZYMES,
TITLE OF INVENTION: SUCH AS PHOSPHOLIPASE AND HYALURONIDASE, AND IMMUNOLOGICAL
TITLE OF INVENTION: THERAPIES BASED THEREON
FILE REFERENCE: 2313/0F138US
CURRENT APPLICATION NUMBER: US/09/166,205B
CURRENT FILING DATE: 1998-10-01

NUMBER OF SEQ ID NOS: 70
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 24
LENGTH: 8
TYPE: PRT
ORGANISM: Dolichovespula maculata
US-09-166-205B-24

Query Match 31.4%; Score 24.5; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9
DB 1 LKR-HNDF 7

RESULT 96
PCT-US94-02629-24
Sequence 24, Application PC/TUS9402629
GENERAL INFORMATION:
APPLICANT: King, Te-Piao
TITLE OF INVENTION: CLONING AND RECOMBINANT PRODUCTION OF
TITLE OF INVENTION: VESPID VENOM ENZYMES, SUCH AS PHOSPHOLIPASE AND
TITLE OF INVENTION: HYALURONIDASE, AND IMMUNOLOGICAL THERAPIES BASED THEREON
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02629
FILING DATE: 10-MAR-1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/180,209
FILING DATE: 11-JAN-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/031,400
FILING DATE: 11-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-074 PCT
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
PCT-US94-02629-24

Query Match 31.4%; Score 24.5; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IKRDNDY 9
DB 1 LKR-HNDF 7

RESULT 97
US-08-724-354D-29
Sequence 29, Application US/08724354D
Patent No. 5994119
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DEGRADATION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/724,354D
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/016,482
FILING DATE: 29-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haller, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-724-354D-29

Query Match 30.8%; Score 24; DB 1; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
DB 3 NDYDK 7

RESULT 98
US-09-270-984A-29
Sequence 29, Application US/09270984A
Patent No. 6048965
GENERAL INFORMATION:
APPLICANT: Dietz, Harry C.
TITLE OF INVENTION: MAMMALIAN REGULATOR OF
TITLE OF INVENTION: NONSENSE-MEDIATED RNA DEGRADATION
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 4225 Executive Square, Suite 1400
CITY: La Jolla
STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/270,984A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/724,354
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07265/090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-678-5070
TELEFAX: 619-678-5099
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-270-984A-29

Query Match 30.8%; Score 24; DB 2; Length 7;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
DB 3 NDYDK 7

RESULT 99
US-08-974-899-15
Sequence 15; Application US/08974899
Patent No. 6037454
GENERAL INFORMATION:
APPLICANT: Presta, Leonard G.
TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,899
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/031971
FILING DATE: 11/27/96
ATTORNEY/AGENT INFORMATION:
NAME: Lee, Wendy M.
REGISTRATION NUMBER: 40,378
REFERENCE/DOCKET NUMBER: P1014R1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1994
TELEFAX: 650/952-9981
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-974-899-15

Query Match 30.8%; Score 24; DB 2; Length 9;

Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9
DB 1 QCHNEY 6

RESULT 100
US-09-336-447A-40
Sequence 40; Application US/09336447A
Patent No. 6310190
GENERAL INFORMATION:
APPLICANT: HANSEN, ERIC J.
APPLICANT: ASBI, CHRISTOPH
APPLICANT: COPE, LESLIE D.
APPLICANT: MACIVER, ISOBEL
APPLICANT: FISKE, MICHAEL J.
APPLICANT: FREDENBURG, ROSS A.
TITLE OF INVENTION: USPA1 AND USPA2 ANTIGENS OF MORAXELLA CATARRHALIS
FILE REFERENCE: AMCY:024
CURRENT APPLICATION NUMBER: US/09/336,447A
CURRENT FILING DATE: 1999-06-21
NUMBER OF SEQ ID NOS: 98
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 40
LENGTH: 9
TYPE: PRT
ORGANISM: Moraxella catarrhalis
US-09-336-447A-40

Query Match 30.8%; Score 24; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10
DB 2 DKNEYS 7

Search completed: January 20, 2006, 19:14:10
Job time : 16.6731 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ! Search time 50.4808 Seconds
(without alignments)
115.878 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78
Sequence: 1 SIRKDNDSKNPM 14

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417629326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

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- 2: /cgn2_6/ptodaca/1/pubpaa/us08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodaca/1/pubpaa/us09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodaca/1/pubpaa/us10_PUBCOMB.pep:*
- 5: /cgn2_6/ptodaca/1/pubpaa/us10A_PUBCOMB.pep:*
- 6: /cgn2_6/ptodaca/1/pubpaa/us10B_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	78	100.0	14	4 US-10-218-743-1	Sequence 1, App1
2	37	47.4	17	3 US-09-992-665-48	Sequence 48, App1
3	34	43.6	20	3 US-09-731-321-58	Sequence 58, App1
4	32	41.0	11	3 US-09-758-318-10	Sequence 10, App1
5	32	41.0	11	4 US-10-340-783-10	Sequence 10, App1
6	32	41.0	11	4 US-10-801-820-10	Sequence 10, App1
7	32	41.0	17	4 US-10-095-373A-22	Sequence 22, App1
8	32	41.0	18	4 US-10-218-743-12	Sequence 12, App1
9	30	38.5	20	3 US-09-731-221-59	Sequence 59, App1
10	30	38.5	20	4 US-10-079-167-98	Sequence 98, App1
11	30	38.5	20	4 US-10-345-000-20	Sequence 20, App1
12	29	37.2	9	4 US-10-365-761B-20	Sequence 20, App1
13	29	37.2	12	4 US-10-131-540-48	Sequence 48, App1
14	29	37.2	12	4 US-10-453-483-25	Sequence 25, App1
15	29	37.2	12	6 US-11-119-889-48	Sequence 22, App1
16	29	37.2	13	4 US-10-345-764-22	Sequence 22, App1
17	29	37.2	14	4 US-10-417-895A-43	Sequence 43, App1
18	29	37.2	16	4 US-10-417-895A-34	Sequence 34, App1
19	29	37.2	20	5 US-10-776-013-382	Sequence 382, App1
20	28.5	36.5	17	4 US-10-095-373A-12	Sequence 12, App1
21	28	35.9	8	5 US-10-996-316-195	Sequence 195, App1
22	28	35.9	10	4 US-10-794-899-21	Sequence 21, App1
23	28	35.9	11	3 US-09-852-910-247	Sequence 247, App1
24	28	35.9	11	4 US-10-411-336A-247	Sequence 247, App1
25	28	35.9	12	5 US-10-884-830-218	Sequence 218, App1
26	28	35.9	14	4 US-10-417-895A-45	Sequence 45, App1
27	28	35.9	15	4 US-10-354-240-47	Sequence 47, App1

ALIGNMENTS

RESULT 1
US-10-218-743-1
; Sequence 1, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PR1
; ORGANISM: Dermatophagoides farinase
US-10-218-743-1

Query Match 100.0%; Score 78; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 3.3e-06;
Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 SIKRDNDYSKNP 14
Db 1 SIKRDNDYSKNP 14
RESULT 2
US-09-992-665-48
; Sequence 48, Application US/09992665
; Publication No. US20030092009A1
; GENERAL INFORMATION:
; APPLICANT: Kala Palm
; TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
; TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
; FILE REFERENCE: CEMINES.002A
; CURRENT APPLICATION NUMBER: US/09/992,665
; CURRENT FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: 60/249,508
; PRIOR FILING DATE: 2000-11-16
; NUMBER OF SEQ ID NOS: 380
; SOFTWARE: PaetSeq for Windows Version 4.0
; SEQ ID NO 48
; LENGTH: 17
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Probe
US-09-992-665-48

Query Match 47.4%; Score 37; DB 3; Length 17;
Best Local Similarity 54.5%; Pred. No. 31;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 3 KRDNDYSKNP 13

Db 1 KRDNDYSKNP 11

RESULT 3
US-09-731-221-58
; Sequence 58, Application US/09731221
; Patent No. US20020018778A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael
; TITLE OF INVENTION: Passive Desensitization
; FILE REFERENCE: 2002834-0103
; CURRENT APPLICATION NUMBER: US/09/731,221
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 58
; LENGTH: 20
; TYPE: PR1
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Arachis
US-09-731-221-58

Query Match 43.6%; Score 34; DB 3; Length 20;
Best Local Similarity 41.7%; Pred. No. 1.2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IRDNDYSKNP 13
Db 5 IORDSDYERDP 16

RESULT 4
US-09-758-318-10
; Sequence 10, Application US/09758318
; Patent No. US20010034021A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Martin
; APPLICANT: Gassmann, Lucz
; TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
; TITLE OF INVENTION: E1 and E2
; NUMBER OF SEQUENCES: 44
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pinnegan, Henderson, Farabow, Garrett &
; ADDRESSEE: Dunner
; STREET: 1300 I Street, N.W., Suite 700
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20005-3315
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/758,318
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/468,337
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Rinaudi, Carol P.
; REGISTRATION NUMBER: 33,220
; REFERENCE/DOCKET NUMBER: 05552-1199-02000
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-408-4000
; TELEFAX: 202-408-4400
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:

LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-758-318-10

Query Match 41.0%; Score 32; DB 3; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12
Db 3 RDHIDYWKH 11

RESULT 5
US-10-340-783-10
Sequence 10, Application US/10340783
Publication No. US20030147915A1
GENERAL INFORMATION:
APPLICANT: Muller, Martin
Giesmann, Lutz
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
R1 and R2
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/340,783
FILING DATE: 13-Jan-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,318
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/468,337
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudt, Carol P.
REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 05552-1199-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-340-783-10

Query Match 41.0%; Score 32; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12
Db 3 RDHIDYWKH 11

RESULT 6

US-10-801-820-10
Sequence 10, Application US/10801820
Publication No. US20040152074A1
GENERAL INFORMATION:
APPLICANT: Muller, Martin
Giesmann, Lutz
TITLE OF INVENTION: Seroreactive Regions on HPV 16 Proteins
R1 and R2
NUMBER OF SEQUENCES: 44
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flinnegan, Henderson, Farabow, Garrett &
Dunner
STREET: 1300 I Street, N.W., Suite 700
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3315
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/801,820
FILING DATE: 17-Mar-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/758,318
FILING DATE: 12-Jan-2001
APPLICATION NUMBER: 08/468,337
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Elnaudt, Carol P.
REGISTRATION NUMBER: 33,220
REFERENCE/DOCKET NUMBER: 05552-1199-02000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-408-4400
TELEFAX: 202-408-4400
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-801-820-10

Query Match 41.0%; Score 32; DB 4; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDHNDYSKN 12
Db 3 RDHIDYWKH 11

RESULT 7
US-10-095-373A-22
Sequence 22, Application US/10095373A
Publication No. US20030199022A1
GENERAL INFORMATION:
APPLICANT: Shapiro, David J.
TITLE OF INVENTION: A TAMOXIFEN AND 4-HYDROXY TAMOXIFEN-ACTIVATED SYSTEM FOR REGULATING PRODUCTION OF PROTEINS IN EUKARYOTIC CELLS
FILING DATE: 10/3/2000
CURRENT APPLICATION NUMBER: US/10/095,373A
FILING DATE: 2002-06-21
NUMBER OF SEQ ID NOS: 83
SOFTWARE: Patentin version 3.1
SEQ ID NO 22
LENGTH: 17
TYPE: PRT

ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Mutant DBD of ER
US-10-095-373A-22

Query Match 41.0%; Score 32; DB 4; Length 17;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KRHDNDY 9
|:|:|:|
DB 11 KQGHNDY 17

RESULT 8
US-10-218-743-12
Sequence 12, Application US/10218743
Publication No. US20030096779A1
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/10/218,743
CURRENT FILING DATE: 2002-08-13
PRIOR APPLICATION NUMBER: US/09/292,225
PRIOR FILING DATE: 1999-04-15
PRIOR APPLICATION NUMBER: 60/098,909
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/085,295
PRIOR FILING DATE: 1998-05-13
PRIOR APPLICATION NUMBER: 60/098,565
PRIOR FILING DATE: 1998-04-17
PRIOR APPLICATION NUMBER: 09/062,013
PRIOR FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 12
LENGTH: 18
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-10-218-743-12

Query Match 41.0%; Score 32; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYSKNP 13
|:|:|:|
DB 1 DYAKNP 6

RESULT 9
US-09-731-221-59
Sequence 59, Application US/09731221
Patent No. US20020018778A1
GENERAL INFORMATION:
APPLICANT: Caplan, Michael
TITLE OF INVENTION: Passive Desensitization
FILE REFERENCE: 2002834-0103
CURRENT APPLICATION NUMBER: US/09/731,221
CURRENT FILING DATE: 2001-12-06
NUMBER OF SEQ ID NOS: 79
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 59
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Arachis
Hypogaea

US-09-731-221-59

Query Match 38.5%; Score 30; DB 3; Length 20;
Best Local Similarity 36.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRHDNDY 13
|:|:|:|
DB 1 QRDSDYERDP 11

RESULT 10
US-10-079-167-98
Sequence 98, Application US/10079167
Publication No. US20030138454A1
GENERAL INFORMATION:
APPLICANT: Hall, Adrian V.S.
APPLICANT: McShane, Helen
APPLICANT: Gilbert, Sarah C.
APPLICANT: Reece, William
APPLICANT: Schneider, Joerg
TITLE OF INVENTION: Vaccination Method
FILE REFERENCE: 2907.1000-001
CURRENT APPLICATION NUMBER: US/10/079,167
CURRENT FILING DATE: 2002-02-19
PRIOR APPLICATION NUMBER: US 09/454,204
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: PCT/GB98/01681
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: GB 97 11957.2
PRIOR FILING DATE: 1997-06-09
PRIOR APPLICATION NUMBER: PCT/GB01/04116
PRIOR FILING DATE: 2001-09-13
PRIOR APPLICATION NUMBER: GB 00 23203.3
PRIOR FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 99
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 98
LENGTH: 20
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Peptide No. US20030138454A1 10 in the TTI-10 pool
US-10-079-167-98

Query Match 38.5%; Score 30; DB 4; Length 20;
Best Local Similarity 63.6%; Pred. No. 5.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
|:|:|:|
DB 10 IIRLHSDASKN 20

RESULT 11
US-10-345-000-20
Sequence 20, Application US/10345000
Publication No. US20040018177A1
GENERAL INFORMATION:
APPLICANT: OXON PHARMACEUTICALS LIMITED
TITLE OF INVENTION: VACCINATION METHOD
FILE REFERENCE: 550-409
CURRENT APPLICATION NUMBER: US/10/345,000
CURRENT FILING DATE: 2003-02-20
NUMBER OF SEQ ID NOS: 21
SOFTWARE: PatentIn version 3.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Plasmodium falciparum
US-10-345-000-20

Query Match 38.5%; Score 30; DB 4; Length 20;

Best Local Similarity 63.6%; Pred. No. 5.4e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKDDNDYSKN 12
Db 10 IIRLHSDASKN 20

RESULT 12
US-10-365-761B-20

/ Sequence 20; Application US/10365761B
/ Publication No. US20040023300A1
/ GENERAL INFORMATION:
/ APPLICANT: Grabe, Niels
/ TITLE OF INVENTION: METHOD FOR THE DETECTION OF A FUNCTIONAL
/ FILE REFERENCE: ABOHM7.001AUS
/ CURRENT APPLICATION NUMBER: US/10/365,761B
/ PRIOR FILING DATE: 2003-04-12
/ PRIOR APPLICATION NUMBER: EP 02003469.0
/ NUMBER OF SEQ ID NOS: 82
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 20
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: synthesized phosphorylacton site
US-10-365-761B-20

Query Match 37.2%; Score 29; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYSKN 12
Db 1 DNMRYNNN 8

RESULT 13
US-10-191-540-48
/ Sequence 48; Application US/10191540
/ Publication No. US20030224494A1
/ GENERAL INFORMATION:
/ APPLICANT: Tsuyoshi Nomoto, Tetsuya Yano, Shinya Kozaki and Tautomu Honma
/ TITLE OF INVENTION: Polyhydroxyalkanoate-containing structure and manufacturing method
/ FILE REFERENCE: CRO16534
/ CURRENT APPLICATION NUMBER: US/10/191,540
/ PRIOR FILING DATE: 2002-07-10
/ PRIOR APPLICATION NUMBER: JP P2001-210052
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: JP P2002-112978
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 186
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 48
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Carbon Black-binding peptide
US-10-191-540-48

Query Match 37.2%; Score 29; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13
Db 3 NNDWSKAP 10

RESULT 14
US-10-453-483-25
/ Sequence 25; Application US/10453483
/ Publication No. US20040005638A1
/ GENERAL INFORMATION:
/ APPLICANT: Tautomu Honma
/ APPLICANT: Tetsuya Yano
/ APPLICANT: Tsuyoshi No. US20040005638A1oto
/ APPLICANT: Shinya Kozaki
/ TITLE OF INVENTION: Immunoassay, reagent for immunoassay, and production method of t
/ FILE REFERENCE: CRO17318
/ CURRENT APPLICATION NUMBER: US/10/453,483
/ PRIOR FILING DATE: 2002-09-05
/ PRIOR APPLICATION NUMBER: JP P2002-173027
/ PRIOR FILING DATE: 2002-06-13
/ PRIOR APPLICATION NUMBER: JP P2003-127099
/ PRIOR FILING DATE: 2003-05-02
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 25
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ OTHER INFORMATION: binding peptide
US-10-453-483-25

Query Match 37.2%; Score 29; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13
Db 3 NNDWSKAP 10

RESULT 15
US-11-119-889-48
/ Sequence 48; Application US/11119889
/ Publication No. US20050208635A1
/ GENERAL INFORMATION:
/ APPLICANT: Tsuyoshi Nomoto, Tetsuya Yano, Shinya Kozaki and Tautomu Honma
/ TITLE OF INVENTION: Polyhydroxyalkanoate-containing structure and manufacturing method
/ FILE REFERENCE: CRO16534
/ CURRENT APPLICATION NUMBER: US/11/119,889
/ PRIOR FILING DATE: 2005-05-03
/ PRIOR APPLICATION NUMBER: US/10/191,540
/ PRIOR FILING DATE: 2002-07-10
/ PRIOR APPLICATION NUMBER: JP P2001-210052
/ PRIOR FILING DATE: 2001-07-10
/ PRIOR APPLICATION NUMBER: JP P2002-112978
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 186
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 48
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Carbon Black-binding peptide
US-11-119-889-48

Query Match 37.2%; Score 29; DB 6; Length 12;
Best Local Similarity 62.5%; Pred. No. 4.6e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13
Db 3 NNDWSKAP 10

RESULT 16
US-10-345-764-22
; Sequence 22, Application US/10345764
; Publication No. US20030138912A1
; GENERAL INFORMATION:
; APPLICANT: Busfield, S.
; APPLICANT: Gearling, D.
; TITLE OF INVENTION: EGF-LIKE NUCLEIC ACIDS AND POLYPEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: 7853-198
; CURRENT APPLICATION NUMBER: US/10/345,764
; CURRENT FILING DATE: 2003-01-16
; PRIOR APPLICATION NUMBER: US/09/443,959
; PRIOR FILING DATE: 1999-11-19
; PRIOR APPLICATION NUMBER: 09/196,269
; PRIOR FILING DATE: 1998-11-19
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 22
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: peptide used to generate polyclonal antibody
US-10-345-764-22

Query Match 37.2%; Score 29; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
Db 5 DHNDHSHQ 12

RESULT 17
US-10-417-895A-43
; Sequence 43, Application US/10417895A
; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 43
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for second complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: Immunoglobulin
US-10-417-895A-43

Query Match 37.2%; Score 29; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
Db 7 DHNDHSHQ 14

RESULT 18
US-10-417-895A-34
; Sequence 34, Application US/10417895A

; Publication No. US20040033569A1
; GENERAL INFORMATION:
; APPLICANT: Crea, Roberto
; APPLICANT: Cappuccilli, Guido
; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
; FILE REFERENCE: 1551.2002-001
; CURRENT APPLICATION NUMBER: US/10/417,895A
; CURRENT FILING DATE: 2003-04-16
; PRIOR APPLICATION NUMBER: 60/373,686
; PRIOR FILING DATE: 2002-04-17
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: variant peptide for second complementarity
; OTHER INFORMATION: determining region of Fv region of an
; OTHER INFORMATION: Immunoglobulin
US-10-417-895A-34

Query Match 37.2%; Score 29; DB 4; Length 16;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKNP 13
Db 6 NDYARTP 12

RESULT 19
US-10-776-013-382
; Sequence 382, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 382
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-382

Query Match 37.2%; Score 29; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 8e+02;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HDYSKXP 13
Db 3 HDNYRNP 10

RESULT 20
US-10-095-373A-12

; Sequence 12, Application US/10095373A
; Publication No. US20030199022A1
; GENERAL INFORMATION:
; APPLICANT: Shaprio, David J.
; TITLE OF INVENTION: A TAMOXIFEN AND 4-HYDROXY TAMOXIFEN-ACTIVATED SYSTEM FOR REGULATING
; FILE REFERENCE: 10322.25
; CURRENT APPLICATION NUMBER: US/10/095,373A
; CURRENT FILING DATE: 2002-06-21
; NUMBER OF SEQ ID NOS: 83
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 12
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Mutant DBD of ER
US-10-095-373A-12

Query Match 36.5%; Score 28.5; DB 4; Length 17;
Best Local Similarity 77.8%; Pred. No. 8.1e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

Qy 1 SIKRDNDY 9
Db 10 SIAR-HNDY 17

RESULT 21
US-10-996-316-195
; Sequence 195, Application US/10996316
; Publication No. US20050129690A1
; GENERAL INFORMATION:
; APPLICANT: Alexion Pharmaceuticals, Inc.
; APPLICANT: Bowdish, Katherine S.
; APPLICANT: McWhirter, John
; APPLICANT: Kretz-Rommel, Anke
; TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC
; TITLE OF INVENTION: LEUKEMIA CELLS AND USES THEREOF
; FILE REFERENCE: 60 CIP IV (1087-43 CIP IV)
; CURRENT APPLICATION NUMBER: US/10/996,316
; CURRENT FILING DATE: 2004-11-23
; PRIOR APPLICATION NUMBER: US 10/894,672
; PRIOR FILING DATE: 2004-07-20
; PRIOR APPLICATION NUMBER: US 10/736,188
; PRIOR FILING DATE: 2003-12-15
; PRIOR APPLICATION NUMBER: US 10/379,151
; PRIOR FILING DATE: 2003-03-04
; PRIOR APPLICATION NUMBER: PCT/US01/47931
; PRIOR FILING DATE: 2001-12-10
; PRIOR APPLICATION NUMBER: US 60/254,113
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 211
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 195
; LENGTH: 8
; TYPE: PRT
; ORGANISM: murine
US-10-996-316-195

Query Match 35.9%; Score 28; DB 5; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KRDNNDY 9
Db 2 KRDFDY 8

RESULT 22
US-10-794-899-21
; Sequence 21, Application US/10794899
; Publication No. US20040146516A1
; GENERAL INFORMATION:
; APPLICANT: Utah Ventures
; TITLE OF INVENTION: Lumen-Exposed Molecules and Methods Targeted Delivery
; FILE REFERENCE: 27110-715
; CURRENT APPLICATION NUMBER: US/10/794,899
; CURRENT FILING DATE: 2004-03-05
; NUMBER OF SEQ ID NOS: 121
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 21
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Tryptic Peptide
US-10-794-899-21

Query Match 35.9%; Score 28; DB 4; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RDNDYS 10
Db 3 QDNDFPS 9

RESULT 23
US-09-852-910-247
; Sequence 247, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method For Identifying Inhibitors of G Protein Coupled Receptor
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 247
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(11)
; OTHER INFORMATION: G11 library peptide
US-09-852-910-247

Query Match 35.9%; Score 28; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IKRDNDY 9
Db 1 LQRDHYEY 8

RESULT 24
US-10-411-336A-247
; Sequence 247, Application US/10411336A
; Publication No. US20040018558A1
; GENERAL INFORMATION:
; APPLICANT: GILCHRIST, ANNETTE

```
/ APPLICANT: HAMM, HEIDI
/ TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
/ TITLE OF INVENTION: SIGNALING
/ FILE REFERENCE: 2661-102
/ CURRENT APPLICATION NUMBER: US/10/411.336A
/ CURRENT FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: US 09/852910
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/275472
/ PRIOR FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 273
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 247
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: G11 library peptide
US-10-411-336A-247
```

```
Query Match          35.9%; Score 28; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      2 IKRDHNDY 9
DB      1 LQRDHVEY 8
```

```
RESULT 25
US-10-884-830-218
/ Sequence 218, Application US/10884830
/ Publication No. US20050004354A1
/ GENERAL INFORMATION:
/ APPLICANT: Jochem, Salfeld et al.
/ TITLE OF INVENTION: Human Antibodies That Bind Human IL-12 And Methods For Producing
/ FILE REFERENCE: BBI-093CP
/ CURRENT APPLICATION NUMBER: US/10/884,830
/ CURRENT FILING DATE: 2004-07-01
/ PRIOR APPLICATION NUMBER: US/09/534,717
/ PRIOR FILING DATE: 2000-03-24
/ PRIOR APPLICATION NUMBER: 60/126,603
/ PRIOR FILING DATE: March 25, 1999
/ NUMBER OF SEQ ID NOS: 675
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 218
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-884-830-218
```

```
Query Match          35.9%; Score 28; DB 5; Length 12;
Best Local Similarity 50.0%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYS 10
DB      2 SYDRGNHNS 11
```

```
RESULT 26
US-10-417-895A-45
/ Sequence 45, Application US/10417895A
/ Publication No. US20040033569A1
/ GENERAL INFORMATION:
/ APPLICANT: Crea, Roberto
/ APPLICANT: Cappuccilli, Guido
/ TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
/ FILE REFERENCE: 1551.2002-001
/ CURRENT APPLICATION NUMBER: US/10/417,895A
/ CURRENT FILING DATE: 2003-04-16
/ PRIOR APPLICATION NUMBER: 60/373,686
/ PRIOR FILING DATE: 2002-04-17
```

```
/ NUMBER OF SEQ ID NOS: 86
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: variant peptide for second complementarity
/ OTHER INFORMATION: determining region of Fv region of an
/ OTHER INFORMATION: Immunoglobulin
US-10-417-895A-45
```

```
Query Match          35.9%; Score 28; DB 4; Length 14;
Best Local Similarity 57.1%; Pred. No. 8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 11
DB      7 DHSDHDK 13
```

```
RESULT 27
US-10-354-240-47
/ Sequence 47, Application US/10354240
/ Publication No. US20030185847A1
/ GENERAL INFORMATION:
/ APPLICANT: Sone, Toshio
/ APPLICANT: Kume, Akinori
/ APPLICANT: Dairiki, Kazuo
/ APPLICANT: Iwama, Akiko
/ APPLICANT: Kino, Kohsuke
/ TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
/ FILE REFERENCE: SPO-103D1
/ CURRENT APPLICATION NUMBER: US/10/354,240
/ CURRENT FILING DATE: 2003-01-29
/ PRIOR APPLICATION NUMBER: PCT/JP97/00740
/ PRIOR FILING DATE: 1997-03-10
/ PRIOR APPLICATION NUMBER: US 09/142,524
/ PRIOR FILING DATE: 1998-09-09
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 47
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Cryptosporidia japonica
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)..(15)
/ OTHER INFORMATION: CryJ1 peptide, Figure 1, Row 33
US-10-354-240-47
```

```
Query Match          35.9%; Score 28; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 12
DB      4 DHNSFSNS 11
```

```
RESULT 28
US-09-949-196-2
/ Sequence 2, Application US/09949196
/ Patent No. US20020147145A1
/ GENERAL INFORMATION:
/ APPLICANT: Zealand Pharmaceuticals A/S
/ TITLE OF INVENTION: MATERIALS AND METHODS RELATING TO THE DEGRADATION OF Cdc25A IN R
/ FILE REFERENCE: 55868 (45487)
/ CURRENT APPLICATION NUMBER: US/09/949,196
/ CURRENT FILING DATE: 2001-07-09
/ NUMBER OF SEQ ID NOS: 45
/ SOFTWARE: PatentIn version 3.1
```


SEQ ID NO 2
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: synthetic peptide sequence
US-09-949-196-2

Query Match 35.9%; Score 28; DB 3; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.9e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDND 8
:|:|:|:
DB 3 ALKSHSD 10

RESULT 29
US-10-772-089-2
Sequence 2, Application US/10772089
Publication No. US20040192609A1
GENERAL INFORMATION:
APPLICANT: The Brigham & Women's Hospital, Inc.
APPLICANT: Farzan, Michael R
TITLE OF INVENTION: Peptides Binding gp120 of HIV-1
FILE REFERENCE: 7570/80211
CURRENT APPLICATION NUMBER: US/10/772,089
CURRENT FILING DATE: 2004-02-05
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
US-10-772-089-2

Query Match 35.9%; Score 28; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHNDYS 10
:|:|:|:
DB 5 DYNDYA 10

RESULT 30
US-10-931-260-42
Sequence 42, Application US/10931260
Publication No. US20050152927A1
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
Pollock, Joanne;
Bond, Julian P.;
Garman, Richard D;
Kuo, Mei-Chang;
Powers, Stephen P.;
Exley, Mark A.;
Chen, Xian;
Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lathive & Cockfield, LLP
STREET: 28 State St
CITY: Boston

STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/931,260
FILING DATE: 30-Aug-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/240,203
FILING DATE: 29-Jan-1999
APPLICATION NUMBER: 08/467,023
FILING DATE: 1995-JUN-06
APPLICATION NUMBER: 08/350,225
FILING DATE: 1994-DEC-06
APPLICATION NUMBER: 08/226,248
FILING DATE: 1994-APR-08
APPLICATION NUMBER: PCT/US93/00139
FILING DATE: 1993-JAN-15
APPLICATION NUMBER: 07/938,990
FILING DATE: 1992-SEP-01
APPLICATION NUMBER: 07/730,452
FILING DATE: 1991-JUL-15
APPLICATION NUMBER: 07/729,134
FILING DATE: 1991-JUL-12
APPLICATION NUMBER: 07/975,179
FILING DATE: 1992-NOV-12
APPLICATION NUMBER: PCT/US92/05661
FILING DATE: 1992-JUL-10
ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras, Esq.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: peptide
FRAGMENT TYPE: internal
SEQUENCE DESCRIPTION: SEQ ID NO: 42:
US-10-931-260-42

Query Match 35.9%; Score 28; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
:|:|:|:
DB 4 DHNSFSNS 11

RESULT 31
US-10-931-260-203
Sequence 203, Application US/10931260
Publication No. US20050152927A1
GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
Pollock, Joanne;
Bond, Julian P.;
Garman, Richard D;
Kuo, Mei-Chang;
Powers, Stephen P.;
Exley, Mark A.;
Chen, Xian;
Shaked, Ze'ev

TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lathive & Cockfield, LLP
STREET: 28 State St

```

1 CITY: Boston
2 STATE: MA
3 COUNTRY: USA
4 ZIP: 02109
5
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patent Release #1.0, Version #1.25
11
12 CURRENT APPLICATION DATA:
13 APPLICATION NUMBER: US/10/931,260
14 FILING DATE: 30-Aug-2004
15 CLASSIFICATION: <Unknown>
16
17 PRIOR APPLICATION DATA:
18 APPLICATION NUMBER: US/09/240,203
19 FILING DATE: 29-Jan-1999
20 APPLICATION NUMBER: 08/467,023
21 FILING DATE: 1995-JUN-06
22 APPLICATION NUMBER: 08/350,225
23 FILING DATE: 1994-DEC-06
24 APPLICATION NUMBER: 08/226,248
25 FILING DATE: 1994-APR-08
26 APPLICATION NUMBER: PCT/US93/00139
27 FILING DATE: 1993-JAN-15
28 APPLICATION NUMBER: 07/938,990
29 FILING DATE: 1992-SEP-01
30 APPLICATION NUMBER: 07/730,452
31 FILING DATE: 1991-JUL-15
32 APPLICATION NUMBER: 07/729,134
33 FILING DATE: 1991-JUL-12
34 APPLICATION NUMBER: 07/975,179
35 FILING DATE: 1992-NOV-12
36 APPLICATION NUMBER: PCT/US92/05661
37 FILING DATE: 1992-JUL-10
38
39 ATTORNEY/AGENT INFORMATION:
40 NAME: Amy E. Mandragouras, Esq.
41 REGISTRATION NUMBER: 36,207
42 REFERENCE/DOCKET NUMBER: INT-028CD2CCPA2
43 TELECOMMUNICATION INFORMATION:
44 TELEPHONE: (617) 742-7400
45 TELEFAX: (617) 742-4214
46
47 INFORMATION FOR SEQ ID NO: 203:
48
49 SEQUENCE CHARACTERISTICS:
50 LENGTH: 20 amino acids
51 TYPE: amino acid
52 TOPOLOGY: linear
53 MOLECULE TYPE: peptide
54 FRAGMENT TYPE: internal
55
56 SEQUENCE DESCRIPTION: SEQ ID NO: 203:
57
58 US-10-931-260-203
59
60 Query Match 35.9%, Score 28, DB 5, Length 20;
61 Best Local Similarity 50.0%, Pred. No. 1.2e+03;
62 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
63
64 Cy 5 DHNDYSKN 12
65 ||| : :
66 ||| : :
67
68 Db 10 DHNSFNS 17
69
70 RESULT 32
71 US-09-901-187B-2
72 Sequence 2, Application US/09901187B
73 Patent No. US20020151464A1
74 GENERAL INFORMATION:
75 APPLICANT: Panacea Pharmaceuticals, Inc.
76 APPLICANT: Wolozin, Benjamin
77 APPLICANT: Ostretova-Golts, Natalie
78 APPLICANT: Lebowitz, Michael S.
79 TITLE OF INVENTION: Methods for Preventing Neural Tissue Damage and for the Treatment
80 TITLE OF INVENTION: Alpha-Synuclein Diseases
81 TITLE REFERENCE: PAM01/002US
82 CURRENT APPLICATION NUMBER: US/09/901,187B

```

```

; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,319
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/279,199
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-901-187B-2

Query Match          34.6%; Score 27; DB 3; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      9 YSKNPM 14
       |:|:|:|
Db      2 YAKNPI 7

RESULT 33
US-10-909-116-2
; Sequence 2, Application US/10909116
; Publication No. US20050032131A1
; GENERAL INFORMATION:
; APPLICANT: Panacea Pharmaceuticals, Inc.
; APPLICANT: Wolozin, Benjamin
; APPLICANT: Ostretova-Golts, Natalie
; APPLICANT: Lebowitz, Michael S.
; TITLE OF INVENTION: Methods for Preventing Neural Tissue Damage and for the Treatment
; FILE REFERENCE: PAN01/002US
; CURRENT APPLICATION NUMBER: US/10/909,116
; CURRENT FILING DATE: 2004-07-30
; PRIOR APPLICATION NUMBER: US/09/901,187
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 60/217,319
; PRIOR FILING DATE: 2000-07-07
; PRIOR APPLICATION NUMBER: US 60/279,199
; PRIOR FILING DATE: 2001-03-28
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 7
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-909-116-2

Query Match          34.6%; Score 27; DB 5; Length 7;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY      9 YSKNPM 14
       |:|:|:|
Db      2 YAKNPI 7

RESULT 34
US-09-852-910-185
; Sequence 185, Application US/09852910
; Publication No. US20030096297A1
; GENERAL INFORMATION:
; APPLICANT: Hamm, Heidi
; APPLICANT: Gilchrist, Annette
; TITLE OF INVENTION: Method for Identifying Inhibitors of G Protein Coupled Receptor S
; FILE REFERENCE: 2661-101
; CURRENT APPLICATION NUMBER: US/09/852,910
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US 60/275,472
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 271

```

```
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 185
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ NAME/KEY: misc feature
/ LOCATION: (1)..(11)
/ OTHER INFORMATION: G alpha library peptide
US-09-852-910-185

Query Match          34.6%; Score 27; DB 3; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      2 IKRDHNDYS 10
DB      1 LQMNHNENY 9

RESULT 35
US-10-411-336A-185
/ Sequence 185, Application US/10411336A
/ Publication No. US20040018558A1
/ GENERAL INFORMATION:
/ APPLICANT: GLICHRIST, ANNETTE
/ APPLICANT: HAMM, HEIDI
/ TITLE OF INVENTION: METHOD FOR IDENTIFYING MODULATORS OF G PROTEIN COUPLED RECEPTOR
/ FILE REFERENCE: 2661-102
/ CURRENT APPLICATION NUMBER: US/10/411.336A
/ PRIOR FILING DATE: 2003-04-11
/ PRIOR APPLICATION NUMBER: US 09/852910
/ PRIOR FILING DATE: 2001-05-11
/ PRIOR APPLICATION NUMBER: US 60/275472
/ PRIOR FILING DATE: 2001-03-14
/ NUMBER OF SEQ ID NOS: 273
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 185
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: G alpha library peptide
US-10-411-336A-185

Query Match          34.6%; Score 27; DB 4; Length 11;
Best Local Similarity 33.3%; Pred. No. 9.1e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY      2 IKRDHNDYS 10
DB      1 LQMNHNENY 9
```

```
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-692-151-33

Query Match          34.6%; Score 27; DB 4; Length 12;
Best Local Similarity 100.0%; Pred. No. 1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HNDY 9
DB      2 TVKGDVHDIGKN 5

RESULT 37
US-10-607-712-9
/ Sequence 9, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607.712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980.326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031.964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050.310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Escherichia coli
US-10-607-712-9

Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY      1 SIKRDHNDYSKN 12
DB      2 TVKGDVHDIGKN 13

RESULT 38
US-10-607-712-10
/ Sequence 10, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607.712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980.326
/ PRIOR FILING DATE: 1997-11-26
```

```
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 10
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Cyanobacterium synechocystis
US-10-607-712-10
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 39
US-10-607-712-11
/ Sequence 11, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Mycobacterium leprae
US-10-607-712-11
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 40
US-10-607-712-12
/ Sequence 12, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
```

```
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ CURRENT FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Hemophilus influenzae
US-10-607-712-12
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 41
US-10-607-712-13
/ Sequence 13, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
/ APPLICANT: Goyette, Philippe
/ APPLICANT: Campeau, Eric
/ TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
/ TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
/ TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
/ FILE REFERENCE: 50004/002005
/ CURRENT APPLICATION NUMBER: US/10/607,712
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 08/980,326
/ PRIOR FILING DATE: 1997-11-26
/ PRIOR APPLICATION NUMBER: 60/031,964
/ PRIOR FILING DATE: 1996-11-27
/ PRIOR APPLICATION NUMBER: 60/050,310
/ PRIOR FILING DATE: 1997-06-20
/ NUMBER OF SEQ ID NOS: 76
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-10-607-712-13
```

```
Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.le+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 SIKRDHNDYSKN 12
       :|:|:|:|
Db      2 TVKGDVHDIGKN 13
```

```
RESULT 42
US-10-607-712-14
/ Sequence 14, Application US/10607712
/ Publication No. US20040073018A1
/ GENERAL INFORMATION:
/ APPLICANT: Gravel, Roy A.
/ APPLICANT: Rozen, Rima
/ APPLICANT: Leclerc, Daniel
```

```

; APPLICANT: Goyette, Philippe
; APPLICANT: Campeau, Eric
; TITLE OF INVENTION: HUMAN METHIONINE SYNTHASE: CLONING, AND
; TITLE OF INVENTION: METHODS FOR EVALUATING RISK OF NEURAL TUBE DEFECTS,
; TITLE OF INVENTION: CARDIOVASCULAR DISEASE, AND CANCER
; FILE REFERENCE: 50004/002005
; CURRENT APPLICATION NUMBER: US/10/607,712
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 08/980,326
; PRIOR FILING DATE: 1997-11-26
; PRIOR APPLICATION NUMBER: 60/031,964
; PRIOR FILING DATE: 1996-11-27
; PRIOR APPLICATION NUMBER: 60/050,310
; PRIOR FILING DATE: 1997-06-20
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 14
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-607-712-14

Query Match          34.6%; Score 27; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 1.1e+03;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSKN 12
DB 2 TVKGDVADIGKN 13

RESULT 43
US-10-354-240-46
; Sequence 46, Application US/10354240
; Publication No. US20030185847A1
; GENERAL INFORMATION:
; APPLICANT: Some, Toshio
; APPLICANT: Kume, Akimori
; APPLICANT: Daitiki, Kazuo
; APPLICANT: Iwama, Akiko
; APPLICANT: Kino, Kohsuke
; TITLE OF INVENTION: Peptide-Based Immunotherapeutic Agent for Treating Allergic Disease
; FILE REFERENCE: SPO-103D1
; CURRENT APPLICATION NUMBER: US/10/354,240
; PRIOR FILING DATE: 2003-01-29
; PRIOR APPLICATION NUMBER: PCT/JP97/00740
; PRIOR FILING DATE: 1997-03-10
; PRIOR APPLICATION NUMBER: US 09/142,524
; PRIOR FILING DATE: 1998-09-09
; NUMBER OF SEQ ID NOS: 174
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 46
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Cryptomeria japonica
; FEATURE:
; NAME/KEY: MISC FEATURE
; LOCATION: (1)..(15)
; OTHER INFORMATION: Cys11 peptide, Figure 1, Row 32
US-10-354-240-46

Query Match          34.6%; Score 27; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHDNDYS 10
DB 9 DHDNSFS 14

RESULT 44
US-10-714-679-1
; Sequence 1, Application US/10714679
; Publication No. US20040170637A1
; GENERAL INFORMATION:
; APPLICANT: McVey, David Scott
; TITLE OF INVENTION: Use of rmlt as a Marker Antigen for Vaccines and as a Synergistic
; TITLE OF INVENTION: Adjuvant with Amphigen
; FILE REFERENCE: P15827 (PC25075)
; CURRENT APPLICATION NUMBER: US/10/714,679
; PRIOR FILING DATE: 2003-11-14
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: Marker peptides from the rmlt sequence
US-10-714-679-1

Query Match          34.6%; Score 27; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHNDY 9
DB 3 RGHNEY 8

RESULT 45
US-10-808-187-1406
; Sequence 1406, Application US/10808187
; Publication No. US2005009009A1
; GENERAL INFORMATION:
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: CHAN, XI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; PRIOR FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1406
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1406

Query Match          34.6%; Score 27; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

Qy 5 HNDYSKN 12
|:|:|
Db 7 DYNDNSHN 14

RESULT 46

US-10-807-1406
; Sequence 1406, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 1406
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1406

Query Match 34.6%; Score 27; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 HNDYSKN 12
|:|:|
Db 7 DYNDNSHN 14

RESULT 47

US-10-946-647-65
; Sequence 65, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3

; SEQ ID NO 65
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Salmonella enterica
US-10-946-647-65

Query Match 34.6%; Score 27; DB 5; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HNDYSKN 12
|:|:|
Db 1 HNDFDLN 7

RESULT 48

US-10-946-647-368
; Sequence 368, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 368
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-10-946-647-368

Query Match 34.6%; Score 27; DB 5; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HNDYSKN 12
|:|:|
Db 1 HNDFDLN 7

RESULT 49

US-10-946-647-517
; Sequence 517, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYLL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: WONDERLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; CURRENT FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 517
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-10-946-647-517

Query Match 34.6%; Score 27; DB 5; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 6 HNDYSKN 12

```
Db      1 HNDPDLN 7

RESULT 50
US-10-946-647-635
; Sequence 635, Application US/10946647
; Publication No. US20050186217A1
; GENERAL INFORMATION:
; APPLICANT: EMERY, DARYL A.
; APPLICANT: STRAUB, DARREN E.
; APPLICANT: MONDEBLING, LAURA
; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
; FILE REFERENCE: 293.00340101
; CURRENT APPLICATION NUMBER: US/10/946,647
; PRIOR FILING DATE: 2004-09-20
; PRIOR APPLICATION NUMBER: 60/504,119
; PRIOR FILING DATE: 2003-09-19
; NUMBER OF SEQ ID NOS: 1448
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 635
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Salmonella enteritidis
US-10-946-647-635

Query Match      34.6%; Score 27; DB 5; Length 16;
Best Local Similarity 57.1%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      6 HNDYSKN 12
Db      1 HNDPDLN 7

RESULT 51
US-09-731-221-57
; Sequence 57, Application US/09731221
; Patent No. US20020018778A1
; GENERAL INFORMATION:
; APPLICANT: Caplan, Michael
; TITLE OF INVENTION: Passive Desensitization
; FILE REFERENCE: 2002834-0103
; CURRENT APPLICATION NUMBER: US/09/731,221
; CURRENT FILING DATE: 2001-12-06
; NUMBER OF SEQ ID NOS: 79
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 57
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Atachis
US-09-731-221-57

Query Match      34.6%; Score 27; DB 3; Length 20;
Best Local Similarity 36.4%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      2 IKRDHNDYSKN 12
Db      10 IQRDEDSYERD 20

RESULT 52
US-09-864-761-39698
; Sequence 39698, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.

APPLICANT: Chen, Wenheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263,6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 39698
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC002127.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.3
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 3.4
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 3
US-09-864-761-39698

Query Match      34.6%; Score 27; DB 3; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      1 SIKRDHNDYS 10
Db      11 TFKKRNNDYT 20

RESULT 53
US-10-931-260-41
; Sequence 41, Application US/10931260
; Publication No. US20050152927A1
```

GENERAL INFORMATION:
APPLICANT: Griffith, Irwin J.;
Pollock, Joanne;
Bond, Julian P.;
Garman, Richard D;
Kuo, Wei-Chang;
Powers, Stephen P.;
Exley, Mark A.;
Shen, Xian;
Shaked, Zeev

TITLE OF INVENTION: Allergenic Proteins And Peptides From
Japanese Cedar Pollen

NUMBER OF SEQUENCES: 283

CORRESPONDENCE ADDRESS:
ADDRESSEE: Lathive & Cockfield, LLP
STREET: 28 State St
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/931,260
FILING DATE: 30-Aug-2004

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/240,203
FILING DATE: 29-Jan-1999
APPLICATION NUMBER: 08/467,023
FILING DATE: 1995-JUN-06
APPLICATION NUMBER: 08/350,225
FILING DATE: 1994-DEC-06
APPLICATION NUMBER: 08/226,248
FILING DATE: 1994-APR-08
APPLICATION NUMBER: PCT/US93/00139
FILING DATE: 1993-JAN-15
APPLICATION NUMBER: 07/938,990
FILING DATE: 1992-SEP-01
APPLICATION NUMBER: 07/730,452
FILING DATE: 1991-JUL-15
APPLICATION NUMBER: 07/729,134
FILING DATE: 1991-JUL-12
APPLICATION NUMBER: 07/975,179
FILING DATE: 1992-NOV-12
APPLICATION NUMBER: PCT/US92/05661
FILING DATE: 1992-JUL-10

ATTORNEY/AGENT INFORMATION:
NAME: Amy E. Mandragouras, Esq.
REGISTRATION NUMBER: 36,207
REFERENCE/DOCKET NUMBER: IMI-028CD2CCPA2

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 227-7400
TELEFAX: (617) 742-4214

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 41:
US-10-931-260-41

Query Match
Best Local Similarity 66.7%; Score 27; DB 5; Length 20;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10
|||:|

Db 14 DHNSFS 19

RESULT 54
US-10-089-549-12
Sequence 12, Application US/10089549
Publication No. US20030194762A1

GENERAL INFORMATION:
APPLICANT: KUBOTA, Michio
APPLICANT: TSUSAKI, Keiji
APPLICANT: HIGASHIYAMA, Takanobu
APPLICANT: FUKUDA, Shigeharu
APPLICANT: MIYAKE, Toshio

TITLE OF INVENTION: ALPHA-1SOMALYOSYLGLUCOSACCHARIDE-FORMING ENZYME, PROCESS AND USE

FILE REFERENCE: KUBOTA-9

CURRENT APPLICATION NUMBER: US/10/089,549
CURRENT FILING DATE: 2002-12-13
PRIOR APPLICATION NUMBER: JP 233364/2000
PRIOR FILING DATE: 2000-08-01
PRIOR APPLICATION NUMBER: JP 234937/2000
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: PCT/JP01/06412
PRIOR FILING DATE: 2001-07-25

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PatentIn version 3.1

SEQ ID NO 12
LENGTH: 8
TYPE: PRT

ORGANISM: Bacillus globisporus
US-10-089-549-12

Query Match
Best Local Similarity 66.7%; Score 26; DB 4; Length 8;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKNP 13
|:|:|

Db 1 DYSNMP 6

RESULT 55
US-10-245-871-459
Sequence 459, Application US/10245871
Publication No. US20030235594A1

GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN

TITLE OF INVENTION: II-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: REH-2013

CURRENT APPLICATION NUMBER: US/10/245,871
CURRENT FILING DATE: 2003-01-09
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 905

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 459
LENGTH: 9
TYPE: PRT

ORGANISM: Homo sapiens
US-10-245-871-459

Query Match
Best Local Similarity 71.4%; Score 26; DB 4; Length 9;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDNNDY 9
|||:|

Db 1 KRHPDPY 7

RESULT 56

US-10-253-286-459
; Sequence 459, Application US/10253286
; Publication No. US2004005881A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: I-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RH-2015
; CURRENT APPLICATION NUMBER: US/10/253, 286
; CURRENT FILING DATE: 2003-01-13
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 905
; SOFTWARE: FastSeq for Windows Version 2.1
; SEQ ID NO 459
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-253-286-459

Query Match 33.3%; Score 26; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRHDNDY 9
|||
Db 1 KRVPDPY 7

RESULT 57

US-09-894-018-263
; Sequence 263, Application US/09894018
; Patent No. US20020119127A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Chestnut, Robert
; APPLICANT: Livingston, Brian
; APPLICANT: Baker, Denlow
; APPLICANT: Newman, Mark
; APPLICANT: Brown, David
; TITLE OF INVENTION: METHODS AND SYSTEM FOR OPTIMIZING
; FILE REFERENCE: 39963-20033.00
; CURRENT APPLICATION NUMBER: US/09/894,018
; CURRENT FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: PCT/US00/35568
; PRIOR FILING DATE: 2000-12-28
; PRIOR APPLICATION NUMBER: US 60/173,390
; PRIOR FILING DATE: 1999-12-28
; PRIOR APPLICATION NUMBER: US 60/284,221
; PRIOR FILING DATE: 2001-04-16
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 263
; LENGTH: 10
; TYPE: PRT
; ORGANISM: P. falciparum
US-09-894-018-263

Query Match 33.3%; Score 26; DB 3; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11
|||
Db 5 HNSYK 10

RESULT 58

US-10-360-836-33

Sequence 33, Application US/10360836
Publication No. US20030185854A1
GENERAL INFORMATION:
APPLICANT: Zavala, Fidel
APPLICANT: Birkett, Ashley
TITLE OF INVENTION: USE OF RECOMBINANT HEPATITIS B CORE
PARTICLES TO DEVELOP VACCINES AGAINST INFECTIOUS PATHOGENS
TITLE OF INVENTION: AND MALDIQUANCES
FILE REFERENCE: 5986/1J876
CURRENT APPLICATION NUMBER: US/10/360,836
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/354,963
PRIOR FILING DATE: 2002-02-08
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 10
TYPE: PRT
ORGANISM: Plasmodium
US-10-360-836-33

Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11
|||
Db 5 HNSYK 10

RESULT 59

US-10-371-525-441
; Sequence 441, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chestnut, Robert W.
; APPLICANT: Epimune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; IMMUNE RESPONSE AND METHODS OF USING THE SAME
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 441
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-525-441

Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11
|||
Db 5 HNSYK 10

RESULT 60

US-10-371-069-441

```
/ Sequence 441, Application US/10371069
/ Publication No. US20030216342A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE Inc.
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ FILE REFERENCE: 39963-20022.10
/ CURRENT APPLICATION NUMBER: US/10/371,069
/ CURRENT FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: US 09/078,904
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 441
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-069-441
```

```
Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 HNDYSK 11
DB 5 HNSYK 10
```

```
RESULT 61
US-10-371-645-441
/ Sequence 441, Application US/10371645
/ Publication No. US20030216343A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE Inc.
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ FILE REFERENCE: 39963-20022.11
/ CURRENT APPLICATION NUMBER: US/10/371,645
/ CURRENT FILING DATE: 2003-06-20
/ PRIOR APPLICATION NUMBER: US 09/078,904
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 441
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-645-441
```

```
Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
```

```
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 6 HNDYSK 11
DB 5 HNSYK 10
```

```
RESULT 62
US-10-371-260-441
/ Sequence 441, Application US/10371260
/ Publication No. US20030220285A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE Inc.
/ APPLICANT: Fikes, John D.
/ APPLICANT: Hermanson, Gary G.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Ishioka, Glenn Y.
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert W.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Expression Vectors for Stimulating an
/ FILE REFERENCE: 39963-20022.13
/ CURRENT APPLICATION NUMBER: US/10/371,260
/ CURRENT FILING DATE: 2003-02-21
/ PRIOR APPLICATION NUMBER: US 09/078,904
/ PRIOR FILING DATE: 1998-05-13
/ PRIOR APPLICATION NUMBER: US 60/085,751
/ PRIOR FILING DATE: 1998-05-15
/ NUMBER OF SEQ ID NOS: 463
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 441
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Pf LSA1 59 (peptide 1167.47)
US-10-371-260-441
```

```
Query Match 33.3%; Score 26; DB 4; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 HNDYSK 11
DB 5 HNSYK 10
```

```
RESULT 63
US-10-474-960A-263
/ Sequence 263, Application US/10474960A
/ Publication No. US20040248113A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Livingston, Brian
/ APPLICANT: Baker, Denise
/ APPLICANT: Newman, Mark
/ APPLICANT: Brown, David
/ TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
/ FILE REFERENCE: 2060.0320004
/ CURRENT APPLICATION NUMBER: US/10/474,960A
/ CURRENT FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: PCT/US02/09877
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 09/894,018
/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/284,221
/ PRIOR FILING DATE: 2001-04-16
/ NUMBER OF SEQ ID NOS: 419
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 263
```

```

; LENGTH: 10
; TYPE: PRT
; ORGANISM: P. falciparum
US-10-474-960A-263

Query Match      33.3%; Score 26; DB 5; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 HNDYSK 11
      |||
Db      5 HNSYK 10

RESULT 64
US-10-697-399-9
; Sequence 9, Application US/10697399
; Publication No. US20040162413A1
; GENERAL INFORMATION:
; APPLICANT: Watkins, Jeffrey D.
; APPLICANT: Huse, William D.
; APPLICANT: Vasselec, Alain P.
; APPLICANT: Margulis, David P.
; APPLICANT: Smith, Eric P.
; TITLE OF INVENTION: Methods of Optimizing Antibody Variable Region Binding Affinity
; FILE REFERENCE: AME-08122
; CURRENT APPLICATION NUMBER: US/10/697,399
; CURRENT FILING DATE: 2003-10-30
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-697-399-9

Query Match      33.3%; Score 26; DB 4; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 SIXRDNDY 9
      |||
Db      1 SASQDINDY 9

RESULT 65
US-10-930-300-129
; Sequence 129, Application US/10930300
; Publication No. US20050014138A1
; GENERAL INFORMATION:
; APPLICANT: Racht, Matthias
; TITLE OF INVENTION: METHOD OF PRODUCING VACCINES FROM PROTEIN SIGNAL
; OLIGOPEPTIDES
; NUMBER OF SEQUENCES: 360
; CORRESPONDENCE ADDRESS:
; ADDRESSER: INHOUSE IP MANAGEMENT
; STREET: 280 Colorado Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94301
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk, 3.50 inch, 1.44MB storage
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: WINDOWS 95
; SOFTWARE: MS WORD 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/930,300
; FILING DATE: 30-Aug-2004
; CLASSIFICATION: <unknown>
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: 08/182,248
; FILING DATE: 14-JAN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: ALI KAMAREI
; REGISTRATION NUMBER: 37000
; REFERENCE/DOCKET NUMBER: 10262-1US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650-322-7371
; TELEFAX: 650-322-7389
; INFORMATION FOR SEQ ID NO: 129:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 129:
US-10-930-300-129

Query Match      33.3%; Score 26; DB 5; Length 11;
Best Local Similarity 40.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY      2 IKRDNDYSK 11
      |||
Db      1 VKRRNRNIK 10

RESULT 66
US-10-193-460A-16
; Sequence 16, Application US/10193460A
; Publication No. US20030082769A1
; GENERAL INFORMATION:
; APPLICANT: BOEHRINGER INGELHEIM (CANADA) LTD.
; TITLE OF INVENTION: HUMAN PAPILLOMAVIRUS E2 TRANSACTIVATION
; TITLE OF INVENTION: DOMAIN/INHIBITOR CO-CRYSTAL AND X-RAY COORDINATES DEFINING
; TITLE OF INVENTION: THE INHIBITOR-BINDING POCKET
; FILE REFERENCE: 13/100
; CURRENT APPLICATION NUMBER: US/10/193,460A
; CURRENT FILING DATE: 2002-07-11
; PRIOR APPLICATION NUMBER: 60/304,412
; PRIOR FILING DATE: 2001-07-12
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 16
; LENGTH: 12
; TYPE: PRT
; ORGANISM: HPV16
US-10-193-460A-16

Query Match      33.3%; Score 26; DB 4; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 DNRDYSK 11
      |||
Db      1 DHIDYWK 7

RESULT 67
US-10-652-407-44
; Sequence 44, Application US/10652407
; Publication No. US20040180823A1
; GENERAL INFORMATION:
; APPLICANT: Pasquale, Elena B.
; APPLICANT: Koolpe, Mitchell
; APPLICANT: Murali, Keith K.
; TITLE OF INVENTION: NOVEL AGENTS THAT MODULATE EPH RECEPTOR ACTIVITY
; FILE REFERENCE: BURHAM, 003A
; CURRENT APPLICATION NUMBER: US/10/652,407
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US 60/413,242
; PRIOR FILING DATE: 2002-09-24
; NUMBER OF SEQ ID NOS: 71
```

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 44
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: EphA4-binding peptide
US-10-652-407-44

Query Match 33.3%; Score 26; DB 4; Length 12;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKP 13
Db 1 DHNHNLNP 9

RESULT 68
US-10-958-765-35
Sequence 35, Application US/10958765
Publication No. US20050191296A1
GENERAL INFORMATION:
APPLICANT: Viasum Research and Development Company of the Hebrew
APPLICANT: University of Jerusalem
TITLE OF INVENTION: Broad Spectrum in vivo effective Superantigen Toxin Antagonists
TITLE OF INVENTION: based on the interaction between CD28 and the Superantigen and
TITLE OF INVENTION: uses thereof
FILE REFERENCE: 1396-16824-17428US+
CURRENT APPLICATION NUMBER: US/10/958,765
PRIOR FILING DATE: 2004-10-04
PRIOR APPLICATION NUMBER: IL 148993
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: PCT/IL03/00278
PRIOR FILING DATE: 2003-04-03
NUMBER OF SEQ ID NOS: 63
SOFTWARE: PatentIn version 3.3
SEQ ID NO 35
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide pbs
US-10-958-765-35

Query Match 33.3%; Score 26; DB 5; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.5e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDYSK 11
Db 4 HHDSK 9

RESULT 69
US-09-992-665-15
Sequence 15, Application US/09992665
Publication No. US20030092009A1
GENERAL INFORMATION:
APPLICANT: Kala Palm
TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF NEOPLASTIC DISEASE
FILE REFERENCE: CEMTRES.002A
CURRENT APPLICATION NUMBER: US/09/992,665
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: 60/249,508
PRIOR FILING DATE: 2000-11-16
NUMBER OF SEQ ID NOS: 380
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 15
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Probe
US-09-992-665-15

Query Match 33.3%; Score 26; DB 3; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYSK 11
Db 3 HDSYSK 8

RESULT 70
US-09-391-104-15
Sequence 15, Application US/09391104
Publication No. US20020031817A1
GENERAL INFORMATION:
APPLICANT: Abbott Laboratories
APPLICANT: Falduto, Michael T.
APPLICANT: Magnuson, Scott R.
APPLICANT: Morgan, Douglas W.
TITLE OF INVENTION: HUMAN MATRIX METALLOPROTEINASE GENE,
TITLE OF INVENTION: PROTEINS ENCODED THEREFROM AND METHODS
FILE REFERENCE: 6073 US P1
CURRENT APPLICATION NUMBER: US/09/391,104
PRIOR FILING DATE: 1999-09-07
PRIOR APPLICATION NUMBER: US 08/814,394
PRIOR FILING DATE: 1997-03-11
NUMBER OF SEQ ID NOS: 35
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 15
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptides
US-09-391-104-15

Query Match 33.3%; Score 26; DB 3; Length 15;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHND 8
Db 4 DHND 7

RESULT 71
US-10-124-986-33
Sequence 33, Application US/10124986
Publication No. US20030036508A1
GENERAL INFORMATION:
APPLICANT: Ford et al.
TITLE OF INVENTION: EGF MOTIF PROTEIN, EGF16, MATERIALS AND METHODS
FILE REFERENCE: 28110/37958
CURRENT APPLICATION NUMBER: US/10/124,986
PRIOR FILING DATE: 2002-04-17
PRIOR APPLICATION NUMBER: US 09/981,649
PRIOR FILING DATE: 2001-10-15
PRIOR APPLICATION NUMBER: US 09/687,860
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/620,312
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: US 09/363,316
PRIOR FILING DATE: 1999-07-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence

```

; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: EGR16 peptide
US-10-124-986-33

Query Match      33.3%; Score 26; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDHNDYSKNP 13
   | : | : |
Db 3 REDDDPDWNP 12

RESULT 72
US-10-116-275-44
; Sequence 44, Application US/10116275
; Publication No. US20030211476A1
; GENERAL INFORMATION:
; APPLICANT: Elian Pharmaceutical Technology
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Brayden, David
; APPLICANT: Byrne, Daragh
; APPLICANT: Lambkin, Imelda
; APPLICANT: Higgins, Lisa
; TITLE OF INVENTION: Genetic Analysis of Peyer's Patches and M Cells and Methods and
; TITLE OF INVENTION: Compositions Targeting Peyer's Patches and M Cell Receptors
; FILE REFERENCE: E1067/20087
; CURRENT APPLICATION NUMBER: US/10/116, 275
; CURRENT FILING DATE: 2002-10-04
; NUMBER OF SEQ ID NOS: 349
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 44
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Listed in Table titled "Peptides that Target to and/or Enhance Up
; OTHER INFORMATION: take Across the GIT"
US-10-116-275-44

Query Match      33.3%; Score 26; DB 4; Length 15;
Best Local Similarity 27.3%; Pred. No. 1.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
   | : | : |
Db 4 LRRNHSKKN 14

RESULT 73
US-10-475-104-129
; Sequence 129, Application US/10475104
; Publication No. US20040171097A1
; GENERAL INFORMATION:
; APPLICANT: Schneider-Mergener, Jens
; APPLICANT: Schutkowski, Mike
; APPLICANT: Reimer, Ulf
; APPLICANT: Dong, Liyang
; APPLICANT: Panse, Soren
; APPLICANT: Scharn, Dirk
; APPLICANT: Oesterkamp, Frank
; APPLICANT: Hummel, Gerd
; APPLICANT: Jodion, Laurence
; TITLE OF INVENTION: Method for Determining the Substrate Specificity of an Enzymatic
; TITLE OF INVENTION: Activity and a Device Therefor
; FILE REFERENCE: 2918-0102
; CURRENT APPLICATION NUMBER: US/10/475, 104
; PRIOR FILING DATE: 2003-10-17
; PRIOR APPLICATION NUMBER: PCT/EP02/04265
; NUMBER OF SEQ ID NOS: 144
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 129

; LENGTH: 15
; TYPE: PRT
; ORGANISM: Unknown
; FEATURE:
; OTHER INFORMATION: synthesized peptide sequence
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (14)..(14)
; OTHER INFORMATION: Xaa = beta-alanine
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (15)..(15)
; OTHER INFORMATION: amino group
US-10-475-104-129

Query Match      33.3%; Score 26; DB 4; Length 15;
Best Local Similarity 36.4%; Pred. No. 1.9e+03;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
   | : | : |
Db 3 ISKNDPDYQDD 13

RESULT 74
US-10-126-845-53
; Sequence 53, Application US/10126845
; Publication No. US20030181367A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; APPLICANT: Philhla, Clemencia
; APPLICANT: Houghten, Richard
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: E1067/20058
; CURRENT APPLICATION NUMBER: US/10/126, 845
; CURRENT FILING DATE: 2002-10-15
; NUMBER OF SEQ ID NOS: 119
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 53
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: D form retroinversion peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: dansylated
; FEATURE:
; NAME/KEY: MISC_FEATURE
; LOCATION: (2)..(16)
; OTHER INFORMATION: D form amino acid
US-10-126-845-53

Query Match      33.3%; Score 26; DB 4; Length 16;
Best Local Similarity 27.3%; Pred. No. 2e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
   | : | : |
Db 5 LRRNHSKKN 15

RESULT 75
US-10-764-235-53
; Sequence 53, Application US/10764235
; Publication No. US20040138132A1
; GENERAL INFORMATION:
; APPLICANT: O'Mahony, Daniel J.
; APPLICANT: Lambkin, Imelda J.
; TITLE OF INVENTION: MEMBRANE TRANSLOCATING PEPTIDE DRUG DELIVERY SYSTEM
; FILE REFERENCE: P26,479-B USA
```

1 CURRENT APPLICATION NUMBER: US/10/764,235
2 CURRENT FILING DATE: 2004-01-23
3 PRIOR APPLICATION NUMBER: 09/671,089
4 PRIOR FILING DATE: 2000-09-27
5 PRIOR APPLICATION NUMBER: 60/156,246
6 PRIOR FILING DATE: 1999-09-27
7 NUMBER OF SEQ ID NOS: 59
8 SOFTWARE: PatentIn version 3.1
9 SEQ ID NO 53
10 LENGTH: 16
11 TYPE: PRT
12 ORGANISM: Artificial Sequence
13 FEATURE:
14 OTHER INFORMATION: D form retroinversion peptide
15 NAME/KEY: MOD_RES
16 LOCATION: (1)..(1)
17 OTHER INFORMATION: danylated
18 FEATURE:
19 NAME/KEY: MISC_FEATURE
20 LOCATION: (2)..(16)
21 OTHER INFORMATION: D form amino acid
22 US-10-764-235-53

Query Match 33.3%; Score 26; DB 4; Length 16;
Best Local Similarity 27.3%; Pred. No. 2e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
DB 5 LRRNHSHKAN 15

RESULT 76
US-10-955-656-53
1 Sequence 53, Application US/10955656
2 Publication No. US20050101762A1
3 GENERAL INFORMATION:
4 APPLICANT: O'Mahony, Daniel J.
5 APPLICANT: Lambkin, Imelda J.
6 APPLICANT: Pinilla, Clemencia
7 APPLICANT: Houghten, Richard
8 TITLE OF INVENTION: CONJUGATES OF MEMBRANE TRANSLOCATING AGENTS AND PHARMACEUTICALLY
9 FILE REFERENCE: P26, 481-A USA
10 CURRENT APPLICATION NUMBER: US/10/955,656
11 CURRENT FILING DATE: 2004-09-30
12 PRIOR APPLICATION NUMBER: 10/126,845
13 PRIOR FILING DATE: 2002-04-19
14 PRIOR APPLICATION NUMBER: 09/671,089
15 PRIOR FILING DATE: 2000-09-27
16 PRIOR APPLICATION NUMBER: 60/156,246
17 PRIOR FILING DATE: 1999-09-27
18 NUMBER OF SEQ ID NOS: 119
19 SOFTWARE: PatentIn version 3.1
20 SEQ ID NO 53
21 LENGTH: 16
22 TYPE: PRT
23 ORGANISM: Artificial Sequence
24 FEATURE:
25 OTHER INFORMATION: D form retroinversion peptide
26 NAME/KEY: MOD_RES
27 LOCATION: (1)..(1)
28 OTHER INFORMATION: danylated
29 FEATURE:
30 NAME/KEY: MISC_FEATURE
31 LOCATION: (2)..(16)
32 OTHER INFORMATION: D form amino acid
33 US-10-955-656-53

Query Match 33.3%; Score 26; DB 5; Length 16;
Best Local Similarity 27.3%; Pred. No. 2e+03;

Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
DB 5 LRRNHSHKAN 15

RESULT 77
US-10-660-370-87
1 Sequence 87, Application US/10660370
2 Publication No. US20050064507A1
3 GENERAL INFORMATION:
4 APPLICANT: Shaw, J. Stephen
5 APPLICANT: National Institutes of Health
6 TITLE OF INVENTION: Determining Kinase Specificity
7 FILE REFERENCE: 1662.009US2
8 CURRENT APPLICATION NUMBER: US/10/660,370
9 CURRENT FILING DATE: 2003-09-11
10 NUMBER OF SEQ ID NOS: 640
11 SOFTWARE: FastSeq for Windows Version 4.0
12 SEQ ID NO 87
13 LENGTH: 17
14 TYPE: PRT
15 ORGANISM: Artificial Sequence
16 FEATURE:
17 OTHER INFORMATION: A synthetic peptide
18 US-10-660-370-87

Query Match 33.3%; Score 26; DB 5; Length 17;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 7; Conservative 2; Mismatches 1; Indels 4; Gaps 1;

QY 1 SIKRDNDYSKNPM 14
DB 8 SIKRD---TVNPL 17

RESULT 78
US-09-839-884-6
1 Sequence 6, Application US/09839884
2 Patent No. US20020076739A1
3 GENERAL INFORMATION:
4 APPLICANT: Aebersold, Rudolf H.
5 APPLICANT: Gelb, Michael H.
6 APPLICANT: Gygi, Steven
7 APPLICANT: Scott, C R
8 APPLICANT: Turecek, Frantisek
9 APPLICANT: Gerber, Scott A
10 APPLICANT: Rist, Beate
11 TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
12 FILE REFERENCE: 64-98A
13 CURRENT APPLICATION NUMBER: US/09/839,884
14 CURRENT FILING DATE: 2001-04-20
15 PRIOR APPLICATION NUMBER: 09/383,062
16 PRIOR FILING DATE: 1999-08-25
17 PRIOR APPLICATION NUMBER: 60/097,788
18 PRIOR FILING DATE: 1998-08-25
19 NUMBER OF SEQ ID NOS: 64
20 SOFTWARE: PatentIn Ver. 2.0
21 SEQ ID NO 6
22 LENGTH: 18
23 TYPE: PRT
24 ORGANISM: Artificial Sequence
25 FEATURE:
26 OTHER INFORMATION: Description of Artificial Sequence: Test peptide
27 US-09-839-884-6

Query Match 33.3%; Score 26; DB 3; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12

Db 1 KDDONPHSN 10

RESULT 79
US-09-371-900-50
Sequence 50, Application US/09371900
Patent No. US20020137700A1
GENERAL INFORMATION:
APPLICANT: FALB, DEAN A
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
NUMBER OF SEQUENCES: 54
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/371,900
FILING DATE: 11-Aug-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: US 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: CORUZZI, LAURA A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-104
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 50:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-09-371-900-50
Query Match 33.3%; Score 26; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 DYSKNP 13
Db 5 EYKNP 10
RESULT 80
US-09-924-417-16
Sequence 16, Application US/09924417
Patent No. US2002014241A1
GENERAL INFORMATION:
APPLICANT: FALB, DEAN
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
DISEASE
NUMBER OF SEQUENCES: 67

CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/924,417
FILING DATE: 07-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/034,286
FILING DATE: 04-MAR-1998
APPLICATION NUMBER: 08/870,434
FILING DATE: 06-JUN-1997
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
APPLICATION NUMBER: 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-114-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-924-417-16
Query Match 33.3%; Score 26; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 8 DYSKNP 13
Db 5 EYKNP 10
RESULT 81
US-09-839-884-6
Sequence 6, Application US/09839884
Publication No. US2003087322A9
GENERAL INFORMATION:
APPLICANT: Aebbersold, Rudolf H.
APPLICANT: Gyl, Michael H
APPLICANT: Gyl, Steven
APPLICANT: Scott, C R
APPLICANT: turecek, Frantisek
APPLICANT: Geiber, Scott A
APPLICANT: Rist, Beate
TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
FUNCTION IN COMPLEX MIXTURE
FILE REFERENCE: 64-98A

/ CURRENT APPLICATION NUMBER: US/09/839,884
/ CURRENT FILING DATE: 2001-04-20
/ PRIOR APPLICATION NUMBER: 09/383,062
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 60/097,788
/ PRIOR FILING DATE: 1998-08-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 6
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Test peptide
US-09-839-884-6

Query Match 33.3%; Score 26; DB 3; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDYSKN 12
DB 1 KDDQNPSSN 10

RESULT 82
US-10-225-567A-1380
/ Sequence 1380, Application US/10225567A
/ Publication No. US2003011379A1
/ GENERAL INFORMATION:
/ APPLICANT: Lifespan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenn C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1380
/ LENGTH: 18
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-225-567A-1380

Query Match 33.3%; Score 26; DB 4; Length 18;
Best Local Similarity 40.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHDYKNPM 14
DB 3 DFRDHAKNAL 12

RESULT 83
US-10-186-950-50
/ Sequence 50, Application US/10186950
/ Publication No. US20030188327A1
/ GENERAL INFORMATION:
/ APPLICANT: PALB, DEAN A
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
/ TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR DISEASE
/ NUMBER OF SEQUENCES: 54
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PENNIE & EDMONDS LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: New York
/ COUNTRY: USA
/ ZIP: 10036-2711

/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/186,950
/ FILING DATE: 02-Jul-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/944,496
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/599,654
/ FILING DATE: 09-FEB-1996
/ APPLICATION NUMBER: US 08/485,573
/ FILING DATE: 07-JUN-1995
/ APPLICATION NUMBER: US 08/386,844
/ FILING DATE: 10-FEB-1995
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CORUZZI, LAURA A
/ REGISTRATION NUMBER: 30,742
/ REFERENCE/DOCKET NUMBER: 7853-104
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (212) 790-9090
/ TELEFAX: (212) 869-8864
/ TELEX: 66141 PENNIE
/ INFORMATION FOR SEQ ID NO: 50:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: unknown
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 50:
US-10-186-950-50

Query Match 33.3%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKNPM 13
DB 5 BYKNPM 10

RESULT 84
US-10-653-872-16
/ Sequence 16, Application US/10653872
/ Publication No. US2004008192A1
/ GENERAL INFORMATION:
/ APPLICANT: Palb, Dean
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
/ THE TREATMENT AND DIAGNOSIS OF CARDIOVASCULAR
/ DISEASE
/ NUMBER OF SEQUENCES: 67
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: PENNIE & EDMONDS LLP
/ STREET: 1155 Avenue of the Americas
/ CITY: New York
/ STATE: NY
/ COUNTRY: USA
/ ZIP: 10036-2711
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/653,872
/ FILING DATE: 03-Sep-2003
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/924,417

FILING DATE: 07-AUG-2001
APPLICATION NUMBER: US/09/034,286
FILING DATE: 04-MAR-1998
APPLICATION NUMBER: 08/870,434
FILING DATE: 06-JUN-1997
APPLICATION NUMBER: 08/799,910
FILING DATE: 13-FEB-1997
APPLICATION NUMBER: 60/011,787
FILING DATE: 16-FEB-1996
APPLICATION NUMBER: 08/599,654
FILING DATE: 09-FEB-1996
APPLICATION NUMBER: 08/485,573
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 08/386,844
FILING DATE: 10-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-114-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)7909090
TELEFAX: (212)8699741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-10-653-872-16

Query Match 33.3%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKRP 13
: : : :
DB 5 EYRNP 10

RESULT 85
US-10-994-815-6
Sequence 6, Application US/10994815
Publication No. US20050233399A1
GENERAL INFORMATION:
APPLICANT: Aebersold, Rudolf H.
APPLICANT: Gelb, Michael H
APPLICANT: Gysli, Steven
APPLICANT: Scott, C R
APPLICANT: Turecek, Frantisek
APPLICANT: Gerber, Scott A
APPLICANT: Rist, Beate
TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
FILE REFERENCE: 64-98A
CURRENT APPLICATION NUMBER: US/10/994,815
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: US/09/839,884
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/383,062
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/097,788
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Test peptide

US-10-994-815-6

Query Match 33.3%; Score 26; DB 5; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12
: : : :
DB 1 KDDQNPSSN 10

RESULT 86
US-10-225-567A-2058
Sequence 2058, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2292
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2058
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-2058

Query Match 33.3%; Score 26; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDYS 10
: : : :
DB 2 SVSYEYGDYS 11

RESULT 87
US-10-378-173-190
Sequence 190, Application US/10378173
Publication No. US20030232014A1
GENERAL INFORMATION:
APPLICANT: Burke et al.
TITLE OF INVENTION: PHOSPHORYLATED PROTEINS AND USES RELATED THERETO
FILE REFERENCE: MDSP-P01-023
CURRENT APPLICATION NUMBER: US/10/378,173
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: 60/360787
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 231
SOFTWARE: PatentIn version 3.2
SEQ ID NO 190
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: phosphorylated peptide
NAME/KEY: MISC FEATURE
LOCATION: (14)-(14)
OTHER INFORMATION: phosphorylation
NAME/KEY: MISC FEATURE
LOCATION: (16)-(16)
OTHER INFORMATION: phosphorylation
US-10-378-173-190

Query Match 33.3%; Score 26; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSKNPM 14
DB 2 YSKNPM 7

RESULT 88
US-10-466-085A-21
; Sequence 21, Application US/10466085A
; Publication No. US20040161835A1
; GENERAL INFORMATION:
; APPLICANT: KUBOTA, Michio
; APPLICANT: MARUTA, Kazuhiko
; APPLICANT: YAMAMOTO, Takuo
; APPLICANT: FUKUDA, Shigeharu
; TITLE OF INVENTION: POLYPEPTIDE HAVING -ISOMALTOXYLGLUCOSACCHARIDE-FORMING ENZYME
; FILE REFERENCE: KUBOTA=14
; CURRENT APPLICATION NUMBER: US/10/466,085A
; CURRENT FILING DATE: 2003-07-11
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: JP 5441/2001
; PRIOR FILING DATE: 2001-01-12
; PRIOR APPLICATION NUMBER: PCT/JP02/00052
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 21
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Bacillus globisporus NT5
US-10-466-085A-21

Query Match 33.3%; Score 26; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNP 13
DB 1 DYSKNP 6

RESULT 89
US-10-025-222A-36
; Sequence 36, Application US/10025222A
; Publication No. US2003003444A1
; GENERAL INFORMATION:
; APPLICANT: PELLETIER, JERRY
; APPLICANT: GROS, PHILIPPE
; APPLICANT: DUBOW, MICHAEL
; TITLE OF INVENTION: COMPOSITIONS AND METHODS INVOLVING AN ESSENTIAL
; TITLE OF INVENTION: STAPHYLOCOCCUS AUREUS GENE AND ITS ENCODED PROTEIN
; FILE REFERENCE: 073406-0701
; CURRENT APPLICATION NUMBER: US/10/025,222A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/256,349
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Staphylococcus aureus
US-10-025-222A-36

Query Match 32.7%; Score 25.5; DB 4; Length 17;
Best Local Similarity 53.8%; Pred. No. 2.6e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 1 SIKRD--HNDYS 10

DB 2 SIKRDIANDLS 14

RESULT 90
US-09-834-765-658
; Sequence 658, Application US/09834765
; Patent No. US20020055478A1
; GENERAL INFORMATION:
; APPLICANT: Mary Paris
; APPLICANT: Pia M. Challita-Eid
; APPLICANT: Arthur B. Raitano
; APPLICANT: Steve Chappell Mitchell
; APPLICANT: Daniel B.H. Afar
; APPLICANT: Aya Jakobovits
; TITLE OF INVENTION: GTP-BINDING PROTEIN USEFUL IN TREATMENT
; TITLE OF INVENTION: AND DETECTION OF CANCER
; FILE REFERENCE: 129,6USU1
; CURRENT APPLICATION NUMBER: US/09/834,765
; CURRENT FILING DATE: 2001-09-21
; PRIOR APPLICATION NUMBER: 60/197,647
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 770
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 658
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-834-765-658

Query Match 32.1%; Score 25; DB 3; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 SIKRDNDY 9
DB 1 STLRDPNEY 9

RESULT 91
US-09-938-864-180
; Sequence 180, Application US/09938864
; Publication No. US20030072767A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Smithgall, Molly
; APPLICANT: Moulton, Gus
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Sleath, Paul R.
; APPLICANT: Moseman, Sally
; APPLICANT: Evans, Lawrence
; APPLICANT: Spies, A. Gregory
; APPLICANT: Boydelton, Jeremy
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY
; FILE REFERENCE: 210121.465C5
; CURRENT APPLICATION NUMBER: US/09/938,864
; CURRENT FILING DATE: 2001-08-24
; NUMBER OF SEQ ID NOS: 413
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-938-864-180

Query Match 32.1%; Score 25; DB 3; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12

Db 1 RHHNMHQRN 9

RESULT 92

US-09-791-477-180

Sequence 180, Application US/09791477

Publication No. US20030082194A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DIAGNOSIS

TITLE OF INVENTION: AND THERAPY OF MALIGNANT MESOTHELIOMA

FILE REFERENCE: 2077,000200

CURRENT APPLICATION NUMBER: US/09/791,477

PRIOR FILING DATE: 2001-02-22

PRIOR APPLICATION NUMBER: 60/184,070

PRIOR FILING DATE: 2000-02-22

NUMBER OF SEQ ID NOS: 326

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 180

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-09-791-477-180

Query Match

Best Local Similarity 32.1%; Score 25; DB 3; Length 9;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12

Db 1 RHHNMHQRN 9

RESULT 93

US-09-785-019-180

Sequence 180, Application US/09785019

Publication No. US20030082196A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Cheever, Martin A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Smithgall, Molly

APPLICANT: Moulton, Gus

APPLICANT: Vedvick, Thomas S.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

FILE REFERENCE: 210121,465C4

CURRENT APPLICATION NUMBER: US/09/785,019

CURRENT FILING DATE: 2001-02-15

NUMBER OF SEQ ID NOS: 376

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 180

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-09-785-019-180

Query Match

Best Local Similarity 33.1%; Score 25; DB 3; Length 9;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12

Db 1 RHHNMHQRN 9

RESULT 94

US-10-125-635A-180

Sequence 180, Application US/10125635A

Publication No. US20030039635A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Smithgall, Molly D.

APPLICANT: Carter, Darrick

APPLICANT: Cheever, Martin A.

APPLICANT: McNeill, Patricia D.

APPLICANT: Sutherland, R. Alec

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

FILE REFERENCE: 210121,465C7

CURRENT APPLICATION NUMBER: US/10/125,635A

CURRENT FILING DATE: 2002-07-19

NUMBER OF SEQ ID NOS: 461

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 180

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-125-635A-180

Query Match

Best Local Similarity 32.1%; Score 25; DB 4; Length 9;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12

Db 1 RHHNMHQRN 9

RESULT 95

US-10-002-603-180

Sequence 180, Application US/10002603

Publication No. US20030095971A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: McNeill, Patricia D.

APPLICANT: Smithgall, Molly

APPLICANT: Moulton, Gus

APPLICANT: Vedvick, Thomas S.

APPLICANT: Sleath, Paul R.

APPLICANT: Mossman, Sally

APPLICANT: Evans, Lawrence

APPLICANT: Spies, A. Gregory

APPLICANT: Boydston, Jeremy

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1

TITLE OF INVENTION: SPECIFIC IMMUNOTHERAPY

FILE REFERENCE: 210121,465C6

CURRENT APPLICATION NUMBER: US/10/002,603

CURRENT FILING DATE: 2001-10-30

NUMBER OF SEQ ID NOS: 413

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 180

LENGTH: 9

TYPE: PRT

ORGANISM: Homo sapiens

US-10-002-603-180

Query Match

Best Local Similarity 32.1%; Score 25; DB 4; Length 9;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

OY 4 RDHNDYSKN 12

Db 1 RHHNMHQRN 9

RESULT 96

US-10-195-835-180

Sequence 180, Application US/10195835

Publication No. US20030198622A1

GENERAL INFORMATION:

APPLICANT: Gaiger, Alexander

APPLICANT: Smithgall, Molly D.

APPLICANT: Carter, Darrick

```

; APPLICANT: Cheever, Martin A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Sutherland, R. Alec
; APPLICANT: Moesman, Sally P.
; APPLICANT: Evans, Lawrence S.
; APPLICANT: Swanson, Ryan M.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C8
; CURRENT APPLICATION NUMBER: US/10/195,835
; PENDING FILING DATE: 2002-07-12
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-195-835-180

```

```

Query Match          32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      |||:|
      1 RHHNMHQRN 9

```

```

RESULT 97
US-10-286-333-180
; Sequence 180, Application US/10286333
; Publication No. US20030215458A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20030215458A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C10
; CURRENT APPLICATION NUMBER: US/10/286,333
; PENDING FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-286-333-180

```

```

Query Match          32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      |||:|
      1 RHHNMHQRN 9

```

```

Query Match          32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      |||:|
      1 RHHNMHQRN 9

```

```

RESULT 98
US-10-244-830-180
; Sequence 180, Application US/10244830
; Publication No. US20030235557A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: Cheever, Martin A.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C9
; CURRENT APPLICATION NUMBER: US/10/244,830
; PENDING FILING DATE: 2002-09-16
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180

```

```

; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-244-830-180

```

```

Query Match          32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      |||:|
      1 RHHNMHQRN 9

```

```

RESULT 99
US-10-427-717-180
; Sequence 180, Application US/10427717
; Publication No. US20040018204A1
; GENERAL INFORMATION:
; APPLICANT: Gaiger, Alexander
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Jaya, No. US20040018204A1a1e
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR WT1
; FILE REFERENCE: 210121.465C11
; CURRENT APPLICATION NUMBER: US/10/427,717
; PENDING FILING DATE: 2003-04-30
; NUMBER OF SEQ ID NOS: 508
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 180
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-427-717-180

```

```

Query Match          32.1% Score 25; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      4 RDHNDYSK 12
      |||:|
      1 RHHNMHQRN 9

```

```

RESULT 100
US-10-363-791-11
; Sequence 11, Application US/10363791
; Publication No. US20040029197A1
; GENERAL INFORMATION:
; APPLICANT: TAKIMOTO, Masao
; APPLICANT: KUZUMAKI, No. US20040029197A1a1yuki
; APPLICANT: SATO, No. US20040029197A1a1yuki
; APPLICANT: SAHARA, Hiroeki
; TITLE OF INVENTION: A novel human cancer/testis-associated gene thereof
; FILE REFERENCE: 4439-4006
; CURRENT APPLICATION NUMBER: US/10/363,791
; PENDING FILING DATE: 2003-03-07
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 11
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-363-791-11

```

```

Query Match          32.1% Score 25; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      3 KRHDNDYSK 11
      |||:|

```

Db 1 KIDNDEFIK 9

Search completed: January 20, 2006, 19:45:35
Job time : 52.4808 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 ; Search time 5.65385 Seconds
(without alignments)
25.093 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78
Sequence: 1 SIKRDHNDYKRW 14Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA New:*
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2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description	
1	30	38.5	20	6	US-10-485-788A-542	Sequence 542, App
2	26	33.3	9	7	US-11-033-039-459	Sequence 459, App
3	26	33.3	11	6	US-10-925-366A-90	Sequence 90, App
4	25	32.1	9	7	US-11-045-024-5857	Sequence 5857, App
5	25	32.1	14	6	US-10-467-657-8922	Sequence 8922, App
6	25	32.1	16	6	US-10-834-397-238	Sequence 238, App
7	25	32.1	18	7	US-11-033-039-1157	Sequence 1157, App
8	25	32.1	18	7	US-11-033-039-1180	Sequence 1180, App
9	25	32.1	18	7	US-11-033-039-1186	Sequence 1186, App
10	25	32.1	18	7	US-11-033-039-1206	Sequence 1206, App
11	25	32.1	20	6	US-10-485-788A-589	Sequence 589, App
12	25	32.1	20	7	US-11-022-562-128	Sequence 128, App
13	24	30.8	9	6	US-10-665-658-15	Sequence 15, App
14	24	30.8	9	6	US-10-665-658-56	Sequence 66, App
15	24	30.8	10	7	US-11-033-039-88	Sequence 88, App
16	24	30.8	11	7	US-11-045-024-427	Sequence 427, App
17	24	30.8	11	7	US-11-045-024-428	Sequence 428, App
18	24	30.8	11	7	US-11-045-024-5104	Sequence 5104, App
19	24	30.8	11	7	US-11-045-024-5105	Sequence 5105, App
20	24	30.8	11	7	US-11-045-024-8154	Sequence 8154, App
21	24	30.8	11	7	US-11-045-024-8155	Sequence 8155, App
22	24	30.8	11	7	US-11-045-024-10738	Sequence 10738, App
23	24	30.8	11	7	US-11-045-024-10739	Sequence 10739, App
24	24	30.8	11	7	US-11-045-024-12504	Sequence 12504, App
25	24	30.8	11	7	US-11-045-024-12505	Sequence 12505, App

26	24	30.8	12	7	US-11-058-727-104	Sequence 104, App
27	24	30.8	12	7	US-11-108-389-104	Sequence 104, App
28	24	30.8	12	7	US-11-069-834-28	Sequence 28, Appl
29	24	30.8	16	6	US-10-467-657-8683	Sequence 8683, App
30	24	30.8	16	7	US-11-054-515-2918	Sequence 2918, App
31	24	30.8	18	7	US-11-033-039-1169	Sequence 1169, App
32	24	30.8	18	7	US-11-033-039-1196	Sequence 1196, App
33	24	30.8	20	7	US-11-033-039-55	Sequence 55, Appl
34	24	30.8	20	7	US-11-037-708-32	Sequence 32, Appl
35	23	29.5	11	7	US-11-045-024-933	Sequence 933, App
36	23	29.5	14	7	US-11-054-315-3215	Sequence 315, App
37	23	29.5	15	7	US-11-106-932-106	Sequence 106, App
38	23	29.5	17	6	US-10-467-657-8975	Sequence 8975, App
39	22.5	28.8	20	7	US-11-094-142-31	Sequence 31, Appl
40	22	28.2	8	7	US-11-054-515-3179	Sequence 3179, App
41	22	28.2	10	6	US-10-859-643-628	Sequence 628, App
42	22	28.2	10	6	US-10-973-977-66	Sequence 66, Appl
43	22	28.2	10	7	US-11-097-864-628	Sequence 628, App
44	22	28.2	10	7	US-11-097-812-628	Sequence 628, App
45	22	28.2	12	7	US-11-058-727-105	Sequence 105, App
46	22	28.2	12	7	US-11-108-389-105	Sequence 105, App
47	22	28.2	13	6	US-10-511-559-554	Sequence 554, App
48	22	28.2	13	6	US-10-511-559-555	Sequence 555, App
49	22	28.2	14	7	US-11-116-144-258	Sequence 258, App
50	22	28.2	15	6	US-10-939-890-199	Sequence 199, App
51	22	28.2	15	7	US-11-045-024-13269	Sequence 13269, App
52	22	28.2	16	6	US-10-939-990-11	Sequence 11, Appl
53	22	28.2	16	6	US-10-939-990-205	Sequence 205, App
54	22	28.2	19	6	US-11-152-846-2	Sequence 2, Appl1
55	22	28.2	19	6	US-10-503-575-173	Sequence 173, App
56	21	26.9	7	7	US-11-129-104-12	Sequence 12, Appl
57	21	26.9	8	7	US-11-045-024-7497	Sequence 7497, App
58	21	26.9	8	7	US-11-045-024-8233	Sequence 8233, App
59	21	26.9	9	6	US-10-473-037-8	Sequence 8, Appl1
60	21	26.9	9	6	US-10-859-643-482	Sequence 482, App
61	21	26.9	9	7	US-11-021-441-102	Sequence 102, App
62	21	26.9	9	7	US-11-097-864-482	Sequence 482, App
63	21	26.9	9	7	US-11-097-812-482	Sequence 482, App
64	21	26.9	9	7	US-11-045-024-5858	Sequence 5858, App
65	21	26.9	9	7	US-11-041-893-66	Sequence 66, Appl
66	21	26.9	10	7	US-11-010-748A-522	Sequence 522, App
67	21	26.9	10	7	US-11-156-843-119	Sequence 119, App
68	21	26.9	10	7	US-11-129-104-54	Sequence 54, Appl
69	21	26.9	10	7	US-11-129-104-55	Sequence 55, Appl
70	21	26.9	11	7	US-11-156-843-30	Sequence 30, Appl
71	21	26.9	11	7	US-11-156-843-37	Sequence 37, Appl
72	21	26.9	11	7	US-11-127-877-88	Sequence 88, Appl
73	21	26.9	11	7	US-11-127-877-90	Sequence 90, Appl
74	21	26.9	12	7	US-11-110-274-321	Sequence 321, App
75	21	26.9	13	6	US-10-511-559-475	Sequence 475, App
76	21	26.9	13	6	US-10-511-559-476	Sequence 476, App
77	21	26.9	13	7	US-11-054-515-3172	Sequence 3172, App
78	21	26.9	13	7	US-11-054-515-3187	Sequence 3187, App
79	21	26.9	13	7	US-11-078-469-111	Sequence 109, App
80	21	26.9	13	7	US-11-078-469-111	Sequence 111, App
81	21	26.9	13	7	US-11-078-469-113	Sequence 113, App
82	21	26.9	13	7	US-11-078-469-117	Sequence 117, App
83	21	26.9	14	7	US-11-129-104-51	Sequence 11, Appl
84	21	26.9	14	6	US-10-989-326-11	Sequence 52, Appl
85	21	26.9	14	6	US-10-632-645-15	Sequence 15, Appl
86	21	26.9	14	7	US-11-054-515-3218	Sequence 3218, App
87	21	26.9	15	6	US-10-952-535A-29	Sequence 29, Appl
88	21	26.9	15	7	US-11-045-024-13379	Sequence 13379, App
89	21	26.9	16	7	US-11-108-185-39	Sequence 39, Appl
90	21	26.9	16	7	US-11-108-185-42	Sequence 42, Appl
91	21	26.9	17	6	US-11-108-185-67	Sequence 67, Appl
92	21	26.9	17	6	US-10-201-825-23	Sequence 23, Appl
93	21	26.9	17	7	US-11-038-880-165	Sequence 165, App
94	21	26.9	18	6	US-10-503-575-177	Sequence 177, Appl
95	21	26.9	18	6	US-10-485-788A-536	Sequence 536, App
96	21	26.9	18	6	US-10-500-878-18	Sequence 18, Appl
97	21	26.9	18	7	US-11-033-039-1304	Sequence 1304, App
98	21	26.9	20	6	US-10-956-155A-5	Sequence 5, Appl1

99 21 26.9 20 7 US-11-054-515-2131
100 21 26.9 20 7 US-11-078-469-55

Sequence 2131, Ap
Sequence 55, Appl

ALIGNMENTS

RESULT 1

US-10-485-788A-542
; Sequence 542, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweitzer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 542
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-542

Query Match 38.5%; Score 30; DB 6; Length 20;
Best Local Similarity 57.1%; Pred. No. 14;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDYSKNP 13
DB 9 NDETPNP 15

RESULT 2

US-11-033-039-459
; Sequence 459, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RSH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 459
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-459

Query Match 33.3%; Score 26; DB 7; Length 9;
Best Local Similarity 71.4%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDPNDY 9
DB 1 KRVPDPY 7

RESULT 3

US-10-925-366A-90
; Sequence 90, Application US/10925366A
; Publication No. US20050271663A1
; GENERAL INFORMATION:
; APPLICANT: Ignatovich, Olga
; APPLICANT: Demildt, Rudolph M.T.
; APPLICANT: Benjamin, Woolven
; APPLICANT: Grant, Steven
; APPLICANT: Jones, Philip
; APPLICANT: Basran, Amrik
; APPLICANT: Brewis, Neil
; TITLE OF INVENTION: Compositions and Methods for Treating Inflammatory Disorders
; FILE REFERENCE: 8039/2105
; CURRENT APPLICATION NUMBER: US/10/925,366A
; CURRENT FILING DATE: 2004-08-24
; PRIOR APPLICATION NUMBER: US 10/744,774
; PRIOR FILING DATE: 2003-12-23
; PRIOR APPLICATION NUMBER: PCT/GB2003/002804
; PRIOR FILING DATE: 2003-06-30
; PRIOR APPLICATION NUMBER: PCT/GB2002/03014
; PRIOR FILING DATE: 2002-06-28
; PRIOR APPLICATION NUMBER: GB 0230202.4
; PRIOR FILING DATE: 2002-12-27
; PRIOR APPLICATION NUMBER: GB 115841.9
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: PCT/GB2004/002829
; PRIOR FILING DATE: 2004-06-30
; PRIOR APPLICATION NUMBER: US 60/535,076
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: PCT/GB2003/005646
; PRIOR FILING DATE: 2003-12-24
; PRIOR APPLICATION NUMBER: GB 0327706.8
; PRIOR FILING DATE: 2003-11-28
; PRIOR APPLICATION NUMBER: US 60/509,613
; PRIOR FILING DATE: 2003-10-08
; NUMBER OF SEQ ID NOS: 368
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 90
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Artificial CDR3 sequence
US-10-925-366A-90

Query Match 33.3%; Score 26; DB 6; Length 11;
Best Local Similarity 60.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 4; Gaps 1;

QY 4 RDNHNDY 9
DB 2 RDNHNSLFDY 11

RESULT 4

US-11-045-024-5857
; Sequence 5857, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esben
; APPLICANT: Kubo, Ralph

APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 5857
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5857

Query Match 32.1% Score 25; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Oy 5 DHNDYSKN 12
Db 1 DHEKHSN 8

RESULT 5
US-10-467-657-8922
Sequence 8922, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: Seqwin99, version 1.04
SEQ ID NO: 8922
LENGTH: 14
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8922

Query Match 32.1% Score 25; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 69;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 6 HNDYK 11
Db 4 HNSYK 9

RESULT 6
US-10-834-397-238
Sequence 238, Application US/10834397
Publication No. US2006000334A1
GENERAL INFORMATION:

APPLICANT: Knappik, Achim

pack, Peter

llag, vic

Ge, Liming

Moroney, Simon

Plueckthun, Andreas

TITLE OF INVENTION: Protein/(Poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESSER: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/834,397

FILING DATE: 29-Apr-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-FEB-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 238:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 238:

US-10-834-397-238

Query Match 32.1% Score 25; DB 6; Length 16;
Best Local Similarity 54.5%; Pred. No. 80;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;

Oy 4 RDHNDYSKNPM 14
Db 5 RDNYSY--DFM 13

RESULT 7
US-11-033-039-1157

Sequence 1157, Application US/11033039

Publication No. US20060002947A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: XU, MINZHEN

TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: RH-2017US01

CURRENT APPLICATION NUMBER: US/11/033,039

CURRENT FILING DATE: 2005-01-11

```
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1157
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1157
```

```
Query Match          32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 11
        | | | | :
Db       7 DFNDYEE 13
```

```
RESULT 8
US-11-033-039-1180
; Sequence 1180, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1180
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1180
```

```
Query Match          32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 11
        | | | | :
Db       10 DFNDYEE 16
```

```
RESULT 9
US-11-033-039-1186
```

```
; Sequence 1186, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1186
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1186
```

```
Query Match          32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSK 11
        | | | | :
Db       7 DFNDYEE 13
```

```
RESULT 10
US-11-033-039-1206
; Sequence 1206, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1206
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1206
```

```
Query Match          32.1%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 91;
```

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 DHNDYSK 11
10 DFNDYER 16

RESULT 11

US-10-485-788A-589
; Sequence 589, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: NO PCT/US02/24655
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 589
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-589

Query Match 32.1%; Score 25; DB 6; Length 20;
Best Local Similarity 44.4%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IKRDNDYS 10
7 VKSEFNSYS 15

RESULT 12

US-11-022-562-128
; Sequence 128, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, JIANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatsSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-128

Query Match 32.1%; Score 25; DB 7; Length 20;
Best Local Similarity 57.1%; Pred. No. 1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDYSK 11

Db 10 DNGDYSE 16

RESULT 13

US-10-665-658-15
; Sequence 15, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPacIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/665,658
; FILING DATE: 19-Sep-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/031971
; FILING DATE: 27-NOV-1996
; APPLICATION NUMBER: 08/974899
; FILING DATE: 20-NOV-1997
; APPLICATION NUMBER: 09/420745
; FILING DATE: 20-OCT-1999
; APPLICATION NUMBER: 09/975798
; FILING DATE: 28-FEB-2001
; ATTORNEY/AGENT INFORMATION:
; NAME: Tan, Lee K.
; REGISTRATION NUMBER: 39,447
; REFERENCE/DOCKET NUMBER: P1014R1C1D1C1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-4462
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 9 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-665-658-15

Query Match 30.8%; Score 24; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 4 RDNDY 9
1 QCHNEY 6

RESULT 14

US-10-665-658-66
; Sequence 66, Application US/10665658
; Publication No. US20050276801A1
; GENERAL INFORMATION:
; APPLICANT: Jardieu, Paula M.
; APPLICANT: Presta, Leonard G.
; TITLE OF INVENTION: Humanized Anti-CD11a Antibodies
; NUMBER OF SEQUENCES: 71
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 MB floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/665,658

FILING DATE: 19-Sep-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/031971

FILING DATE: 27-NOV-1996

APPLICATION NUMBER: 08/974899

FILING DATE: 20-NOV-1997

APPLICATION NUMBER: 09/420745

FILING DATE: 20-OCT-1999

APPLICATION NUMBER: 09/975798

FILING DATE: 28-FEB-2001

ATTORNEY/AGENT INFORMATION:

NAME: Tan, Lee K.

REGISTRATION NUMBER: 39,447

REFERENCE/DOCKET NUMBER: P1014R1C1D1C1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-4462

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 66:

SEQUENCE CHARACTERISTICS:

LENGTH: 9 amino acids

TYPE: Amino Acid

TOPOLOGY: <Unknown>

SEQUENCE DESCRIPTION: SEQ ID NO: 66:

US-10-665-658-66

Query Match 30.8%; Score 24; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9

Db 1 QQHNEY 6

RESULT 15

US-11-033-039-88

Sequence 88, Application US/11033039

Publication No. US20060002947A1

GENERAL INFORMATION:

APPLICANT: HUMPHREYS, ROBERT

APPLICANT: XU, MINZHEN

TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES

FILE REFERENCE: REH-2017US01

CURRENT APPLICATION NUMBER: US/11/033,039

PRIOR FILING DATE: 2005-01-11

PRIOR APPLICATION NUMBER: 10/245,871

PRIOR FILING DATE: 2002-09-17

PRIOR APPLICATION NUMBER: 10/197,000

PRIOR FILING DATE: 2002-07-17

PRIOR APPLICATION NUMBER: 09/336,813

PRIOR FILING DATE: 1999-09-14

NUMBER OF SEQ ID NOS: 1452

SOFTWARE: PatentIn version 3.3

SEQ ID NO 88

LENGTH: 10

TYPE: PRT

ORGANISM: Archaea hypogaea

US-11-033-039-88

Query Match 30.8%; Score 24; DB 7; Length 10;

Best Local Similarity 50.0%; Pred. No. 70;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRDNDY 9

Db 2 IORDSDY 9

RESULT 16

US-11-045-024-427

Sequence 427, Application US/11045024

Publication No. US20050271676A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert

APPLICANT: Baker, Denise Marie

APPLICANT: Celis, Esben

APPLICANT: Kubo, Ralph

APPLICANT: Grey, Howard M.

APPLICANT: Eptimmune Inc.

TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency

FILE REFERENCE: 2060.0040007

CURRENT APPLICATION NUMBER: US/11/045,024

PRIOR FILING DATE: 2005-01-28

PRIOR APPLICATION NUMBER: US 09/412,863

PRIOR FILING DATE: 1999-10-05

PRIOR APPLICATION NUMBER: US 08/027,146

PRIOR FILING DATE: 1993-03-05

PRIOR APPLICATION NUMBER: US 08/073,205

PRIOR FILING DATE: 1993-06-04

PRIOR APPLICATION NUMBER: US 08/103,396

PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/159,339

PRIOR FILING DATE: 1993-11-29

PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04

PRIOR APPLICATION NUMBER: US 08/347,610

PRIOR FILING DATE: 1994-12-01

NUMBER OF SEQ ID NOS: 14528

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 427

LENGTH: 11

TYPE: PRT

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

US-11-045-024-427

Query Match 30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDNDY 9

Db 6 RDDSDY 11

RESULT 17

US-11-045-024-428

Sequence 428, Application US/11045024

Publication No. US20050271676A1

GENERAL INFORMATION:

APPLICANT: Sette, Alessandro

APPLICANT: Sidney, John

APPLICANT: Southwood, Scott

APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert

APPLICANT: Baker, Denise Marie

APPLICANT: Celis, Esben

```
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 428
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-428
```

```
Query Match 30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 RDHNDY 9
||:|
Db 6 RDSDDY 11
```

```
RESULT 18
US-11-045-024-5104
Sequence 5104, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
```

```
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5104
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5104
```

```
Query Match 30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 RDHNDY 9
||:|
Db 6 RDSDDY 11
```

```
RESULT 19
US-11-045-024-5105
Sequence 5105, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
PRIOR FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5105
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5105
```

```
Query Match 30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 4 RDHNDY 9
||:|
Db 6 RDSDDY 11
```

```
RESULT 20
US-11-045-024-8154
; Sequence 8154, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8154
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8154

Query Match          30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
RESULT 21
US-11-045-024-8155
; Sequence 8155, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024

RESULT 22
US-11-045-024-10738
; Sequence 10738, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10738
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8155

Query Match          30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```

; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10738

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDNDY 9
      ||:|
      6 RDDS DY 11

Db

RESULT 23
US-11-045-024-10739
; Sequence 10739, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 10739
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10739

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDNDY 9
      ||:|
      6 RDDS DY 11

Db

RESULT 24
US-11-045-024-12504
; Sequence 12504, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
```

```

; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: PaSeq for Windows Version 4.0
; SEQ ID NO 12504
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12504

Query Match      30.8%; Score 24; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 78;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      4 RDNDY 9
      ||:|
      6 RDDS DY 11

Db

RESULT 25
US-11-045-024-12505
; Sequence 12505, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
```


RESULT 29
US-10-467-657-8683
Sequence 8683, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASTIGNANI Vega
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
PRIOR FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqW4n99, version 1.04
SEQ ID NO 8683
LENGTH: 16
TYPE: PRT
ORGANISM: *Neisseria gonorrhoeae*
US-10-467-657-8683

Query Match 30.8%; Score 24; DB 6; Length 16;
Best Local Similarity 36.4%; Pred. No. 1.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRDNHDSKNP 13
| | | | |
Db 6 KQDDADITQHP 16

RESULT 30
US-11-054-515-2918
Sequence 2918, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2918
LENGTH: 16
TYPE: PRT
ORGANISM: *Homo sapiens*
US-11-054-515-2918

Query Match 30.8%; Score 24; DB 7; Length 16;

Best Local Similarity 80.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
| | | | |
Db 9 DHNVY 13

RESULT 31
US-11-033-039-1169
Sequence 1169, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1169
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)-(5)
OTHER INFORMATION: Ava
US-11-033-039-1169

Query Match 30.8%; Score 24; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDND 8
: | | | :
Db 6 TIKRSYNN 13

RESULT 32
US-11-033-039-1196
Sequence 1196, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197,000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1196
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1196

Query Match 30.8%; Score 24; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDHND 8
|:|:|:
Db 6 TIKRSTYNN 13

RESULT 33
US-11-033-039-55
/ Sequence 55, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 55
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Arachis hypogaea
US-11-033-039-55

Query Match 30.8%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKRDHNDY 9
|:|:|:
Db 12 IQRDEDSY 19

RESULT 34
US-11-057-708-32
/ Sequence 32, Application US/11057708
/ Publication No. US20050250702A1
/ GENERAL INFORMATION:
/ APPLICANT: Universiteit Utrecht
/ APPLICANT: Strous, Gerardus
/ APPLICANT: Van Kerkhof, Petrus
/ APPLICANT: Govers, Roland
/ TITLE OF INVENTION: CONTROLLING AVAILABILITY OR ACTIVITY OF PROTEINS BY USE OF PROTEIN
/ FILE REFERENCE: 2183-4525US
/ CURRENT APPLICATION NUMBER: US/11/057,708
/ CURRENT FILING DATE: 2005-02-14
/ PRIOR APPLICATION NUMBER: US/09/660,302
/ PRIOR FILING DATE: 2000-09-12
/ PRIOR APPLICATION NUMBER: PCT/NL99/00136
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: EP98200799.9
/ PRIOR FILING DATE: 1998-03-12
/ NUMBER OF SEQ ID NOS: 51
/ SOFTWARE: PatentIn version 3.0

/ SEQ ID NO 32
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Unnaure, RHESUS BLOOD GROUP-ASSOCIATED GLYCOPROTEIN
US-11-057-708-32

Query Match 29.5%; Score 23; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 1e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HNDY 9
|:|:|:
Db 2 HNEY 5

RESULT 35
US-11-045-024-933
/ Sequence 933, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Spilmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 933
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-933

Query Match 29.5%; Score 23; DB 7; Length 11;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12
|:|:|:
Db 3 HTNYTSN 9

RESULT 36
US-11-054-515-3215
/ Sequence 3215, Application US/11054515

Publication No. US2005025532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS23P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 3215
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-3215

Query Match 29.5%; Score 23; DB 7; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 5 DHNDYKRP 13
Db 4 DHNGDGP 12

RESULT 37
US-11-106-932-106
Sequence 106, Application US/11106932
Publication No. US20050260697A1
GENERAL INFORMATION:
APPLICANT: WANG, KA-WANG KEVIN
APPLICANT: HAYES, RONALD
APPLICANT: LITV, MING CHEN
APPLICANT: OLI, MONIKA
TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
FILE REFERENCE: 5853-549-1
CURRENT APPLICATION NUMBER: US/11/106,932
CURRENT FILING DATE: 2005-04-15
NUMBER OF SEQ ID NOS: 147
SOFTWARE: PatentIn version 3.2
SEQ ID NO 106
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-11-106-932-106

Query Match 29.5%; Score 23; DB 7; Length 15;
Best Local Similarity 37.5%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 4 RDHNDYK 11
Db 7 KKHEDFDK 14

RESULT 38
US-10-467-657-8975
Sequence 8975, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqMan99, version 1.04
SEQ ID NO 8975
LENGTH: 17
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8975

Query Match 29.5%; Score 23; DB 6; Length 17;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

Qy 2 IKRDNDYKRP 13
Db 7 IFRHNN-IKRP 16

RESULT 39
US-11-094-142-31
Sequence 31, Application US/11094142
Publication No. US20050260770A1
GENERAL INFORMATION:
APPLICANT: Cohen, Irun R.
APPLICANT: Quintana, Francisco Javier
APPLICANT: Doman, Bryan
APPLICANT: Elizur, Gad
APPLICANT: Hagedorn, Peter H.
TITLE OF INVENTION: ANTIGEN ARRAY AND DIAGNOSTIC USES THEREOF
FILE REFERENCE: 29462
CURRENT APPLICATION NUMBER: US/11/094,142
CURRENT FILING DATE: 2005-03-31
NUMBER OF SEQ ID NOS: 47
SOFTWARE: PatentIn version 3.3
SEQ ID NO 31
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial sequence
FEATURES:
OTHER INFORMATION: Synthetic peptide
US-11-094-142-31

Query Match 28.8%; Score 22.5; DB 7; Length 20;
Best Local Similarity 54.5%; Pred. No. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

Qy 3 KRDNNDYKRN 12
Db 6 KRKKKQDISQV 16

RESULT 40
US-11-054-515-3179
Sequence 3179, Application US/11054515
Publication No. US2005025532A1
GENERAL INFORMATION:

```

; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: P5523p3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3179
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3179

```

```

Query Match      28.2%; Score 22; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.Se+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      2 IKRDHNDY 9
      :|||:
Db      1 VKRYTFDY 8

```

```

RESULT 41
US-10-859-643-628
; Sequence 628, Application US/10859643
; Publication No. US2006002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Encited 161p2f10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-628

```

```

Query Match      28.2%; Score 22; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

```

```

Qy      3 KRDHNDYSKN 12
      |||:|
Db      3 KRLH--YAKN 10

```

```

RESULT 42
US-10-973-977-66
; Sequence 66, Application US/10973977
; Publication No. US20060008467A1
; GENERAL INFORMATION:
; APPLICANT: HAYNES, BARTON F.
; APPLICANT: LIAO, HUA-XIN
; APPLICANT: LETVIN, NORMAN
; TITLE OF INVENTION: HUMAN IMMUNODEFICIENCY VIRUS VACCINE
; FILE REFERENCE: 1579-942
; CURRENT APPLICATION NUMBER: US/10/973,977
; CURRENT FILING DATE: 2004-10-27
; PRIOR APPLICATION NUMBER: 09/775,805
; PRIOR FILING DATE: 2001-02-05
; PRIOR APPLICATION NUMBER: 09/497,497
; PRIOR FILING DATE: 2000-02-04
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 66
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Macaque sp.
US-10-973-977-66

```

```

Query Match      28.2%; Score 22; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

```

Qy      9 YSNMFM 14
      |||||
Db      4 YDNKQM 9

```

```

RESULT 43
US-11-097-864-628
; Sequence 628, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Faris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161p2f10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 628
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-628

```

```

Query Match      28.2%; Score 22; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Qy      3 KRDHNDYSKN 12
      |||:|
Db      3 KRLH--YAKN 10

```

RESULT 44
US-11-097-912-628
Sequence 628, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 51158206204
CURRENT APPLICATION NUMBER: US/11/097,912
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 628
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-912-628

Query Match 28.2%; Score 22; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

Cy 3 KRDNDYSKN 12
|||
Db 3 KRLH-YAKN 10

RESULT 45
US-11-058-727-105
Sequence 105, Application US/11058727
Publication No. US20050261483A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Prensall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/287809
CURRENT APPLICATION NUMBER: US/11/058,727
CURRENT FILING DATE: 2005-02-15
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105
LENGTH: 12
TYPE: PRT
ORGANISM: Bacillus thuringiensis (mutated)
US-11-058-727-105

Query Match 28.2%; Score 22; DB 7; Length 12;

Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 5 DHNDYS 10
|||
Db 1 DYKDYA 6

RESULT 46
US-11-108-389-105
Sequence 105, Application US/11108389
Publication No. US20050261188A1
GENERAL INFORMATION:
APPLICANT: Andre R. Abad
APPLICANT: Ronald D. Flannagan
APPLICANT: Rafael Herrmann
APPLICANT: Theodore W. Kahn
APPLICANT: Albert L. Lu
APPLICANT: Billy Fred McCutchen
APPLICANT: James K. Prensall
APPLICANT: James F.H. Wong
APPLICANT: Cao-Guo Yu
TITLE OF INVENTION: Gene Encoding Proteins With Pesticidal
TITLE OF INVENTION: Activity
FILE REFERENCE: 35718/291049
CURRENT APPLICATION NUMBER: US/11/108,389
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: 60/391,786
PRIOR FILING DATE: 2002-06-26
PRIOR APPLICATION NUMBER: 60/460,787
PRIOR FILING DATE: 2003-04-04
PRIOR APPLICATION NUMBER: 10/606,320
PRIOR FILING DATE: 2003-06-25
NUMBER OF SEQ ID NOS: 134
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 105
LENGTH: 12
TYPE: PRT
ORGANISM: Bacillus thuringiensis (mutated)
US-11-108-389-105

Query Match 28.2%; Score 22; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 5 DHNDYS 10
|||
Db 1 DYKDYA 6

RESULT 47
US-10-511-559-554
Sequence 554, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis, J.
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: PCT/EP03/04063
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: EP 02008712.8
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 03006554.4
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 554
LENGTH: 13
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-554

Query Match 28.2%; Score 22; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDHNYSKN 12
DB 3 IORTGKNSLN 13

RESULT 48

US-10-511-559-555
Sequence 555, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
APPLICANT: CAR, Francis, J.
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: PCT/EP03/04063
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: EP 02008712.8
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 03006554.4
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 555
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-555

Query Match 28.2%; Score 22; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDHNYSKN 12
DB 1 IORTGKNSLN 11

RESULT 49

US-11-116-144-258
Sequence 258, Application US/11116144
Publication No. US2005027181A1
GENERAL INFORMATION:
APPLICANT: BERTHE, FRANCOIS XAVIER
APPLICANT: CASADEVAL, FRANCESC VAYREDA
APPLICANT: SANZ MARIA, MARIA CRUZ
APPLICANT: GARCIA, TERESA LLOP
APPLICANT: OLE, ANGELS MOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
FILE REFERENCE: INT-084
CURRENT APPLICATION NUMBER: US/11/116,144
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: PCT/ES04/000581
PRIOR FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: EP 03380307.3
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 258

LENGTH: 14
TYPE: PRT
ORGANISM: Plasmodium yoelii
US-11-116-144-258

Query Match 28.2%; Score 22; DB 7; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
DB 5 DHGKSGKN 12

RESULT 50

US-10-939-890-199
Sequence 199, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen B.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pocheon, Sibylla
APPLICANT: Ramalingam, Kondaredi
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf B.
APPLICANT: Von Wronski, Matthew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617.70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 199
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-199

Query Match 28.2%; Score 22; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 2.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDHND 8
DB 5 VKRDHND 11

RESULT 51

US-11-045-024-13269

```
/ Sequence 13269, Application US/11045024
/ Publication No. US2005027676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13269
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-13269

Query Match      28.2%; Score 22; DB 7; Length 15;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Matthew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or VEGF/KDR Binding Polypeptide
/ US-10-939-890-11

Query Match      28.2%; Score 22; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

NUMBER OF SEQ ID NOS: 883
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 205
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-205

Query Match 28.2%; Score 22; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHDYSKN 12
|:|:|:
Db 1 DHDYCLHN 8

RESULT 54
US-11-152-846-2
Sequence 2, Application US/11152846
Publication No. US20060002862A1
GENERAL INFORMATION:
APPLICANT: Medimmune Vaccines, Inc.
APPLICANT: Truong-Le, Vu
APPLICANT: Scherer, Tom
TITLE OF INVENTION: HIGH PRESSURE SPRAY-DRY OF ANTIBODIES
FILE REFERENCE: 26-000630US
CURRENT APPLICATION NUMBER: US/11/152,846
CURRENT FILING DATE: 2005-06-13
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.2
SEQ ID NO 2
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-11-152-846-2

Query Match 28.2%; Score 22; DB 7; Length 16;
Best Local Similarity 40.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRDNDSKN 12
|:|:|:
Db 7 KRDYNSPLKS 16

RESULT 55
US-10-503-575-173
Sequence 173, Application US/10503575
Publication No. US20050244823A1
GENERAL INFORMATION:
APPLICANT: Drifflhout, Jan Wouter
APPLICANT: van Veele, Petrus Antonius
APPLICANT: Konig, Frits
TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
FILE REFERENCE: 2799/72843-PCT-US
CURRENT APPLICATION NUMBER: US/10/503,575
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: PCT/NL03/00077
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: EP 02075456.0
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.1
SEQ ID NO 173
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-575-173

Query Match 28.2%; Score 22; DB 6; Length 19;
Best Local Similarity 33.3%; Pred. No. 3.2e+02;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHDYSKNP 13
|:|:|:
Db 4 DFGNTYQGP 12

RESULT 56
US-11-129-104-12
Sequence 12, Application US/11129104
Publication No. US20050287644A1
GENERAL INFORMATION:
APPLICANT: CHIU, YI-PANG
APPLICANT: CHEN, LEE-HSIUAN
APPLICANT: HUANG, JEN-PIN
TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
FILE REFERENCE: 09468.0005-00000
CURRENT APPLICATION NUMBER: US/11/129,104
CURRENT FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/571,440
PRIOR FILING DATE: 2004-05-14
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 12
LENGTH: 7
TYPE: PRT
ORGANISM: Unknown Organism
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
US-11-129-104-12

Query Match 26.9%; Score 21; DB 7; Length 7;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YSKNPM 14
|:|:|:
Db 2 YDKTFL 7

RESULT 57
US-11-045-024-7497
Sequence 7497, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Stefan
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Eplimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06

PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7497
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7497

Query Match 26.9%; Score 21; DB 7; Length 8;
Best Local Similarity 42.9%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KRDNDY 9
Db 2 QEDHEKY 8

RESULT 58
US-11-045-024-8233
Sequence 8233, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Eserben
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.004007
CURRENT APPLICATION NUMBER: US/11/045.024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8233
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8233

Query Match 26.9%; Score 21; DB 7; Length 8;
Best Local Similarity 42.9%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KRDNDY 9
Db 2 QEDHEKY 8

RESULT 59
US-10-473-037-8
Sequence 8, Application US/10473037
Publication No. US20050260206A1
GENERAL INFORMATION:
APPLICANT: KYOWA HAKKO KOGYO CO., LTD.
TITLE OF INVENTION: Agents for treatment of cancer using recombinant anti-CD3 antibo
TITLE OF INVENTION: The antibody fragments
FILE REFERENCE: 11374W01
CURRENT APPLICATION NUMBER: US/10/473.037
CURRENT FILING DATE: 2003-09-26
PRIOR APPLICATION NUMBER: JP2001-097483
PRIOR FILING DATE: 2001-03-29
NUMBER OF SEQ ID NOS: 50
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 8
LENGTH: 9
TYPE: PRT
ORGANISM: Mus musculus
US-10-473-037-8

Query Match 26.9%; Score 21; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 7 NDYSKP 13
Db 1 HOYSKLP 7

RESULT 60
US-10-859-643-482
Sequence 482, Application US/10859643
Publication No. US2006002993A1
GENERAL INFORMATION:
APPLICANT: Raitano, Arthur B.
APPLICANT: Fatis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 1612F10B Useful in Treatment and Detection of
FILE REFERENCE: 511582006203
CURRENT APPLICATION NUMBER: US/10/859.643
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 482
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-859-643-482

Query Match 26.9%; Score 21; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 5 DNDYSKN 12
Db 1 DNNMYDVN 8

RESULT 61
US-11-021-441-102

```
/ Sequence 102, Application US/11021441
/ Publication No. US20050249748A1
/ GENERAL INFORMATION:
/ APPLICANT: DUBENSKY, Thomas W., Jr.
/ APPLICANT: PORTNOY, Daniel A.
/ APPLICANT: LOCKETT, William S., Jr.
/ APPLICANT: COOK, David N.
/ TITLE OF INVENTION: RECOMBINANT NUCLEIC ACID MOLECULES,
/ TITLE OF INVENTION: EXPRESSION CASSETTES, AND BACTERIA, AND METHODS OF USE
/ TITLE OF INVENTION: THEREOF
/ FILE REFERENCE: 282172003900
/ CURRENT APPLICATION NUMBER: US/11/021,441
/ CURRENT FILING DATE: 2004-12-23
/ PRIOR APPLICATION NUMBER: US 60/616,750
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/615,287
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR APPLICATION NUMBER: US 60/599,377
/ PRIOR FILING DATE: 2004-08-05
/ PRIOR APPLICATION NUMBER: PCT/US2004/23881
/ PRIOR FILING DATE: 2004-07-23
/ PRIOR APPLICATION NUMBER: US 10/883,599
/ PRIOR FILING DATE: 2004-06-30
/ PRIOR APPLICATION NUMBER: US 60/556,744
/ PRIOR FILING DATE: 2004-03-26
/ NUMBER OF SEQ ID NOS: 129
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 102
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Listeria monocytogenes
US-11-021-441-102
```

```
Query Match          26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      4 RDHNDY 9
         |||||
Db       3 KDGNEY 8
```

```
RESULT 62
US-11-097-864-482
/ Sequence 482, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 482
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-11-097-864-482
```

```
Query Match          26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
         |||||
Db       1 DNNMVDVN 8
```

```
RESULT 63
US-11-097-912-482
/ Sequence 482, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 482
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-11-097-912-482
```

```
Query Match          26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 DHNDYSKN 12
         |||||
Db       1 DNNMVDVN 8
```

```
RESULT 64
US-11-045-024-5858
/ Sequence 5858, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
```

PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5858
LENGTH: 9
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5858

Query Match 26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 37.5%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 DHNDYSKN 12
DB 1 EHEKTHSN 8

RESULT 65
US-11-041-893-66
Sequence 66, Application US/11041893
Publication No. US2006002941A1
GENERAL INFORMATION:
APPLICANT: Mahabirab, Gregory G.
TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
FILE REFERENCE: 100123.401
CURRENT APPLICATION NUMBER: US/11/041,893
CURRENT FILING DATE: 2005-01-24
PRIOR APPLICATION NUMBER: US 60/616,855
PRIOR FILING DATE: 2004-10-06
PRIOR APPLICATION NUMBER: US 60/538,713
PRIOR FILING DATE: 2004-01-23
NUMBER OF SEQ ID NOS: 295
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 66
LENGTH: 9
TYPE: PRT
ORGANISM: Listeria monocytogenes
US-11-041-893-66

Query Match 26.9%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHNDY 9
DB 3 KDGNEY 8

RESULT 66
US-11-010-748A-522
Sequence 522, Application US/11010748A
Publication No. US2005024421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMATTER, Wolfgang
APPLICANT: WOLL, Heidrun
APPLICANT: SCHIAR, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MRR-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926

SOFTWARE: PatentIn version 3.1
SEQ ID NO 522
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CD64 peptide fragment
US-11-010-748A-522

Query Match 26.9%; Score 21; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDN 6
DB 5 SLOEDH 10

RESULT 67
US-11-156-843-119
Sequence 119, Application US/11156843
Publication No. US20050267035A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Fox, Brian
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
FILE REFERENCE: 00-33
CURRENT APPLICATION NUMBER: US/11/156,843
CURRENT FILING DATE: 2005-06-20
PRIOR APPLICATION NUMBER: US/09/883,727
PRIOR FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 119
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C1s exosite binding moiety
US-11-156-843-119

Query Match 26.9%; Score 21; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
DB 3 DYEDY 7

RESULT 68
US-11-129-104-54
Sequence 54, Application US/11129104
Publication No. US20050287644A1
GENERAL INFORMATION:
APPLICANT: CHIU, YI-FANG
APPLICANT: CHEN, LEE-HSIUAN
APPLICANT: HUANG, JEN-PIN
TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
FILE REFERENCE: 09468.0005-00000
CURRENT APPLICATION NUMBER: US/11/129,104
CURRENT FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/571,440
PRIOR FILING DATE: 2004-05-14
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 54
LENGTH: 10
TYPE: PRT

ORGANISM: Homo sapiens
US-11-129-104-54

Query Match 26.9%; Score 21; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YSKNPM 14
| | | |
Db 5 YDKTPL 10

RESULT 69
US-11-129-104-55
Sequence 55, Application US/11129104
Publication No. US20050287644A1
GENERAL INFORMATION:
APPLICANT: CHIU, YI-PANG
APPLICANT: CHEN, LEE-HSIUAN
APPLICANT: HUANG, JEN-PIN
TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
TITLE OF INVENTION: RABBIT-MOUSE HYBRIDOMAS
FILE REFERENCE: 09468.0005-00000
CURRENT FILING DATE: 2005-05-13
PRIORITY FILING DATE: 2005-05-13
PRIORITY FILING DATE: 2004-05-14
NUMBER OF SEQ ID NOS: 100
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 55
LENGTH: 10
TYPE: PRT
ORGANISM: Homo sapiens
US-11-129-104-55

Query Match 26.9%; Score 21; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YSKNPM 14
| | | |
Db 2 YDKTPL 7

RESULT 70
US-11-156-843-30
Sequence 30, Application US/11156843
Publication No. US20050267035A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Fox, Brian
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
FILE REFERENCE: 00-33
CURRENT FILING DATE: 2005-06-20
PRIORITY FILING DATE: 2005-06-20
PRIORITY FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 30
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C1s exosite binding moiety
NAME/KEY: MUTAGEN
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
US-11-156-843-30

Query Match 26.9%; Score 21; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
| | | |
Db 4 DYEDY 8

RESULT 71
US-11-156-843-37
Sequence 37, Application US/11156843
Publication No. US20050267035A1
GENERAL INFORMATION:
APPLICANT: West, Robert R.
APPLICANT: Sheppard, Paul O.
APPLICANT: Fox, Brian
TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
TITLE OF INVENTION: Complement C1s
FILE REFERENCE: 00-33
CURRENT FILING DATE: 2005-06-20
PRIORITY FILING DATE: 2005-06-20
PRIORITY FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 140
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 37
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: C1s exosite binding moiety
NAME/KEY: MUTAGEN
LOCATION: (10)...(10)
OTHER INFORMATION: Xaa = sulfated tyrosine
US-11-156-843-37

Query Match 26.9%; Score 21; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
| | | |
Db 4 DYEDY 8

RESULT 72
US-11-127-677-88
Sequence 88, Application US/11127677
Publication No. US20050272107A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Rabbits, Terence H
APPLICANT: Tanaka, Tomoyuki
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2462
CURRENT FILING DATE: 2005-05-12
PRIORITY FILING DATE: 2003-11-14
PRIORITY FILING DATE: 2003-11-14
PRIORITY FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Derived protein sequence of intracellular Dab
US-11-127-677-88

Query Match 26.9%; Score 21; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9
Db 6 NHNTY 10

RESULT 73
US-11-127-677-90
Sequence 90, Application US/11127677
Publication No. US20050272107A1
GENERAL INFORMATION:
APPLICANT: Medical Research Council
APPLICANT: Rabbitts, Terence H
APPLICANT: Tanaka, Tomoyuki
TITLE OF INVENTION: Intracellular antibodies
FILE REFERENCE: 18396/2462
CURRENT APPLICATION NUMBER: US/11/127,677
CURRENT FILING DATE: 2005-05-12
PRIOR APPLICATION NUMBER: PCT/GB03/04942
PRIOR FILING DATE: 2003-11-14
PRIOR APPLICATION NUMBER: GB 0226729.2
PRIOR FILING DATE: 2002-11-15
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.1
SEQ ID NO 90
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Derived protein sequence of intracellular Dab
US-11-127-677-90

Query Match 26.9%; Score 21; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9
Db 6 NHNTY 10

RESULT 74
US-11-110-274-321
Sequence 321, Application US/11110274
Publication No. US20050266502A1
GENERAL INFORMATION:
APPLICANT: Merchlers, Pascal G.
APPLICANT: Hofmann, Marcel
TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
TITLE OF INVENTION: Amyloid-Beta Protein Production
FILE REFERENCE: P27,657-A USA
CURRENT APPLICATION NUMBER: US/11/110,274
CURRENT FILING DATE: 2005-04-20
PRIOR APPLICATION NUMBER: US 60/563,661
PRIOR FILING DATE: 2004-04-20
NUMBER OF SEQ ID NOS: 620
SOFTWARE: PatentIn version 3.3
SEQ ID NO 321
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
US-11-110-274-321

Query Match 26.9%; Score 21; DB 7; Length 12;
Best Local Similarity 44.4%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 HNDYKMPM 14

Db 2 HNSLRAPM 10

RESULT 75
US-10-511-559-475
Sequence 475, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis, J.
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: PCT/EP03/04063
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: EP 02008712.8
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 03006554.4
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 475
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-475

Query Match 26.9%; Score 21; DB 6; Length 13;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SIKRDND 8
Db 4 SLSEKND 11

RESULT 76
US-10-511-559-476
Sequence 476, Application US/10511559
Publication No. US20050256304A1
GENERAL INFORMATION:
APPLICANT: JONES, Tim
APPLICANT: BAKER, Matthew
APPLICANT: CARR, Francis, J.
TITLE OF INVENTION: MODIFIED FACTOR VIII
FILE REFERENCE: MER-133
CURRENT APPLICATION NUMBER: US/10/511,559
CURRENT FILING DATE: 2004-10-15
PRIOR APPLICATION NUMBER: PCT/EP03/04063
PRIOR FILING DATE: 2003-04-17
PRIOR APPLICATION NUMBER: EP 02008712.8
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: EP 03006554.4
PRIOR FILING DATE: 2003-03-24
NUMBER OF SEQ ID NOS: 1147
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 476
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-476

Query Match 26.9%; Score 21; DB 6; Length 13;
Best Local Similarity 37.5%; Pred. No. 3.1e+02;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDND 8
|:|:
Db 2 SLSENNND 9

RESULT 77

US-11-054-515-3172
; Sequence 3172, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3172
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3172

Query Match 26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
|:|:
Db 2 DYTIDY 6

RESULT 78

US-11-054-515-3187
; Sequence 3187, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 3187
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-3187

Query Match 26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 60.0%; Pred. No. 3.1e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
|:|:
Db 2 DYTIDY 6

RESULT 79

US-11-078-469-109
; Sequence 109, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHLEIDT, THOMAS
; APPLICANT: STOLOW, DAVID
; APPLICANT: CONGER, DEE
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; TITLE OF INVENTION: THERIOP
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; PRIOR FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 109
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide moiety
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)_RES
; OTHER INFORMATION: Lauryl-Ary
US-11-078-469-109

Query Match 26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYSKNPM 14
|:|:
Db 6 DMSRNPM 12

RESULT 80

US-11-078-469-111
; Sequence 111, Application US/11078469
; Publication No. US20050282755A1

GENERAL INFORMATION:
APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, THOMAS
APPLICANT: STOLOV, DAVID
APPLICANT: CONGER, DEE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 60/618,948
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 111
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: peptide moiety
FEATURE:
OTHER INFORMATION: This sequence is composed of all D-isomers
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Lauryl-Arg
US-11-078-469-111

Query Match 26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 8 DYSKRP 14
Db 6 DMSRPM 12

RESULT 81
US-11-078-469-113
Sequence 113, Application US/11078469
Publication No. US20050282755A1
GENERAL INFORMATION:
APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, THOMAS
APPLICANT: STOLOV, DAVID
APPLICANT: CONGER, DEE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 60/618,948
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 113
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: peptide moiety
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Ac-Arg

US-11-078-469-113

Query Match 26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 8 DYSKRP 14
Db 6 DMSRPM 12

RESULT 82
US-11-078-469-117
Sequence 117, Application US/11078469
Publication No. US20050282755A1
GENERAL INFORMATION:
APPLICANT: HART, SCOTT A.
APPLICANT: ZEH, KARIN
APPLICANT: MACHLEIDT, THOMAS
APPLICANT: STOLOV, DAVID
APPLICANT: CONGER, DEE
TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
FILE REFERENCE: ANS-2001-UT
CURRENT APPLICATION NUMBER: US/11/078,469
CURRENT FILING DATE: 2005-03-11
PRIOR APPLICATION NUMBER: 60/554,526
PRIOR FILING DATE: 2004-03-18
PRIOR APPLICATION NUMBER: 60/618,948
PRIOR FILING DATE: 2004-10-15
NUMBER OF SEQ ID NOS: 294
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 117
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
OTHER INFORMATION: peptide moiety
FEATURE:
OTHER INFORMATION: This sequence is composed of all D-isomers
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (1)
OTHER INFORMATION: Ac-Arg
US-11-078-469-117

Query Match 26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Cy 8 DYSKRP 14
Db 6 DMSRPM 12

RESULT 83
US-11-129-104-11
Sequence 11, Application US/11129104
Publication No. US20050287644A1
GENERAL INFORMATION:
APPLICANT: CHIU, YI-PANG
APPLICANT: CHEN, LEE-HSIUAN
APPLICANT: HUANG, JEN-PIN
TITLE OF INVENTION: METHODS FOR PRODUCING RABBIT-MOUSE
TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
FILE REFERENCE: 09468.0005-00000
CURRENT APPLICATION NUMBER: US/11/129,104
CURRENT FILING DATE: 2005-05-13
PRIOR APPLICATION NUMBER: 60/571,440
PRIOR FILING DATE: 2004-05-14
NUMBER OF SEQ ID NOS: 100

```
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 11
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
/ OTHER INFORMATION: Canine peptide
US-11-129-104-11
```

```
Query Match          26.9%; Score 21; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      9 YSKNPM 14
        |||
Db       5 YDKTFL 10
```

```
RESULT 84
US-10-989-226-52
/ Sequence 52, Application US/10989226
/ Publication No. US20050255491A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Frank D.
/ APPLICANT: Meng, Xun
/ APPLICANT: Afeyan, Noubar B.
/ APPLICANT: Gordon, Neal F.
/ TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: EP1M-P01-005
/ CURRENT APPLICATION NUMBER: US/10/989,226
/ PRIOR FILING DATE: 2004-11-15
/ PRIOR APPLICATION NUMBER: US 60/519,530
/ PRIOR FILING DATE: 2003-11-13
/ PRIOR APPLICATION NUMBER: US 60/532,687
/ PRIOR FILING DATE: 2003-12-24
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 52
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-989-226-52
```

```
Query Match          26.9%; Score 21; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      7 NDYSKNPM 14
        |||
Db       6 NDYGNPI 13
```

```
RESULT 85
US-10-632-645-15
/ Sequence 15, Application US/10632645
/ Publication No. US20050276787A1
/ GENERAL INFORMATION:
/ APPLICANT: Couto, Linda B.
/ APPLICANT: Colosi, Peter C.
/ TITLE OF INVENTION: Adeno-Associated Vectors for Expression of Factor VIII
/ FILE REFERENCE: Avigen-04082
/ CURRENT APPLICATION NUMBER: US/10/632,645
/ CURRENT FILING DATE: 2003-08-01
/ PRIOR APPLICATION NUMBER: US/09/740,211
/ PRIOR FILING DATE: 2000-12-18
/ PRIOR APPLICATION NUMBER: 09/470,618
/ PRIOR FILING DATE: 1999-12-22
/ PRIOR APPLICATION NUMBER: 60/125,974
/ PRIOR FILING DATE: 1999-03-24
/ PRIOR APPLICATION NUMBER: 60/104,394
```

```
/ PRIOR FILING DATE: 1998-10-20
/ NUMBER OF SEQ ID NOS: 15
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 15
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-632-645-15
```

```
Query Match          26.9%; Score 21; DB 6; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 YSKNP 13
        |||
Db       2 FSCNP 6
```

```
RESULT 86
US-11-054-515-3218
/ Sequence 3218, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS3P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3218
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-3218
```

```
Query Match          26.9%; Score 21; DB 7; Length 14;
Best Local Similarity 60.0%; Pred. No. 3.4e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 DHNDY 9
        |||
Db       6 DYGDY 10
```

```
RESULT 87
US-10-952-535A-29
/ Sequence 29, Application US/10952535A
/ Publication No. US20050255113A1
/ GENERAL INFORMATION:
/ APPLICANT: Huston, James S.
```


APPLICANT: Messer, Anne
APPLICANT: Lecercf, Jean-Michel
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR INHIBITING POLYPEPTIDE
TITLE OF INVENTION: ACCUMULATION ASSOCIATED WITH NEUROLOGICAL DISORDERS
FILE REFERENCE: INR-004CP
CURRENT APPLICATION NUMBER: US/10/952,535A
CURRENT FILING DATE: 2004-09-27
PRIOR APPLICATION NUMBER: 60/146,047
PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-952-535A-29

Query Match 26.9%; Score 21; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 5 HNDYSKNPM 14
Db 2 DVPDYATPPL 11

RESULT 88
US-11-045-024-13379
Sequence 13379, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Eteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Eplimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13379
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13379

Query Match 26.9%; Score 21; DB 7; Length 15;
Best Local Similarity 36.4%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IKRDNDYSKN 12
Db 5 IBSQNOQERN 15

RESULT 89
US-11-108-185-39
Sequence 39, Application US/1108185
Publication No. US20050262591A1
GENERAL INFORMATION:
APPLICANT: Debonte, Lorin R.
APPLICANT: Fan, Zhongong
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: FATY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
FILE REFERENCE: 07148-063003
CURRENT APPLICATION NUMBER: US/11/108,185
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/09/771,904
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 39
LENGTH: 16
TYPE: PRT
ORGANISM: Arabidopsis thaliana
US-11-108-185-39

Query Match 26.9%; Score 21; DB 7; Length 16;
Best Local Similarity 33.3%; Pred. No. 3.9e+02;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 HNDYSKNPM 14
Db 4 YGKTYLNPL 12

RESULT 90
US-11-108-185-42
Sequence 42, Application US/1108185
Publication No. US20050262591A1
GENERAL INFORMATION:
APPLICANT: Debonte, Lorin R.
APPLICANT: Fan, Zhongong
APPLICANT: Miao, Guo-Hua
TITLE OF INVENTION: FATY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
FILE REFERENCE: 07148-063003
CURRENT APPLICATION NUMBER: US/11/108,185
CURRENT FILING DATE: 2005-04-18
PRIOR APPLICATION NUMBER: US/09/771,904
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: US 08/874,109
PRIOR FILING DATE: 1997-06-12
NUMBER OF SEQ ID NOS: 70
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 42
LENGTH: 16
TYPE: PRT
ORGANISM: Ricinus communis
US-11-108-185-42

Query Match 26.9%; Score 21; DB 7; Length 16;
Best Local Similarity 40.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 RDNDYSKNP 13
Db 2 RWISKTYLNPL 11

RESULT 91

US-11-108-185-67
 ; Sequence 67, Application US/11108185
 ; Publication No. US20050262591A1
 ; GENERAL INFORMATION:
 ; APPLICANT: DeBonte, Lorin R.
 ; APPLICANT: Fan, Zhegong
 ; APPLICANT: Miao, Guo-Hua
 ; TITLE OF INVENTION: FATTY ACID DESATURASES AND MUTANT SEQUENCES THEREOF
 ; FILE REFERENCE: 07148-063003
 ; CURRENT APPLICATION NUMBER: US/11/108,185
 ; CURRENT FILING DATE: 2005-04-18
 ; PRIOR APPLICATION NUMBER: US/09/771,904
 ; PRIOR FILING DATE: 2001-01-29
 ; PRIOR APPLICATION NUMBER: US 08/874,109
 ; PRIOR FILING DATE: 1997-06-12
 ; NUMBER OF SEQ ID NOS: 70
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 67
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Brassica napus
 US-11-108-185-67

Query Match 26.9%; Score 21; DB 7; Length 16;
 Best Local Similarity 33.3%; Pred. No. 3.9e+02;
 Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 6 HNDYSKNPM 14
 : | | | |
 Db 4 YGKYNLNP 12

RESULT 92
 US-10-201-525-23
 ; Sequence 23, Application US/10201525
 ; Publication No. US2006009631A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Board of Regents of the University of Oklahoma
 ; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
 ; FILE REFERENCE: 5827.005
 ; CURRENT APPLICATION NUMBER: US/10/201,525
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: 09/785,343
 ; PRIOR FILING DATE: 2001-02-16
 ; PRIOR APPLICATION NUMBER: PCT/US99/16750
 ; PRIOR FILING DATE: 1999-07-23
 ; NUMBER OF SEQ ID NOS: 45
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 23
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-201-525-23

Query Match 26.9%; Score 21; DB 6; Length 17;
 Best Local Similarity 60.0%; Pred. No. 4.2e+02;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9
 | : | | |
 Db 5 DYEDY 9

RESULT 93
 US-11-038-980-165
 ; Sequence 165, Application US/11038980
 ; Publication No. US20060002893A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Centellon SAS
 ; APPLICANT: Emmanuelle Vigne

; APPLICANT: Jean-Francois Dedieu
 ; APPLICANT: Martine Iatta
 ; APPLICANT: Patrice Yeh
 ; APPLICANT: Michel Perricaudet
 ; TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery Of Heterologous Genes
 ; FILE REFERENCE: P26,992-C USA
 ; CURRENT APPLICATION NUMBER: US/11/038,980
 ; CURRENT FILING DATE: 2005-01-20
 ; PRIOR APPLICATION NUMBER: US 09/791,524
 ; PRIOR FILING DATE: 2001-02-22
 ; PRIOR APPLICATION NUMBER: PCT/IB99/01524
 ; PRIOR FILING DATE: 1999-08-27
 ; PRIOR APPLICATION NUMBER: US 60/098,028
 ; PRIOR FILING DATE: 1998-08-27
 ; NUMBER OF SEQ ID NOS: 165
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 165
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Human
 US-11-038-980-165

Query Match 26.9%; Score 21; DB 7; Length 17;
 Best Local Similarity 40.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 RDNDYSKNP 13
 | : | | |
 Db 5 RGRNONSRRP 14

RESULT 94
 US-10-503-575-77
 ; Sequence 77, Application US/10503575
 ; Publication No. US20050244823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Drijfhout, Jan Wouter
 ; APPLICANT: van Veele, Petrus Antonius
 ; APPLICANT: Konig, Frits
 ; TITLE OF INVENTION: NOVEL EPTOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
 ; FILE REFERENCE: 2799/72843-PCT-US
 ; CURRENT APPLICATION NUMBER: US/10/503,575
 ; CURRENT FILING DATE: 2004-08-04
 ; PRIOR APPLICATION NUMBER: PCT/NL03/00077
 ; PRIOR FILING DATE: 2003-02-04
 ; PRIOR APPLICATION NUMBER: EP 02075456.0
 ; PRIOR FILING DATE: 2002-02-04
 ; NUMBER OF SEQ ID NOS: 340
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 77
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-503-575-77

Query Match 26.9%; Score 21; DB 6; Length 18;
 Best Local Similarity 37.5%; Pred. No. 4.5e+02;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 6 HNDYSKNP 13
 | : | | |
 Db 4 HCNVQQQP 11

RESULT 95
 US-10-485-788A-536
 ; Sequence 536, Application US/10485788A
 ; Publication No. US20050282743A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lu, Peter S.
 ; APPLICANT: Rabinowitz, Joshua D.
 ; APPLICANT: Schweizer, Johannes

```

; APPLICANT: Carrick, Deanna Marie
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-003320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; PRIOR FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 536
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-788A-536
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Query Match      26.9%; Score 21; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 DHNDY 9
        |::||
Db      8 DNDY 12
```

RESULT 96
US-10-500-878-18

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; Sequence 18, Application US/10500878
; Publication No. US20050287527A1
; GENERAL INFORMATION:
; APPLICANT: National Research Council of Canada
; APPLICANT: NI, Feng
; APPLICANT: SU, Zhengding
; APPLICANT: XU, Ping
; APPLICANT: TOLKACHEV, Dmitri
; APPLICANT: OSBORNE, Michael J.
; APPLICANT: KOTLYCHENKO, Anatol
; TITLE OF INVENTION: QUANTITATIVE RANKING OF TRANSIENT LIGAND
; TITLE OF INVENTION: BINDING TO TARGET BIOMOLECULES BY USE OF NUCLEAR MAGNETIC
; TITLE OF INVENTION: RESONANCE
; FILE REFERENCE: 2139-24PCT
; CURRENT APPLICATION NUMBER: US/10/500,878
; CURRENT FILING DATE: 2004-07-07
; PRIOR APPLICATION NUMBER: US 60/346,894
; PRIOR FILING DATE: 2002-01-11
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 18
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Anti-thrombin peptide
US-10-500-878-18
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Query Match      26.9%; Score 21; DB 6; Length 18;
Best Local Similarity 60.0%; Pred. No. 4.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
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```
QY      4 RDHND 8
        :|||
Db      2 QSHND 6
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RESULT 97
US-11-033-039-1304
; Sequence 1304, Application US/11033039
; Publication No. US2006002947A1
; GENERAL INFORMATION:

```

; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RSH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 1304
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; NAME/KEY: MOD RES
; LOCATION: (5)-(5)
; OTHER INFORMATION: Ava
US-11-033-039-1304
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```
Query Match      26.9%; Score 21; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
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```
QY      2 IKRDHND 8
        :|||
Db      3 MKXDPND 9
```

RESULT 98
US-10-956-755A-5
; Sequence 5, Application US/10956755A
; Publication No. US20050282747A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Prestwich, Glenn
; TITLE OF INVENTION: Methods and Compositions for Wound Healing
; FILE REFERENCE: STONYB-09223
; CURRENT APPLICATION NUMBER: US/10/956,755A
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-755A-5

```
Query Match      26.9%; Score 21; DB 6; Length 20;
Best Local Similarity 41.7%; Pred. No. 5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
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```
QY      2 IKRDHNDYSKNP 13
        :|||
Db      9 IPREDVDYHLYP 20
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RESULT 99
US-11-054-515-2131
; Sequence 2131, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

```

; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,448
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2131
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2131

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Query Match      26.9%; Score 21; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY      6 HANDYS 10
      |||
      8 HNKYA 12
DB

```

```

RESULT 100
US-11-078-469-55
; Sequence 55, Application US/11078469
; Publication No. US20050282755A1
; GENERAL INFORMATION:
; APPLICANT: HART, SCOTT A.
; APPLICANT: ZEH, KARIN
; APPLICANT: MACHEIDT, THOMAS
; APPLICANT: STOLW, DAVID
; APPLICANT: CONGER, DEB
; TITLE OF INVENTION: COMPOSITIONS HAVING ANTIMICROBIAL ACTIVITY AND USES
; FILE REFERENCE: ANS-2001-UT
; CURRENT APPLICATION NUMBER: US/11/078,469
; CURRENT FILING DATE: 2005-03-11
; PRIOR APPLICATION NUMBER: 60/554,526
; PRIOR FILING DATE: 2004-03-18
; PRIOR APPLICATION NUMBER: 60/618,948
; PRIOR FILING DATE: 2004-10-15
; NUMBER OF SEQ ID NOS: 294
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 55
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide moiety
; FEATURE:
; OTHER INFORMATION: This sequence is composed of all D-isomers
; NAME/KEY: MOD_RES
; LOCATION: (1)

```

```

; OTHER INFORMATION: Ac-Thr
US-11-078-469-55
Query Match      26.9%; Score 21; DB 7; Length 20;
Best Local Similarity 57.1%; Pred. No. 5e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY      8 DYSGNDP 14
      |||
      13 DMSRNP 19
DB

```

Search completed: January 20, 2006, 19:46:27
 Job time : 6.65385 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 : Search time 7.94231 Seconds
(without alignments)
169.602 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78

Sequence: 1 SIXRDNDYSKNPM 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	25.5	32.7	20	2	665605
2	25	32.1	20	2	S56005
3	24.5	31.4	19	2	S63476
4	24	30.8	15	2	S27248
5	23	29.5	11	2	S65395
6	23	29.5	18	2	PH1629
7	22	28.2	17	2	S32587
8	22	28.2	20	2	A53875
9	21	26.9	11	2	PC2330
10	21	26.9	11	2	A26930
11	21	26.9	14	2	PS0252
12	21	26.9	14	2	A45889
13	21	26.9	15	2	I67525
14	21	26.9	17	2	PH0769
15	21	26.9	18	2	H64711
16	21	26.9	18	2	B41589
17	21	26.9	19	2	PT0244
18	20	25.6	9	2	S66608
19	20	25.6	9	2	PT0272
20	20	25.6	10	2	S62208
21	20	25.6	11	2	S65377
22	20	25.6	14	1	NYPE14
23	20	25.6	16	2	PH1778
24	20	25.6	16	2	S03084
25	20	25.6	17	2	B42965
26	20	25.6	20	2	E61497
27	20	25.6	20	2	S77992
28	19	24.4	9	2	PT0299
29	19	24.4	10	2	A13687

30	19	24.4	10	2	S74176
31	19	24.4	10	2	S23370
32	19	24.4	11	2	S23926
33	19	24.4	12	2	S65730
34	19	24.4	15	2	PH1342
35	19	24.4	15	2	PL0143
36	19	24.4	15	2	A35417
37	19	24.4	16	2	PH0791
38	19	24.4	16	2	S22040
39	19	24.4	18	2	C56211
40	19	24.4	19	2	I45957
41	19	24.4	19	2	S59485
42	19	24.4	19	2	PH1360
43	19	24.4	19	2	A61377
44	19	24.4	20	2	PH1338
45	19	24.4	20	2	T48881
46	19	24.4	20	2	A61506
47	19	24.4	20	2	B56894
48	18	23.1	7	2	A28709
49	18	23.1	11	2	A38841
50	18	23.1	11	2	S00616
51	18	23.1	13	2	S47365
52	18	23.1	14	2	PH1471
53	18	23.1	14	2	PA0007
54	18	23.1	15	1	SFR7
55	18	23.1	15	2	PA0090
56	18	23.1	15	2	G35141
57	18	23.1	15	2	C44101
58	18	23.1	15	2	S62641
59	18	23.1	15	2	S77987
60	18	23.1	16	1	MTDPBS
61	18	23.1	16	2	D58501
62	18	23.1	16	2	S11760
63	18	23.1	16	2	B44820
64	18	23.1	16	2	B28027
65	18	23.1	17	2	A61117
66	18	23.1	17	2	S57991
67	18	23.1	17	2	B28027
68	18	23.1	17	2	B61491
69	18	23.1	18	2	PH1815
70	18	23.1	18	2	T08159
71	18	23.1	18	2	A59137
72	18	23.1	19	2	S43657
73	18	23.1	19	2	S31613
74	18	23.1	20	2	S50741
75	18	23.1	20	2	S71017
76	18	23.1	20	2	A44773
77	18	23.1	20	2	I54283
78	18	23.1	20	2	H49164
79	17.5	22.4	13	2	A26999
80	17	21.8	7	2	S17976
81	17	21.8	8	2	B54823
82	17	21.8	9	2	S30494
83	17	21.8	9	2	B24362
84	17	21.8	11	2	S18385
85	17	21.8	12	2	B41171
86	17	21.8	12	2	PH1605
87	17	21.8	12	2	T46794
88	17	21.8	13	2	PT0331
89	17	21.8	13	4	T70075
90	17	21.8	14	2	PT0029
91	17	21.8	15	2	A58945
92	17	21.8	15	2	PH1631
93	17	21.8	15	2	B26501
94	17	21.8	15	2	PA0059
95	17	21.8	16	2	C45133
96	17	21.8	16	2	PT0224
97	17	21.8	17	2	S48655
98	17	21.8	17	2	B44923
99	17	21.8	17	2	A46592
100	17	21.8	18	2	S24780

glucocortikase (EC
T-cell receptor al
major glycoprotein
hemoglobin, extrac
Ig heavy chain DJ
carbon-monoxide de
28K serine protein
T-cell receptor al
cob protein - comm
progesterone recep
protein kinase (EC
hydroxyproline-rich
Ig heavy chain DJ
endometrial secret
Ig heavy chain DJ
leader peptide [Im
alpha-1-antitrypsin
intracystalline c
phosphonocetaldh
rhodopsin homolog
paraspinal crystal
T-cell antigen rec
T-cell receptor be
lectin B1 - Peop
scotophobin - rat
protein QP100022 -
T-cell receptor de
calmodulin, vasoac
porphobilinogen sy
cytochrome-c oxida
melanotropin beta
26K kidney and gal
flg protein - Cau
7K protein - Esche
protein P8 - curle
homotocystatin precu
hydroxyproline-ric
protein P4 - curle
seed protein ws-2
T cell receptor al
S locus-linked pro
protein P11 - gold
hep90 protein homo
beta-1,3-glucanase
probable trypsin I
hypothetical prote
pollen allergen I
arylsulfatase A -
chromogranin-B - r
carboxylesterase (
glucose isomerase
olfactory receptor
cat gene leader pe
chloramphenicol O-
NMP-cytochrome P4
chondroitin sulfat
Ig H chain V-D-J r
hypothetical prote
Ig heavy chain CDR
glycophorin B (mis
karatsain - karata
anti-neoplastic ur
Ig H chain V-D-J r
lipoprotein lipase
protein QP200021 -
casein kinase II (
Ig heavy chain CDR
glutathione dehydr
carboxypeptidase 3
lactase-phlorizin
protein-tyrosine k

ALIGNMENTS

RESULT 1
S65605
dimeric protein (BDP) - barley (fragment)
C:Species: Hordeum vulgare (barley)
C:Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S65605
R:Garcia-Casado, G.; Armenia, A.; Sanchez-Monge, R.; Sanchez, L.M.; Lopez-Otin, C.; Sal
FEBs Lett. 364, 36-40, 1995
A:Title: A major baker's asthma allergen from rye flour is considerably more active than
A:Reference number: S65604; MUID:95269763; PMID:7750539
A:Accession: S65605
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <GAR>
A:Cross-references: UNIPROT:Q9S8H1; UNIPARC:UPI00009D53B

Query Match 32.7%; Score 25.5; DB 2; Length 20;
Best Local Similarity 26.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 5; Mismatches 2; Indels 7; Gaps 1;

Oy 3 KRDNHYSK-----NPM 14
| | | | | | | | | | | | | | | | | | | | | |
Db 1 ERDGYEYCRVGSIPINPL 19

RESULT 2
S56005
lysosomal protein 22K - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 10-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999
C:Accession: S56005
R:Kuwana, T.; Mullock, B.M.; Luzzio, J.P.
Biochem. J. 308, 937-946, 1995
A:Title: Identification of a lysosomal protein causing lipid transfer, using a fluoresce
A:Reference number: S56005; MUID:97104296; PMID:8948454
A:Accession: S56005
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <KUM>
A:Cross-references: UNIPARC:UPI0000E7C21

Query Match 32.1%; Score 25; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 5.7e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Oy 5 DHNDYSKNP 13
| | | | | | | | | | | | | | | | | | | | | |
Db 4 DNDDEKDP 12

RESULT 3
S63476
dihydrolipoamide dehydrogenase (EC 1.8.1.4) beta chain E1 - Pseudomonas putida (fragment)
N:Alternate names: branched-chain oxoacid dehydrogenase chain E1
C:Species: Pseudomonas putida
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S63476; S63477
R:Heister, K.; Luo, J.; Burns, G.; Braswell, E.H.; Sokatch, J.R.
Eur. J. Biochem. 233, 828-836, 1995
A:Title: Purification of active E1-alpha(2)-beta(2) of Pseudomonas putida branched-chain
A:Reference number: S63475; MUID:96085147; PMID:8521848
A:Accession: S63476
A:Molecule type: protein
A:Residues: 1-19 <HES>
A:Cross-references: UNIPROT:Q7MOQ1; UNIPARC:UPI000017A9F

A:Accession: S63477
A:Molecule type: protein
A:Residues: 15-19 <HEW>
A:Cross-references: UNIPARC:UPI000017A990
C:Comment: Dihydrolipoamide dehydrogenase beta chain E1 exists in two forms (37K and 39K

C:Genetics:
A:Gene: bkdA2
C:Keywords: alternative initiators; PAD; flavoprotein; lipoamide; NAD; oxidoreductase
F:1-19/Product: dihydrolipoamide dehydrogenase beta chain E1, 39K (fragment) #status ex
F:15-19/Product: dihydrolipoamide dehydrogenase beta chain E1, 37K (fragment) #status e

Query Match 31.4%; Score 24.5; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 6.6e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Oy 5 DHNDYSKNP 13
| | | | | | | | | | | | | | | | | | | | | |
Db 3 DHNN-SINP 10

RESULT 4
S27248
pseudogerm - wheat
C:Species: Triticum aestivum (common wheat)
C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Aug-1997
C:Accession: S27248
R:Lane, B.G.; Cuming, A.C.; Fregeau, J.; Carpica, N.C.; Hurkman, W.J.; Bernier, F.; Dra
Eur. J. Biochem. 209, 961-969, 1992
A:Title: Germ in isoforms are discrete temporal markers of wheat development. Pseudogerm
ated embryos, it is incorporated into cell walls.
A:Reference number: S27247; MUID:93049354; PMID:1425703
A:Accession: S27248
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <LAN>
A:Cross-references: UNIPARC:UPI000017B14D

Query Match 30.8%; Score 24; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 6.3e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Oy 8 DYSKNP 13
| | | | | | | | | | | | | | | | | | | | | |
Db 3 DYXNP 8

RESULT 5
S65395
chemical-sense-related lipophilic-ligand-binding protein - fruit fly (Drosophila melano
C:Species: Drosophila melanogaster
C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S65395
R:Ozaki, M.; Morisaki, K.; Idei, W.; Ozaki, K.; Tokunaga, F.
Eur. J. Biochem. 230, 298-308, 1995
A:Title: A putative lipophilic stimulant carrier protein commonly found in the taste an
A:Reference number: S65394; MUID:95324537; PMID:7601113
A:Accession: S65395
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <OZA>
A:Cross-references: UNIPROT:Q8MYT1; UNIPROT:Q9VR97; UNIPARC:UPI000017BB82

Query Match 29.5%; Score 23; DB 2; Length 11;
Best Local Similarity 80.0%; Pred. No. 6.8e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Oy 2 IKRDH 6
| | | | | | | | | | | | | | | | | | | | | |
Db 4 INRDH 8

RESULT 6
P11629
IG H chain V-D-J region (clone B-1e6 155) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: P11629
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993
 A>Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
 A'Reference number: PH1580; MUID:93301609; PMID:8315387
 A'Accession: PH1629
 A'Molecule type: DNA
 A'Residuals: 1-18 <LEV>
 A'Cross-references: UNIPARC:UPI000017C695
 A'Experimental source: bone marrow pre-B lymphocyte
 C'Keywords: immunoglobulin

Query Match 29.5%; Score 23; DB 2; Length 18;
 Best Local Similarity 44.4%; Pred. No. 1.1e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IRDNDYS 10
 |||:
 DB 2 VARDYDGS 10

RESULT 7

S32587
 L-ascorbate peroxidase (EC 1.11.1.11) isozyme II - spinach (fragment)
 C'Species: Spinacia oleracea (spinach)
 C'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 30-Sep-1993
 C'Accession: S32587; S15878
 R'Kudo, A.; Saij, H.; Tanaka, K.; Kondo, N.
 Plant Mol. Biol. 18, 691-701, 1992
 A>Title: Cloning and sequencing of a cDNA encoding ascorbate peroxidase from Arabidopsis
 A'Reference number: S20866; MUID:92216045; PMID:1558944
 A'Accession: S32587
 A'Molecule type: protein
 A'Residuals: 1-17 <KUB>

A'Cross-references: UNIPARC:UPI000017A924
 A'Note: This is a revision to the sequence from reference S15878
 R'Tanaka, K.; Takeuchi, E.; Kudo, A.; Sakaki, T.; Haraguchi, K.; Kawamura, Y.
 Arch. Biochem. Biophys. 286, 371-375, 1991
 A>Title: Two immunologically different isozymes of ascorbate peroxidase from spinach leaf
 A'Reference number: S15878; MUID:91378325; PMID:1897962
 A'Accession: S15878
 A'Molecule type: protein
 A'Residuals: 1,3-17 <TAN>

A'Cross-references: UNIPARC:UPI000017A925
 A'Note: This sequence has been revised in reference S20866
 C'Keywords: chloroplast; oxidoreductase

Query Match 28.2%; Score 22; DB 2; Length 17;
 Best Local Similarity 42.9%; Pred. No. 1.6e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12
 |||:
 DB 8 HENYQKS 14

RESULT 8

A53875
 creatine kinase (EC 2.7.3.2) CK-MM - coho salmon (fragment)
 C'Species: Oncorhynchus kisutch (coho salmon)
 C'Date: 26-Sep-1994 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C'Accession: A53875
 R'White, K.C.; Babbitt, P.C.; Buechter, D.D.; Kenyon, G.L.
 J. Protein Chem. 11, 489-494, 1992
 A>Title: The principal islet of the coho salmon (*Oncorhynchus kisutch*) contains the BB is
 A'Reference number: A53875; MUID:93080727; PMID:1449598
 A'Accession: A53875
 A'Status: preliminary; not compared with conceptual translation
 A'Molecule type: nucleic acid
 A'Residuals: 1-20 <WHI>

A'Cross-references: UNIPROT:Q9PS15; UNIPARC:UPI00000PB530
 A'Experimental source: Brockmann body, principal islet
 A'Note: sequence extracted from NCBI backbone (NCBIP:120599)
 C'Superfamily: creatine kinase; creatine kinase repeat homology
 C'Keywords: phosphotransferase

Query Match 28.2%; Score 22; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 1.9e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12
 |||:
 DB 6 HNNPFLN 12

RESULT 9

PC2330
 cyclomaltoglucosaccharide fructanotransferase (EC 2.4.-.-) - Bacillus circulans (MCI-2
 C'Species: Bacillus circulans
 C'Date: 21-Mar-1995 #sequence_revision 26-May-1995 #text_change 09-Jul-2004
 C'Accession: PC2330
 R'Kushibe, S.; Mitsu, K.; Yamagishi, M.; Yamada, K.; Morimoto, Y.
 Biosci. Biotechnol. Biochem. 59, 31-34, 1995
 A>Title: Purification and characterization of cyclomaltoglucosaccharide fructanotransf
 A'Reference number: PC2330; MUID:95201377; PMID:7765973
 A'Accession: PC2330
 A'Molecule type: protein
 A'Residuals: 1-11 <KUS>

A'Cross-references: UNIPROT:Q7M0L3; UNIPARC:UPI000017AC93
 A'Comment: This enzyme hydrolyzes beta-(2-1) glycosidic linkages and acts in intermole
 C'Keywords: glycosyltransferase; hexosyltransferase

Query Match 26.9%; Score 21; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 6 HNDYSKNP 13
 |||:
 DB 2 HLFYQWNP 9

RESULT 10

A26930
 ermG leader peptide 1 - Bacillus sphaericus
 C'Species: Bacillus sphaericus
 C'Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
 C'Accession: A26930
 R'Monod, M.; Mohan, S.; Dubnau, D.
 J. Bacteriol. 169, 340-350, 1987
 A>Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B res

A'Reference number: A91840; MUID:87083389; PMID:3025178
 A'Accession: A26930
 A'Molecule type: DNA
 A'Residuals: 1-11 <MON>

A'Cross-references: UNIPROT:P26840; UNIPARC:UPI000016B856; GB:M15332; NID:G142881; PIDR
 Query Match 26.9%; Score 21; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
 |||:
 DB 2 NKYSK 6

RESULT 11

PS0252
 16k protein 5404 - rice (strain Nihonbare) (fragment)
 C'Species: Oryza sativa (rice)
 C'Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Apr-1995
 C'Accession: PS0252
 R'Tsugita, A.
 Submitted to JIPID, April 1993

A'Reference number: PS0206
 A'Accession: PS0252
 A'Molecule type: protein
 A'Residuals: 1-14 <TSU>
 A'Cross-references: UNIPARC:UPI000017B0EF

A:Experimental source: strain Nihonbare
C:Comment: Molecular weight 16k, pI 4.9.

Query Match 26.9%; Score 21; DB 2; Length 14;
Best Local Similarity 37.5%; Pred. No. 2e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKRDHNY 9
:|:|:|
DB 3 LEADDDY 10

RESULT 12
A41589
25K elastin-binding protein - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: A41589
R:Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.; Me
J. Biol. Chem. 266, 23399-23406, 1991
A:Title: Binding of elastin to Staphylococcus aureus.
A:Reference number: A41589; MUID:92078218; PMID:11744133
A:Accession: A41589
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-14 <PAR>
A:Cross-references: UNIPROT:Q9RSR5; UNIPARC:UPI00000BC64C

Query Match 26.9%; Score 21; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKN 12
:|:|:|
DB 6 DDFEKN 11

RESULT 13
I67525
CD3 antigen homolog - mouse (fragment)
C:Species: Mus sp. (mouse)
C:Date: 29-May-1998 #sequence_revision 29-May-1998 #text_change 09-Jul-2004
C:Accession: I67525
R:Chies, J.A.; Lembezat, M.P.; Freltas, A.A.
Eur. J. Immunol. 24, 1657-1664, 1994
A:Title: Entry of B lymphocytes into the persistent cell pool in non-immunized mice is r
A:Reference number: I53392; MUID:94298870; PMID:8026526
A:Accession: I67525
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-15 <RES>
A:Cross-references: UNIPROT:Q7M0G8; UNIPARC:UPI000017C992; GB:S71349; NID:9550037
A:Gene: Ig VH7183

Query Match 26.9%; Score 21; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDH 6
:|:|:|
DB 4 RRDH 7

RESULT 14
PH0769
T-cell receptor beta chain (J2) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C:Accession: PH0769
R:Caenova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A:Title: T cell receptor genes in a series of class I major histocompatibility complex-

allelic exclusion and antigen-specific repertoire.
A:Reference number: PH0746; MUID:92078846; PMID:1836010
A:Accession: PH0769
A:Molecule type: mRNA
A:Residues: 1-17 <CAS>
A:Cross-references: UNIPARC:UPI0000115FBC; EMBL:X60863; NID:952743; PIDN:CAA43253.1; PI
A:Experimental source: T lymphocyte
C:Keywords: T-cell receptor

Query Match 26.9%; Score 21; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 2.4e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
:|:|:|
DB 6 RDRGNVAF 13

RESULT 15
H64711
hypothetical protein HP1536 - Helicobacter pylori (strain 26695)
C:Species: Helicobacter pylori
C:Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004
C:Accession: H64711
R:Tomb, J.F.; White, O.; Kurlavsky, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.I
Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen
son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Wathey, I
Nature 388, 539-547, 1997
A:Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpk, P.D.; Smith, H.O.; Fraser, C
A:Title: The complete genome sequence of the gastric pathogen Helicobacter pylori.
A:Reference number: A64520; MUID:97394467; PMID:9252185
A:Accession: H64711
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-18 <TOM>
A:Cross-references: UNIPROT:Q26062; UNIPARC:UPI00000C07C3; GB:AE006651; GB:AE00511; NI

Query Match 26.9%; Score 21; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKNP 13
:|:|:|
DB 9 NHPSRNP 15

RESULT 16
B41589
40K elastin-binding protein - Staphylococcus aureus (fragment)
C:Species: Staphylococcus aureus
C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C:Accession: B41589
R:Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parks, W.C.; Rosenbloom, J.; Abrams, W.R.; M
J. Biol. Chem. 266, 23399-23406, 1991
A:Title: Binding of elastin to Staphylococcus aureus.
A:Reference number: A41589; MUID:92078218; PMID:11744133
A:Accession: B41589
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-18 <PAR>
A:Cross-references: UNIPROT:Q9RSR6; UNIPARC:UPI00000B32A9

Query Match 26.9%; Score 21; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.6e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSKN 12
:|:|:|
DB 6 DDFEKN 11

RESULT 17
PT0244

Ig heavy chain CDR3 region (clone 2-103B) - human (fragment)
CISpecies: Homo sapiens (man)
CDate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 06-Jun-1997
CAccession: P10244
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A.Reference number: P10222; MUID:91108337; PMID:1899102
ACcession: P10244
A.Molecule type: DNA
A.Residues: 1-19 <YAM>
A.Cross-references: UNIPARC:UPI000017693B
A.Experimental source: B lymphocyte
C:Superfamily: immunoglobulin V region, immunoglobulin homology
C:Keywords: heterotrimer; immunoglobulin

Query Match 26.9%; Score 21; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
DB 6 DYGDY 10

RESULT 18
S66608
quinoline 2-oxidoreductase gamma chain - Comamonas testosteroni (fragment)
CISpecies: Comamonas testosteroni
CDate: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
CAccession: S66608
R.Schach, S.; Ishisaka, B.; Petzner, S.; Lingens, F.
Eur. J. Biochem. 232, 536-544, 1995
A>Title: Quinoline 2-oxidoreductase and 2-oxo-1,2-dihydroquinoline 5,6-dioxygenase from
A.Reference number: S66606; MUID:96035889; PMID:7556104
ACcession: S66608
A.Molecule type: protein
A.Residues: 1-9 <SCH>
A.Cross-references: UNIPARC:UPI000017A956
A.Experimental source: strain 63

Query Match 25.6%; Score 20; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 11 KNPM 14
DB 6 KNPL 9

RESULT 19
P10272
Ig heavy chain CDR3 region (clone 3-103B) - human (fragment)
CISpecies: Homo sapiens (man)
CDate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
CAccession: P10272
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A.Reference number: P10222; MUID:91108337; PMID:1899102
ACcession: P10272
A.Molecule type: DNA
A.Residues: 1-9 <YAM>
A.Cross-references: UNIPARC:UPI000017C1F4
A.Experimental source: B lymphocyte
C:Keywords: heterotrimer; immunoglobulin

Query Match 25.6%; Score 20; DB 2; Length 9;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKN 12
DB 11

DB 4 NDEMKN 9

RESULT 20
S62208
polyferredoxin - Methanosarcina barkeri (fragment)
CISpecies: Methanosarcina barkeri
CDate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 31-Mar-1997
CAccession: S62208
R.Vorholt, J.A.; Vaupel, M.; Thauer, R.K.
Eur. J. Biochem. 236, 309-317, 1996
A>Title: A polyferredoxin with eight (4Fe-4S) clusters as a subunit of molybdenum formy
A.Reference number: S62194; MUID:96184912; PMID:8617280
ACcession: S62208
A.Molecule type: protein
A.Status: preliminary
A.Residues: 1-10 <VOR>
A.Cross-references: UNIPARC:UPI000017AB9C

Query Match 25.6%; Score 20; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.1e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 HNDYSKN 12
DB 2 NTDYDNN 8

RESULT 21
S65377
cytochrome-c oxidase (EC 1.9.3.1) chain VIA-H, cardiac - rat (fragment)
CISpecies: Rattus norvegicus (Norway rat)
CDate: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
CAccession: S65377
R.Schaeffer, H.; Noack, H.; Halanck, W.; Brandt, U.; von Jagow, G.
Eur. J. Biochem. 230, 235-241, 1995
A>Title: Cytochrome-c oxidase in developing rat heart. Enzymic properties and amino-ter
A.Reference number: S65372; MUID:95324529; PMID:7601105
ACcession: S65377
A.Status: preliminary
A.Molecule type: protein
A.Residues: 1-11 <SCH>
A.Cross-references: UNIPROT:Q7MOD4; UNIPARC:UPI000017C8FD
C:Keywords: cardiac muscle; heart; oxidoreductase

Query Match 25.6%; Score 20; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 2.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDH 6
DB 2 SAKGDH 7

RESULT 22
NYPG14
hypothalamic tetradecapeptide - pig
CISpecies: Sus scrofa domestica (domestic pig)
CDate: 13-Jul-1991 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
CAccession: A01419
R.Schleisinger, D.H.; Niall, H.D.; Linthicum, G.L.; Dupont, A.; Schally, A.V.
submitted to the Atlas, November 1976
A.Reference number: A01419
ACcession: A01419
A.Molecule type: protein
A.Residues: 1-14 <SCH>
A.Cross-references: UNIPROT:P01155; UNIPARC:UPI000012CFC3
C:Superfamily: hypothalamic tetradecapeptide
C:Keywords: amidated carboxyl end; hypothalamus
P14/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 25.6%; Score 20; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. No. 2.9e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 9 YSKNP 13
| | |
| | |
Db 3 YKSP 7

RESULT 23

PH1778

T cell receptor alpha chain V region (clone 1PBL V alpha 24-5) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1778

R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.F.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1778

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-16 <POR>

A/Cross-references: UNIPARC:UPI000017C36C

Query Match 25.6%; Score 20; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDHNY 9
| | |
| | |
Db 5 VRPTFNDY 12

RESULT 24

S09084

Proteasome chain 3 - rat (fragment)

N/Alternate names: multicatalytic proteinase chain 3

C/Species: Rattus norvegicus (Norway rat)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C/Accession: S09084

R/Lilley, K.S.; Davison, M.D.; Rivett, A.J.

FEBS Lett. 262, 337-329, 1990

A/Title: N-terminal sequence similarities between components of the multicatalytic prote

A/Reference number: S09082; MUID:90242957; PMID:2335214

A/Accession: S09084

A/Molecule type: protein

A/Residues: 1-16 <LIR>

A/Cross-references: UNIPROT:P34067; UNIPARC:UPI000017C99E

Query Match 25.6%; Score 20; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 SKNPM 14
| | |
| | |
Db 1 TONPM 5

RESULT 25

B42965

talin (glycosylated sites) - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C/Accession: B42965

R/Hagmann, J.; Grob, M.; Burger, M.M.

J. Biol. Chem. 267, 14424-14428, 1992

A/Title: The cytoskeletal protein talin is O-glycosylated.

A/Reference number: A42965; MUID:92332560; PMID:1629228

A/Accession: B42965

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-17 <HAG>

A/Cross-references: UNIPARC:UPI000017C03A

A/Experimental source: gizzard
A/Note: sequence extracted from NCBI backbone (NCBIP:108592)

Query Match 25.6%; Score 20; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
| | |
| | |
Db 9 NDYQ 13

RESULT 26

E61497

seed protein ws-20 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: E61497

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two di-

A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: E61497

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <HIR>

A/Cross-references: UNIPROT:Q9S8J4; UNIPARC:UPI000017B06E

C/Keywords: glycoprotein; seed

Query Match 25.6%; Score 20; DB 2; Length 20;
Best Local Similarity 28.6%; Pred. No. 4.3e+03;
Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSKPM 14
| | | | |
| | | | |
Db 5 SFNPDHRENSNEL 18

RESULT 27

S77992

cytochrome-c oxidase (EC 1.9.3.1) chain VIIb - bigeye tuna (fragment)

C/Species: Thunnus obesus (bigeye tuna)

C/Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C/Accession: S77992

R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Lindner, D.; Lottspeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A/Reference number: S77980

A/Accession: S77992

A/Molecule type: protein

A/Residues: 1-20 <ARN>

A/Cross-references: UNIPROT:P80981; UNIPARC:UPI0000128164

A/Experimental source: liver

C/Genetics:

A/Genome: nuclear

C/Function:

A/Pathway: oxidative phosphorylation; respiratory chain

C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membran

Query Match 25.6%; Score 20; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 4.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 HNDYSKPM 14
| | | | |
| | | | |
Db 9 HSPFYGTNLM 17

RESULT 28

PT0299

Ig heavy chain CRD3 region (clone 5-103B) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0299

R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Royera, G.

J. Exp. Med. 173, 395-407, 1991

A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A/Reference number: P10222; MUID:91108337; PMID:1899102

A/Accession: P10299

A/Molecule type: DNA

A/Residues: 1-9 <YAM>

A/Cross-references: UNIPARC:UPI000017C209

A/Experimental source: B lymphocyte

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 9;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 4 RDNDYS 10

DB 1 RSDMYS 7

RESULT 29

A13687

caerulein-like peptide - African tree frog (Kassina maculata)

C/Species: Kassina maculata

C/Date: 13-Mar-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: A13687

R.Montecucchi, P.; Falconieri, E.; G. Vissier, J.

Experientia 33, 1138-1139, 1977

A>Title: Occurrence of Asn(2), Leu(5)-caerulein in the skin of the African frog Hyalambate

A/Reference number: A13687; MUID:77246547; PMID:891852

A/Accession: A13687

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <MON>

A/Cross-references: UNIPROT:Q7LZC5; UNIPARC:UPI000017668C

C/Species: gasterin

C/Keywords: amidated carboxyl end; neuropeptide; pyroglutamic acid; skin; sulfoprotein

F.1/Modified site: pyroglutamate carboxylic acid (Gln #status experimental

F.10/Modified site: sulfatate (Tyr) (covalent) #status experimental

Query Match

Best Local Similarity 100.0%; Pred. No. 3.1e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 7 NDY 9

DB 2 NDY 4

RESULT 30

874176

glucosyltransferase (EC 2.7.1.12), thermoresistant - *Escherichia coli* (fragment)

C/Species: *Escherichia coli*

C/Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 07-May-1999

C/Accession: 874176

R.Izu, H.; Adachi, O.; Yamada, M.

FEBS Lett. 394, 14-16, 1996

A>Title: Purification and characterization of the *Escherichia coli* thermoresistant gluc

A/Reference number: 874176; MUID:97074194; PMID:8925917

A/Accession: 874176

A/Molecule type: protein

A/Residues: 1-10 <IZU>

A/Cross-references: UNIPARC:UPI000017A3B

A/Experimental source: strain K-12

C/Keywords: dimer; phosphotransferase

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 DHNDY 9

DB 6 DHNTY 10

RESULT 31

S23370

T-cell receptor alpha chain J region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S23370

R.Plusck, G.; Ricker, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Eichma

Bur. J. Immunol. 21, 2743-2754, 1991

A>Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of the

A/Reference number: S23364; MUID:92037820; PMID:1657615

A/Accession: S23370

A/Status: preliminary; translation not shown

A/Molecule type: mRNA

A/Residues: 1-10 <PLU>

A/Cross-references: UNIPARC:UPI000017C391; EMBL:X58165

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 10;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 5 DHND 8

DB 4 DHND 7

RESULT 32

S23926

major glycoprotein PAS-6 - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 09-Jul-2004

C/Accession: S23926

R.Kim, D.H.; Kanno, C.; Mizokami, Y.

Biochim. Biophys. Acta 1122, 203-211, 1992

A>Title: Purification and characterization of major glycoproteins, PAS-6 and PAS-7, fro

A/Reference number: S23926; MUID:92351107; PMID:1643094

A/Accession: S23926

A/Molecule type: protein

A/Residues: 1-11 <KIM>

A/Cross-references: UNIPROT:Q7M2M1; UNIPARC:UPI000017C53F

C/Keywords: glycoprotein; milk; blocked amino end

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 11;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 10 SKNP 13

DB 4 NKNP 7

RESULT 33

S65730

hemoglobin, extracellular, component - earthworm (*Lumbricus terrestris*) (fragment)

C/Species: *Lumbricus terrestris* (common earthworm)

C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C/Accession: S65730

R.Fuehltan, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.

Biochim. Biophys. Acta 1292, 273-280, 1996

A>Title: Characterization of the constituent polypeptides of the extracellular hemoglob

A/Reference number: S65721; MUID:96176855; PMID:8857573

A/Accession: S65730

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <FUS>

A/Cross-references: UNIPARC:UPI000017BD88

Query Match

Best Local Similarity 24.4%; Score 19; DB 2; Length 12;

Best Local Similarity 100.0%; Pred. No. 3.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDH 6
|||
Db 6 RDH 8

RESULT 34

PH1342
Ig heavy chain DJ region (clone C507-95) - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1342
R/Masseran, R.; Galli, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DH joining in young children with B precursor lymphoma
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1342
A/Molecule type: DNA
A/Residues: 1-15 <MAS>
A/Cross-references: UNIPARC:UPI000017C240
C/Keywords: heterotrimer; immunoglobulin

Query Match 24.4%; Score 19; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDH 6
|||
Db 13 RDH 15

RESULT 35

PL0143

carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydohydrogen

C/Species: Pseudomonas carboxydohydrogen
C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C/Accession: PL0143
R/Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A/Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogen
A/Reference number: PL0138; MUID:9055678; PMID:2818128
A/Accession: PL0143
A/Molecule type: protein
A/Residues: 1-15 <KRA>
A/Cross-references: UNIPROT:P19917; UNIPARC:UPI0000128FDB
C/Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, me

C/Keywords: oxidoreductase
Query Match 24.4%; Score 19; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.7e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSK 11
|||
Db 6 HFDYHR 11

RESULT 36

A35417

28K serine proteinase homolog - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)
C/Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C/Accession: A35417
R/Ho, P.L.; Carpenter, M.R.; Smillie, L.B.; Gambarini, A.G.
Biochem. Biophys. Res. Commun. 170, 769-774, 1990
A/Title: Co-purification of proteinases with basic fibroblast growth factor (FGF).
A/Reference number: A35417; MUID:90343797; PMID:2200404
A/Accession: A35417
A/Status: Preliminary
A/Molecule type: protein
A/Residues: 1-15 <HOA>

A/Cross-references: UNIPROT:Q7M3G3; UNIPARC:UPI000017C48D

Query Match 24.4%; Score 19; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYSK 11
|||
Db 3 DSIDYRK 9

RESULT 37

PH0791

T-cell receptor alpha chain (OB7.3.2 V-alpha-8.F3.2) - mouse (fragment)

C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0791
R/Cabanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0791
A/Molecule type: mRNA
A/Residues: 1-16 <CAS>
A/Cross-references: UNIPARC:UPI000017C783; EMBL:X60896
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 24.4%; Score 19; DB 2; Length 16;
Best Local Similarity 27.3%; Pred. No. 5.1e+03;
Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSK 11
::|::|:|
Db 2 ALSGDSDGYNK 12

RESULT 38

S22040

cob protein - common sunflower

C/Species: Helianthus annuus (common sunflower)
C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C/Accession: S22040
R/Koehler, R.H.
submitted to the EMBL Data Library, October 1991
A/Reference number: S22040
A/Accession: S22040
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-16 <KOR>
A/Cross-references: UNIPROT:Q34699; UNIPARC:UPI000008DA3A; EMBL:X62592; NID:q12990; PID

Query Match 24.4%; Score 19; DB 2; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 NDY 9
|||
Db 13 NDY 15

RESULT 39

C56211

progesterone receptor-related protein p23 - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 20-Jun-2000
C/Accession: C56211
R/Johnson, J.L.; Belto, T.G.; Krco, C.J.; Toft, D.O.
Mol. Cell. Biol. 14, 1956-1963, 1994
A/Title: Characterization of a novel 23-kilodalton protein of inactive progesterone rec
A/Reference number: A56211; MUID:94158868; PMID:8114727
A/Accession: C56211

A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-18 <JON>
 A:Cross-references: UNIPARC:UPI00001796B8
 C:Superfamily: Caenorhabditis elegans hypothetical protein ZC395.10
 C:Keywords: steroid hormone receptor

Query Match 24.4%; Score 19; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNDY 9
 DB 10 DNDY 14

RESULT 40
 145957
 protein kinase (EC 2.7.1.37), cAMP-dependent, type I-alpha regulatory chain - bovine (fr
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 05-Oct-2004
 C:Accession: 145957
 R:Lee, D.C.; Carmichael, D.F.; Krebs, B.G.; McKnight, G.S.
 Proc. Natl. Acad. Sci. U.S.A. 80, 3608-3612, 1983
 A:Title: Isolation of a cDNA clone for the type I regulatory subunit of bovine cAMP-depe
 A:Reference number: 145957; MUID:83221645; PMID:6190178
 A:Accession: 145957
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-19 <LEB>
 A:Cross-references: UNIPROT:P00514; UNIPARC:UPI000016C361; GB:K00833; NID:q163533; PIDN:
 C:Superfamily: cAMP-dependent protein kinase regulatory subunit; cAMP receptor protein c
 C:Keywords: phosphotransferase

Query Match 24.4%; Score 19; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 6.1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IKRDN 7
 DB 12 IDRSN 17

RESULT 41
 559485
 hydroxyproline-rich cell wall glycoprotein (42k and others) - kidney bean (fragment)
 C:Species: Phaseolus vulgaris (kidney bean)
 C:Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
 C:Accession: 559485; 559484; 559483
 R:Wojtaszek, P.; Trechman, U.; Bolwell, G.P.
 Plant Mol. Biol. 28, 1075-1087, 1995
 A:Title: Specificity in the immobilisation of cell wall proteins in response to differer
 A:Reference number: 559481; MUID:96011753; PMID:7548825
 A:Accession: 559485
 A:Molecule type: protein
 A:Residues: 1-19 <WOU>
 A:Cross-references: UNIPROT:Q7M1W8; UNIPARC:UPI0000177B5D
 A:Note: hydroxyproline-rich cell wall glycoprotein, 42k
 A:Accession: 559484
 A:Molecule type: protein
 A:Residues: 1-15 <WOW>
 A:Cross-references: UNIPARC:UPI0000177B5E
 A:Note: hydroxyproline-rich cell wall glycoprotein, 84k
 A:Accession: 559483
 A:Molecule type: protein
 A:Residues: 1-14 <WOP>
 A:Cross-references: UNIPARC:UPI0000177B5F
 A:Note: hydroxyproline-rich cell wall glycoprotein, 136k, minor component
 C:Superfamily: proline-rich protein 3
 C:Keywords: glycoprotein; hydroxyproline
 R/6/11/16/Modified site: hydroxyproline (Pro) #status experimental

Query Match 24.4%; Score 19; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 6.1e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKNPM 14
 DB 1 NYDKRPV 7

RESULT 42
 PH1360
 Ig heavy chain DJ region (clone C178-122) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1360
 R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lym
 A:Reference number: PH1302; MUID:93094761; PMID:1460419
 A:Accession: PH1360
 A:Molecule type: DNA
 A:Residues: 1-19 <WAS>
 A:Cross-references: UNIPARC:UPI000017C231
 C:Keywords: heterotrimer; immunoglobulin

Query Match 24.4%; Score 19; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDH 6
 DB 17 RDH 19

RESULT 43
 A61377
 endometrial secretory protein - sheep (fragment)
 C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C:Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 17-Mar-1999
 C:Accession: A61377
 R:Vallet, J.L.; Barker, P.J.; Lamming, G.E.; Skinner, N.; Huettsen, N.S.
 J. Endocrinol. 130, R1-R4, 1991
 A:Title: A low molecular weight endometrial secretory protein which is increased by ovi
 A:Reference number: A61377; MUID:92013712; PMID:1919388
 A:Accession: A61377
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-19 <VAL>
 A:Cross-references: UNIPARC:UPI000017C59D

Query Match 24.4%; Score 19; DB 2; Length 19;
 Best Local Similarity 60.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 YSKNP 13
 DB 10 YSDP 14

RESULT 44
 PH1338
 Ig heavy chain DJ region (clone C372-115) - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C:Accession: PH1338
 R:Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A:Title: Predominance of fetal type DJH joining in young children with B precursor lym
 A:Reference number: PH1302; MUID:93094761; PMID:1460419
 A:Accession: PH1338
 A:Molecule type: DNA
 A:Residues: 1-20 <MAS>
 A:Cross-references: UNIPARC:UPI000017C23D
 C:Keywords: heterotrimer; immunoglobulin

Query Match 24.4%; Score 19; DB 2; Length 20;
A: Molecule type: protein
A: Residues: 1-20 <CUS>
A: Cross-references: UNIPROT:Q7M466; UNIPARC:UP1000017CAC
A: Note: Sequence extracted from NCBI backbone (NCBI:114883)
C: Keywords: chromoprotein

QY 4 RDH 6
|||
DB 18 RDH 20

RESULT 45

leader peptide [imported] - Vibrio sp.
C: Species: Vibrio sp.
C: Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C: Accession: T48881
R: Xu, Y.; Zhang, Y.; Liang, Z.Y.; Van de Casteele, M.; Legrain, C.; Glansdorff, N.
Microbiology 144, 1435-1441, 1998
A: Title: Aspartate carboxyltransferase from a psychrophilic deep-sea bacterium, Vibrio
A: Reference number: Z24845
A: Accession: T48881
A: Status: preliminary; translated from GB/EMBL/DBJ
A: Molecule type: DNA
A: Residues: 1-20 <XUY>
A: Cross-references: UNIPROT:P96173; UNIPARC:UP1000003BBB; EMBL:X09786; PIRN:CAAT0922.1
A: Experimental source: strain 2693

Query Match 24.4%; Score 19; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHND 8
|||
DB 16 RPHNN 20

RESULT 46

alpha-1-antitrypsin - golden hamster (fragment)
A: Accession: A61506
C: Species: Mesocricetus auratus (golden hamster)
C: Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
C: Accession: A61506
R: Amemiya, S.; Yamamoto, K.; Shinohara, H.
Comp. Biochem. Physiol. B 100, 293-296, 1991
A: Title: Purification, characterization, and acute phase response of plasma alpha-1-anti
A: Reference number: A61506; MUID:92191572; PMID:1724745
A: Accession: A61506
A: Status: preliminary
A: Molecule type: protein
A: Residues: 1-20 <AME>
A: Cross-references: UNIPROT:Q7MOE1; UNIPARC:UP1000017C610

Query Match 24.4%; Score 19; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDH 6
|||
DB 18 RDH 20

RESULT 47

B56894
intracrySTALLine chromoprotein 1 - Waltonia inconspicua (fragment)
C: Species: Waltonia inconspicua
C: Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004
C: Accession: B56894
R: Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.
Comp. Biochem. Physiol. B 102, 93-95, 1992
A: Title: An intracrySTALLine chromoprotein from red brachiopod shells: implications for
A: Reference number: B56894; MUID:92405551; PMID:1526140
A: Contents: Bowerly, red brachiopod shells
A: Accession: B56894

A: Status: preliminary
A: Molecule type: protein
A: Residues: 1-20 <CUS>
A: Cross-references: UNIPROT:Q7M466; UNIPARC:UP1000017CAC
A: Note: Sequence extracted from NCBI backbone (NCBI:114883)
C: Keywords: chromoprotein

Query Match 24.4%; Score 19; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 6.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 SKNP 13
|||
DB 17 AKNP 20

RESULT 48

A28709
phosphonoacetaldehyde hydrolase - Bacillus cereus (fragment)
C: Species: Bacillus cereus
C: Date: 22-Aug-1988 #sequence_revision 22-Aug-1988 #text_change 30-Sep-1993
C: Accession: A28709
R: Olsen, D.B.; Hepburn, T.W.; Moos, M.; Mariano, P.S.; Dunaway-Mariano, D.
Biochemistry 27, 2229-2234, 1988
A: Title: Investigation of the Bacillus cereus phosphonoacetaldehyde hydrolase. Evidence
A: Reference number: A28709; MUID:88241058; PMID:3132206
A: Accession: A28709
A: Status: preliminary
A: Molecule type: protein
A: Residues: 1-7 <OLS>
A: Cross-references: UNIPARC:UP1000017AC8C

Query Match 23.1%; Score 18; DB 2; Length 7;
Best Local Similarity 60.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDH 6
|||
DB 1 LKIDH 5

RESULT 49

A38841
rhodopsin homolog - squid (Watasenia scintillans) (fragment)
N: Alternate names: visual pigment protein
C: Species: Watasenia scintillans (sparkling enope)
C: Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
C: Accession: A38841
R: Seidou, M.; Kubota, I.; Hiraki, K.; Kito, Y.
Biochim. Biophys. Acta 957, 318-321, 1988
A: Title: Amino acid sequence of the retinal binding site of squid visual pigment.
A: Reference number: PT0063; MUID:89051045; PMID:3191148
A: Accession: A38841
A: Molecule type: protein
A: Residues: 1-11 <SR>
A: Cross-references: UNIPROT:Q7M3Y2; UNIPARC:UP1000017412E
C: Superfamily: vertebrate rhodopsin
C: Keywords: chromoprotein; retinal
F/3/Binding site: retinal (Lys) (covalent) #status experimental

Query Match 23.1%; Score 18; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 NPM 14
|||
DB 9 NPM 11

RESULT 50

S00616
paraporal crystal protein, wax moth-specific - Bacillus thuringiensis (strain gallera

N:Alternate names: delta-endotoxin; parasporal crystal protein positive chain
 C:Species: *Bacillus thuringiensis*
 C>Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 05-Oct-2004
 C:Accession: S00616
 R:ChemUnkName, G.G.; Kostina, L.I.; Zalunin, I.A.; Khodova, O.M.; Stepanov, V.M.
 FBS Lett. 232, 249-251, 1988
 A>Title: *Bacillus thuringiensis* ssp. *galleriae* simultaneously produces two delta-endotox
 A:Reference number: S00615
 A:Accession: S00616
 A:Molecule type: protein
 A:Residues: 1-11 <CH2>
 A:Cross-references: UNIPROT:Q7M154; UNIPARC:UPI00001781A1
 C:Comment: This toxin is effective against the larvae of *Galleria mellonella* (greater wax
 C:Keywords: delta-endotoxin

Query Match 23.1%; Score 18; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 5.1e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYGR 11
 DB 5 NNPYSQ 10

RESULT 51

847365
 T-cell antigen receptor VJ junction beta chain - human
 C:Species: *Homo sapiens* (man)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 C:Accession: S47365; S47375; S47379; S47397; S47398; S47355
 R:Lehner, P.J.
 submitted to the EMBL Data Library, August 1994

A:Description: Human HLA-A0201 restricted recognition of Influenza A is dominated by T C
 A:Reference number: S47355
 A:Accession: S47365
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-13 <LEH>

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35690; NID:G527471; PIDN:CAA84759.1; PI
 A:Accession: S47375
 A:Molecule type: mRNA
 A:Status: preliminary
 A:Residues: 1-13 <LE3>

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35700; NID:G527493; PIDN:CAA84769.1; PI
 A:Accession: S47379
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35708; NID:G527509; PIDN:CAA84777.1; PI
 A:Accession: S47396
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35674; NID:G527527; PIDN:CAA84743.1; PI
 A:Accession: S47397
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35675; NID:G527529; PIDN:CAA84744.1; PI
 A:Accession: S47398
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

A:Cross-references: UNIPARC:UPI0000116673; EMBL:Z35676; NID:G527531; PIDN:CAA84745.1; PI
 A:Accession: S47399
 A:Molecule type: mRNA
 A:Status: preliminary

RESULT 52

PH1471
 T-cell receptor beta chain (clone A24/BEF4) - mouse (fragment)

C:Species: *Mus musculus* (house mouse)
 C>Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004
 C:Accession: PH1471
 R:Casanova, J.L.; Martini, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; J.
 Exp. Med. 177, 811-820, 1993

A>Title: T cell receptor selection by and recognition of two class I major histocompat
 A:Reference number: PH1430; MUID:93171821; PMID:8436911
 A:Accession: PH1471
 A:Molecule type: mRNA

A:Residues: 1-14 <CAS>
 A:Cross-references: UNIPARC:UPI000017C79B
 A:Experimental source: cytolytic T-lymphocyte

C:Keywords: receptor; T-cell

Query Match 23.1%; Score 18; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDHND 8
 DB 5 RDNDQ 9

RESULT 53

PA0007
 lectin B1 - *Psophocarpus scandens* (fragment)
 C:Species: *Psophocarpus scandens*
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C:Accession: PA0007
 R:Kortt, A.A.

A>Title: Isolation and characterization of the lectins from the seeds of *Psophocarpus*
 A:Reference number: PA0005
 A:Accession: PA0007
 A:Molecule type: protein

A:Residues: 1-14 <KOR>
 A:Cross-references: UNIPROT:P22584; UNIPARC:UPI000012E3DA
 A:Experimental source: seed
 C:Comment: The seeds of *Psophocarpus* contain two distinct groups of lectins which can b

C:Keywords: lectin

Query Match 23.1%; Score 18; DB 2; Length 14;
 Best Local Similarity 25.0%; Pred. No. 6.6e+03;
 Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SIKRDHNDYSKN 12
 DB 2 TISNPNQFOON 13

RESULT 54
 SPRT
 scotophobin - rat

C:Species: *Rattus norvegicus* (Norway rat)
 C>Date: 23-Oct-1981 #sequence_revision 23-Oct-1981 #text_change 09-Jul-2004
 C:Accession: A93164; A92757; A01423
 R:Ungar, G.; Desiderio, D.M.; Parr, W.

A>Title: Isolation, identification and synthesis of a specific-behaviour-inducing brain
 A:Reference number: A93164; MUID:72240741; PMID:4558348
 A:Accession: A93164
 A:Molecule type: protein

A:Residues: 1-15 <UNG>
 A:Cross-references: UNIPROT:P01159; UNIPARC:UPI000013567B
 A:Note: chemical synthesis

R:Desiderio, D.M.; Ungar, G.; White, P.A.
 J. Chem. Soc. D Chem. Commun. 1971, 432-433, 1971
 A>Title: The use of mass spectrometry in the structural elucidation of scotophobin -- a

A:Reference number: A92757
A:Accession: A92757
A:Molecule type: protein
A:Residues: 1-15 <DES>
A:Cross-references: UNIPARC:UPI0000135678
A:Experimental source: brain
A>Note: the sequence was determined by mass spectrometry
R:Stewart, W.W.
Nature 238, 202-209, 1972
A:Title: Comments on the chemistry of scotophobin.
A:Reference number: A93165; MUID:72240742; PMID:4558349
A:Contents: annotation; referee's comments on first reference above
R:Ungar, G.; Desiderio, D.M.; Parr, W.
Nature 238, 209-210, 1972
A:Reference number: A93166
A:Contents: annotation
A>Note: reply to referee's comments
R:Wilson, D.
Nature 320, 313-314, 1986
A:Title: Scotophobin resurrected as a neuropeptide.
A:Reference number: A93076; MUID:86175024; PMID:3960116
A:Contents: annotation
A>Note: comparison with other neuropeptides; author presents scotophobin sequence in the
C:Superfamily: scotophobin
C:Keywords: amidated carboxyl end
F:15/Modified site: amidated carboxyl end (Tyr) #status experimental

Query Match 23.1%; Score 18; DB 1; Length 15;
Best Local Similarity 37.5%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 DHNDYSKN 12
|:|:|:
Db 2 DNNQGGKS 9

RESULT 55
Protein QP100022 - fungus (Fusarium sporotrichioides) (fragment)
C:Species: Fusarium sporotrichioides
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 23-Mar-2001
C:Accession: PA0090
R:Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.
submitted to JIPID, October 1994
A:Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichi
A:Reference number: PA0051
A:Accession: PA0090
A:Molecule type: protein
A:Residues: 1-15 <CHO>
A:Cross-references: UNIPARC:UPI0000178407
C:Keywords: pyroglutamic acid
F:11/Modified site: pyroglutamic acid (Gln) #status experimental

Query Match 23.1%; Score 18; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 10 SKNPM 14
|:|:|:
Db 4 SXNPL 8

RESULT 56
T-cell receptor delta chain V region (105-7) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997
C:Accession: G35141
R:Sim, G.K.; Augustin, A.
Cell 61, 397-405, 1990
A:Title: Dominantly inherited expression of BID, an invariant undiversified T cell recep
A:Reference number: A35141; MUID:90242386; PMID:2110506

A:Accession: G35141
A>Status: preliminary; not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-15 <SIM>
A:Cross-references: UNIPARC:UPI000017C85F
C:Keywords: T-cell receptor

Query Match 23.1%; Score 18; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KRDNND 8
|:|:|:
Db 8 RRDTS D 13

RESULT 57
C44101
calmodulin, vasoactive intestinal peptide-binding protein, VIP binding protein, p18 - gr
C:Species: Cavia porcellus (guinea pig)
C:Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997
C:Accession: C44101
R:Stallwood, D.; Brügger, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shitaga, H.; Landers, J.
J. Biol. Chem. 267, 19617-19621, 1992
A:Title: Identity of a membrane-bound vasoactive intestinal peptide-binding protein with
A:Reference number: A44101; MUID:92406918; PMID:1527080
A:Accession: C44101
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <STG>
A:Cross-references: UNIPARC:UPI000017CA28
A:Experimental source: lung membranes
A>Note: sequence extracted from NCBI backbone (NCBIP:114109)
C:Keywords: intestine

Query Match 23.1%; Score 18; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 4 RDNDY 9
|:|:|:
Db 4 KDGXNY 9

RESULT 58
S62641
porphobilinogen synthase (BC 4.2.1.24) - green alga (Scenedesmus obliquus) (fragment)
N:Alternate names: 5-aminolevulinic acid dehydratase
C:Species: Scenedesmus obliquus
C:Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C:Accession: S62641
R:Stolz, M.; Doernemann, D.
Eur. J. Biochem. 236, 600-608, 1996
A:Title: Purification, metal cofactor, N-terminal sequence and subunit composition of a
A:Reference number: S62641; MUID:96195670; PMID:8612634
A:Accession: S62641
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <STO>
A:Cross-references: UNIPROT:Q9S8B1; UNIPARC:UPI000009F06E
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 23.1%; Score 18; DB 2; Length 15;
Best Local Similarity 25.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 2 IKRDNDYSKNP 13
|:|:|:
Db 3 VNDSKNDIIVSP 14

RESULT 59
S77987

Cytochrome-c oxidase (BC 1.9.3.1) chain Vic.2 - bigeye tuna (fragments)

C.Species: Thunnus obesus (bigeye tuna)
C.Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C.Accession: S77987

R.Artnold, S.; Lee, J.; Kim, M.; Song, B.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997

A.Reference number: S77980

A.Accession: S77987

A.Molecule type: protein

A.Residues: 1-819-15 <ARN>

A.Cross-references: UNIPROT:P80978; UNIPARC:UPI000017BF73; UNIPARC:UPI000017BF74

A.Experimental source: heart

C.Genetics:

A.Genome: nuclear

A.Function: oxidative phosphorylation; respiratory chain

A.Pathway: electron transfer; membrane-associated complex; mitochondrial inner membrane

C.Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 23.1%; Score 18; DB 2; Length 15;

Best Local Similarity 42.9%; Pred. No. 7.6e+03;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KDNDY 9

Db 8 KKPMDDY 14

RESULT 60

MTDFB8

melanotropin beta - spiny dogfish

C.Species: Squalus acanthias (spiny dogfish)

C.Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004

C.Accession: A01471

R.Bennett, H.P.; Lowry, P.J.; McMartin, C.; Scott, A.P.

Biochem. J. 141, 439-444, 1974

A.Title: Structural studies of alpha-melanocyte-stimulating hormone and a novel beta-mel

A.Reference number: A90277; MUID:75127390; PMID:4375978

A.Accession: A01471

A.Molecule type: protein

A.Residues: 1-16 <BEN>

A.Cross-references: UNIPROT:P01207; UNIPARC:UPI000012FLC2

C.Superfamily: corticotropin-lipotropin

C.Keywords: hormone

Query Match 23.1%; Score 18; DB 1; Length 16;

Best Local Similarity 60.0%; Pred. No. 7.6e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 5 DHNDY 9

Db 1 DGDY 5

RESULT 61

D58501

26K kidney and gallbladder stone protein - unidentified bacterium (fragment)

C.Species: unidentified bacterium

C.Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004

C.Accession: D58501

R.Binette, J.P.; Binette, M.B.

submitted to the Protein Sequence Database, October 1996

A.Description: The proteins of kidney and gallbladder stones.

A.Reference number: A58501

A.Accession: D58501

A.Status: preliminary

A.Molecule type: protein

A.Residues: 1-16 <BIN>

A.Cross-references: UNIPROT:Q7MDJ3; UNIPARC:UPI000017A8CE

A.Experimental source: human kidney and gallbladder stones

Query Match

Best Local Similarity 23.1%; Score 18; DB 2; Length 16;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 7 NDYSKN 12

Db 7 NEVSEN 12

RESULT 62

S11760

flgB protein - Caulobacter crescentus (fragment)

C.Species: Caulobacter crescentus

C.Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C.Accession: P00126; A25882; S11760

R.Schoenlein, P.V.; Gallman, L.S.; Winkler, M.E.; Ely, B.

Gene 93, 17-25, 1990

A.Title: Nucleotide sequence of the Caulobacter crescentus flgB and flgT genes and an

A.Reference number: J00741; MUID:91033011; PMID:1699845

A.Accession: P00126

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-16 <SCH>

A.Cross-references: UNIPROT:P18914; UNIPARC:UPI000016EAB1; GB:X15134; NID:G40418; PIDN

R.Mimlich, S.A.; Newton, A.

Proc. Natl. Acad. Sci. U.S.A. 84, 1142-1146, 1987

A.Title: Promoter mapping and cell cycle regulation of flagellin gene transcription in

A.Reference number: A25882; MUID:87147229; PMID:3465658

A.Accession: A25882

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-12, 'V', 14-16 <MIN>

A.Cross-references: UNIPARC:UPI000016EABE; GB:M15688; NID:G144267; PIDN:AAA23050.1; PTL

C.Genetics:

A.Gene: flgB

Query Match 23.1%; Score 18; DB 2; Length 16;

Best Local Similarity 42.9%; Pred. No. 7.6e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDYSKN 13

Db 3 NSINTNP 9

RESULT 63

B44820

7K protease - Escherichia coli

C.Species: Escherichia coli

C.Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C.Accession: B44820

R.Lopez, J.; Delgado, D.; Andree, I.; Ortiz, J.M.; Rodriguez, J.C.

J. Gen. Microbiol. 137, 1093-1099, 1991

A.Title: Isolation and evolutionary analysis of a RepFVB replicon of the plasmid pSU21

A.Reference number: A44820; MUID:91324851; PMID:1865183

A.Contents: IncFVI plasmid pSU212

A.Accession: B44820

A.Status: preliminary

A.Molecule type: DNA

A.Residues: 1-16 <LOP>

A.Cross-references: UNIPROT:Q8KQF9; UNIPARC:UPI000017AA2D

A.Note: sequence extracted from NCBI backbone (NCBIN:45962, NCBI:45966)

Query Match 23.1%; Score 18; DB 2; Length 16;

Best Local Similarity 75.0%; Pred. No. 7.6e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 SKNP 13

Db 9 SENP 12

RESULT 64

B28027

protein P8 - curled-leaved tobacco (fragment)

C.Species: Nicotiana glauca (curled-leaved tobacco)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004
C/Accession: B28027
R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid-
A/Reference number: A94167
A/Accession: B28027
A/Molecule type: protein
A/Residues: 1-16 <BAU>
A/Cross-references: UNIPROT:Q7M1V7; UNIPARC:UPI000017B09F
A/Note: 10-Lys was also found

Query Match 23.1%; Score 18; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 7.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
| | | |
Db 10 NDGSK 14

RESULT 65
A61117
somatostatin precursor processing enzyme (EC 3.4.21.-) - American goosefish (fragment)
C/Species: Lophius americanus (American goosefish)
C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 13-Sep-1996
C/Accession: A61117
R/Mackin, R.B.; Noe, B.D.; Spiess, J.
Endocrinology 129, 2263-2265, 1991
A/Title: Identification of a somatostatin-14-generating propeptide converting enzyme as
A/Reference number: A61117; MUID:9207528; PMID:1680673
A/Accession: A61117
A/Molecule type: protein
A/Residues: 1-17 <MAC>
A/Cross-references: UNIPARC:UPI0000175CD6
A/Experimental source: pancreatic islets
C/Superfamily: kexin; subtilisin homology
C/Keywords: hydrolase; serine proteinase

Query Match 23.1%; Score 18; DB 2; Length 17;
Best Local Similarity 44.4%; Pred. No. 8.1e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDNDYSKN 12
| : | | |
Db 3 RNNDIEVN 11

RESULT 66
S57991
hydroxyproline-rich protein - Sesbania rostrata (fragment)
C/Species: Sesbania rostrata
C/Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004
C/Accession: S57991
R/Gormachitzy, S.; Valerio-Lepintec, M.; Szczylowski, K.; van Montagu, M.; Holsters, M.
submitted to the EMBL Data Library, March 1995
A/Description: Use of differential display to identify novel Sesbania rostrata genes ent
A/Reference number: S57991
A/Accession: S57991
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-17 <GOO>
A/Cross-references: UNIPROT:Q41400; UNIPARC:UPI00000ACDP95; EMBL:Z48673; NID:g899484; PIC
C/Superfamily: hydroxyproline-rich glycoprotein

Query Match 23.1%; Score 18; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 YSKNP 13
| : | |
Db 6 YKSP 10

RESULT 67
B28027
protein P4 - curled-leaved tobacco (fragment)
C/Species: Nicotiana glauca (curled-leaved tobacco)
C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 18-Jun-1993
C/Accession: B28027
R/Bauw, G.; De Loose, M.; Inze, D.; Van Montagu, M.; Vandekerckhove, J.
Proc. Natl. Acad. Sci. U.S.A. 84, 4806-4810, 1987
A/Title: Alterations in the phenotype of plant cells studied by NH2-terminal amino acid
A/Reference number: A94167
A/Accession: B28027
A/Molecule type: protein
A/Residues: 1-17 <BAU>
A/Cross-references: UNIPARC:UPI000017B09D

Query Match 23.1%; Score 18; DB 2; Length 17;
Best Local Similarity 28.6%; Pred. No. 8.1e+03;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKNPM 14
| : | : |
Db 8 EYNQNAL 14

RESULT 68
B61491
seed protein ws-2 - winged bean (fragment)
C/Species: Psophocarpus tetragonolobus (winged bean)
C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
C/Accession: B61491
R/Hirano, H.
J. Protein Chem. 8, 115-130, 1989
A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two di-
A/Reference number: A61491; MUID:9351606; PMID:2765119
A/Accession: B61491
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-17 <HR>
A/Cross-references: UNIPROT:Q7M1H7; UNIPARC:UPI000017B06D
C/Keywords: seed

Query Match 23.1%; Score 18; DB 2; Length 17;
Best Local Similarity 25.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 1 SIKRDNDYSKN 12
| : | : | : |
Db 2 TISFNFQPDON 13

RESULT 69
PH1815
T cell receptor alpha chain V region (clone 4PB1 V alpha 24-7) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1815
R/Poccellil, S.; Jockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1815
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-18 <POR>
A/Cross-references: UNIPARC:UPI000017C387

Query Match 23.1%; Score 18; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 8.6e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDYS 10

Db 5 DLMRYs 10

RESULT 70

T08159
8 locus-linked protein SLR1a - rape
C/Species: Brassica napus (rape)
C/Date: 21-May-1999 #sequence_revision 21-May-1999 #text_change 09-Jul-2004
C/Accession: T08159
R/Yu, K.; Schuster, U.; Glavin, T.L.; Goring, D.R.; Rothstein, S.J.
Plant Cell 8, 2269-2380, 1996
A/Title: Molecular characterization of the S locus in two self-incompatible Brassica nap
A/Reference number: Z16388; MUID:97143881; PMID:8989868
A/Accession: T08159
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-18 <YUK>
A/Cross-references: UNIPROT:Q96345; UNIPARC:UPI00000A8040; EMBL:U66192; NID:g1518109; PI

Query Match

Best Local Similarity 23.1%; Score 18; DB 2; Length 18;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 YSKNP 13
Db 10 YSDDP 14

RESULT 71

A59137
protein P11 - golden needle mushroom (fragment)
C/Species: Flammulina velutipes (golden needle mushroom)
C/Date: 12-Nov-1999 #sequence_revision 12-Nov-1999 #text_change 09-Jul-2004
C/Accession: A59137
R/Sakamoto, Y.; Ando, A.; Tamai, Y.; Miura, K.
submitted to the Protein Sequence Database, November 1999
A/Description: Differences of proteins expressed in the fruiting dikaryon and the non-fr
A/Reference number: A59137
A/Accession: A59137
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-18 <SAK>
A/Cross-references: UNIPROT:Q7M4W6; UNIPARC:UPI000017CB27

Query Match

Best Local Similarity 23.1%; Score 18; DB 2; Length 18;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 SKNP 13
Db 12 SQNP 15

RESULT 72

S43657
hsp90 protein homolog - qual1 (fragments)
N/Alternate names: p89 protein
C/Species: Phasliandae gen. sp. (qual1)
C/Date: 19-Mar-1997 #sequence_revision 01-Feb-1999 #text_change 01-Feb-1999
C/Accession: S43657
R/Lovric, J.; Blischof, O.; Moelling, K.
FEBS Lett. 343, 15-21, 1994
A/Title: Cell cycle-dependent association of Gag-M1 and hsp90.
A/Reference number: S43657; MUID:94215698; PMID:8163010
A/Accession: S43657
A/Molecule type: protein
A/Residues: 1-19 <LOV>
A/Cross-references: UNIPARC:UPI0000177D66
A/Experimental source: embryo fibroblasts
C/Superfamily: heat shock protein 90
C/Keywords: heat shock

Query Match 23.1%; Score 18; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 9.1e+03;
Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KRHDNDYK 11
Db 11 KKFYEQFSK 19

RESULT 73

S31613
beta-1,3-glucanase homolog (clone A28) - rape (fragment)
C/Species: Brassica napus (rape)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S31613
R/Hird, D.; Worrall, D.; Hodge, R.; Paul, W.; Smartt, S.; Draper, J.; Scott, R.
submitted to the EMBL Data Library, December 1992
A/Description: The anther-specific protein encoded by the Brassica napus and Arabidops
A/Reference number: S31612
A/Accession: S31613
A/Molecule type: mRNA
A/Residues: 1-19 <HIR>
A/Cross-references: UNIPROT:Q06914; UNIPARC:UPI000009FB3B; EMBL:X69890; NID:g17735; PI
A/Experimental source: clone A28
C/Superfamily: beta-1,3-glucanase

Query Match 23.1%; Score 18; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 9.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 7 NDYSKNP 13
Db 9 NDRCKFP 15

RESULT 74

S50741
probable trypsin inhibitor - potato (fragment)
N/Alternate names: PKPI major protein
C/Species: Solanum tuberosum (potato)
C/Date: 14-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
C/Accession: S50741
R/Mitsumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.
Plant Mol. Biol. 26, 961-969, 1994
A/Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibit
A/Reference number: S50741; MUID:95093035; PMID:8000008
A/Accession: S50741
A/Molecule type: protein
A/Residues: 1-20 <MIT>
A/Cross-references: UNIPROT:Q9S8K2; UNIPARC:UPI00000A9BBF
C/Superfamily: cathepsin D inhibitor

Query Match 23.1%; Score 18; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 9.6e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 8 DYSKNPM 14
Db 8 DQDGNPL 14

RESULT 75

S71017
hypothetical protein - Streptococcus pneumoniae (fragment)
C/Species: Streptococcus pneumoniae
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C/Accession: S71017
R/Martin, B.; Sharples, G.U.; Humbert, O.; Lloyd, R.G.; Claverys, J.P.
Mol. Microbiol. 19, 1035-1045, 1996
A/Title: The mmsA locus of Streptococcus pneumoniae encodes a RecG-like protein involve
A/Reference number: S71015; MUID:96249697; PMID:8830261
A/Accession: S71017
A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA
A:Residues: 1-20 <MAR>
A:Cross-references: UNIPROT:Q97PE0, UNIPROT:Q8DNUL, UNIPARC:UPI000017AC6F, EMBL:249988
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995
C:Superfamily: cephalosporin-C deacetylase

Query Match 23.1%; Score 18; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KNP 13
| | |
| | |
Db 2 KNP 4

RESULT 76
A44773
pollen allergen I - Japanese cedar (fragment)
C:Species: Cryptomeria japonica (Japanese cedar)
C:Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 09-Jul-2004
C:Accession: A44773
R:Tanaka, M.; Ando, S.; Usui, M.; Kurimoto, M.; Sakaguchi, M.; Inouye, S.; Matsushi, T.
FEBS Lett. 239, 329-332, 1988
A:Title: N-terminal amino acid sequence of a major allergen of Japanese cedar pollen (Cr
A:Reference number: A44773; MUID:89031257; PMID:3181436
A:Accession: A44773
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <TAN>
A:Cross-references: UNIPROT:P18632, UNIPARC:UPI0000157693
C:Superfamily: pectate lyase LAM59
C:Keywords: pollen

Query Match 23.1%; Score 18; DB 2; Length 20;
Best Local Similarity 27.3%; Pred. No. 9.6e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 4 RDNDYSKNPM 14
| : : : : |
| : : : : |
Db 9 RGSNMAQNRM 19

RESULT 77
I54283
aryl sulfatase A - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 21-Jul-2000
C:Accession: I54283
R:Regis, S.; Carozzo, R.; Filocamo, M.; Serra, G.; Mastropalo, C.; Gatti, R.
Hum. Genet. 96, 233-235, 1995
A:Title: An AT-deletion causing a frameshift in the arylsulfatase A gene of a late infan
A:Reference number: I54283; MUID:95362256; PMID:7635478
A:Accession: I54283
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <RES>
A:Cross-references: UNIPARC:UPI00001177BE, GB:S78735; NID:G1037139; PIDN:AAB35013.1; PIT

Query Match 23.1%; Score 18; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 9.6e+03;
Matches 2; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYSK 11
| : : : : |
| : : : : |
Db 3 HSDHCR 8

RESULT 78
H49164
chromogranin-B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C:Accession: H49164

R:Nielsen, B.; Wellinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides t
A:Reference number: H49164; MUID:92063871; PMID:1954895
A:Accession: H49164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <NIE>
A:Cross-references: UNIPARC:UPI0000086626
A:Note: sequence extracted from NCBI backbone (NCBIP:66364)

Query Match 23.1%; Score 18; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 RDND 8
| | :
| | :
Db 6 RDXNME 10

RESULT 79
A26999
carboxylesterase (EC 3.1.1.1), intestinal - Caenorhabditis elegans (fragment)
C:Species: Caenorhabditis elegans
C:Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 09-Jul-2004
C:Accession: A26999
R:McGhee, J.D.
Biochemistry 26, 4101-4107, 1987
A:Title: Purification and characterization of a carboxylesterase from the intestine of
A:Reference number: A26999; MUID:88000636; PMID:3651439
A:Accession: A26999
A:Molecule type: protein
A:Residues: 1-13 <MCS>
A:Cross-references: UNIPROT:Q7M3Q8, UNIPARC:UPI0000176B3
C:Keywords: carboxylic ester hydrolase; intestine

Query Match 22.4%; Score 17.5; DB 2; Length 13;
Best Local Similarity 57.1%; Pred. No. 7.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 5 DHNDYSK 11
| : : : : |
| : : : : |
Db 5 EHN-YGK 10

RESULT 80
S17976
glucose isomerase - Thermoaerobacterium saccharolyticum (fragment)
C:Species: Thermoaerobacterium saccharolyticum
C:Date: 12-Feb-1998 #sequence_revision 12-Feb-1998 #text_change 09-Jul-2004
C:Accession: S17976
R:Lee, C.; Zeikus, J.G.
Biochem. J. 273, 565-571, 1991
A:Title: Purification and characterization of thermostable glucose isomerase from Clost
A:Reference number: S15119; MUID:91144536; PMID:1996956
A:Accession: S17976
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-7 <LBS>
A:Cross-references: UNIPROT:P30435, UNIPARC:UPI0000173053
A:Note: the sequence from page 568 is inconsistent with that from page 565 in having 6-

Query Match 21.8%; Score 17; DB 2; Length 7;
Best Local Similarity 50.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NDYSKN 12
| | :
| | :
Db 2 NKYPEN 7

RESULT 81

B54823
Olfactory receptor 17 - western wild mouse (fragment)
C:Species: Mus spretus (western wild mouse)
C:Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 17-Mar-1999
C:Accession: B54823
R:Cheser, A.; Simon, I.; Cedar, H.; Axel, R.
Cell 78, 823-834, 1994
A:Title: Allelic inactivation regulates olfactory receptor gene expression.
A:Reference number: A54823; PMID:94373818; PMID:8087849
A:Accession: B54823
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-8 <CH2>
A:Cross-references: UNIPARC:UPI000017C89B

Query Match 21.8%; Score 17; DB 2; Length 8;
Best Local Similarity 40.0%; Pred. No. 2.8e+05;
Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDN 7
DB 3 RKNHS 7

RESULT 82
S30494
cat gene leader peptide - Streptococcus agalactiae plasmid pIP501
C:Species: Streptococcus agalactiae
C:Date: 12-Feb-1998 #sequence_revision 20-Feb-1998 #text_change 16-Aug-2004
C:Accession: S30494
R:Trieu-Quoc, P.; de Cespedes, G.; Horud, T.
Plasmid 28, 272-276, 1992
A:Title: Nucleotide sequence of the chloramphenicol resistance determinant of the Strept
A:Reference number: J01950; PMID:93096867; PMID:1461942
A:Accession: S30494
A:Molecule type: DNA
A:Residues: 1-9 <TRI>
A:Cross-references: UNIPROT:P36884; UNIPARC:UPI00000004AB; EMBL:X65462; NID:949071; PIDN
A:Genome: plasmid pIP501

Query Match 21.8%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYS 10
DB 6 DYS 8

RESULT 83
B24362
chloramphenicol O-acetyltransferase leader peptide - Staphylococcus aureus plasmid pUB1
C:Species: Staphylococcus aureus
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 05-Oct-2004
C:Accession: B24362
R:Bruckner, R.; Matzura, H.
EMBO J. 4, 2295-2300, 1985
A:Title: Regulation of the inducible chloramphenicol acetyltransferase gene of the Staph
A:Reference number: A24362; PMID:86081739; PMID:1385770
A:Accession: B24362
A:Molecule type: DNA
A:Residues: 1-9 <BN>
A:Cross-references: UNIPROT:P36884; UNIPARC:UPI00000004AB; GB:X02872; NID:946536; PIDN:
C:Comment: Ribosome stalling in the translation of this leader peptide, caused by the ef
ficient translation of the chloramphenicol O-acetyltransferase from a ribosome binding site located
A:Genome: plasmid

Query Match 21.8%; Score 17; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 DYS 10
DB 6 DYS 8

RESULT 84
S18385
NADP-cytochrome P450 reductase-related protein - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 22-Nov-1993 #sequence_revision 12-Apr-1996 #text_change 07-Feb-1997
C:Accession: S18385
R:Nadler, S.G.; Strobel, H.W.
Arch. Biochem. Biophys. 290, 277-284, 1991
A:Title: Identification and characterization of an NADPH-cytochrome P450 reductase der
A:Reference number: S18385; PMID:92027739; PMID:1929397
A:Accession: S18385
A:Molecule type: protein
A:Residues: 1-11 <NAD>
A:Cross-references: UNIPARC:UPI000017C961
C:Keywords: NADP

Query Match 21.8%; Score 17; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 7.6e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DHNDY 9
DB 5 DPEDY 9

RESULT 85
B47171
chondroitin sulfate proteoglycan PG-M core protein, splice form VI - chicken (fragment)
N:Alternate names: versican-like chondroitin sulfate proteoglycan
C:Species: Gallus gallus (chicken)
C:Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Feb-1997
C:Accession: B47171
R:Shinomura, T.; Nishida, Y.; Ito, K.; Kimata, K.
J. Biol. Chem. 268, 14461-14469, 1993
A:Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed durin
A:Reference number: A47171; PMID:93300846; PMID:8314802
A:Accession: B47171
A:Status: preliminary
A:Molecule type: nucleic acid
A:Residues: 1-12 <SHI>
A:Cross-references: UNIPARC:UPI000017BPF2
A:Experimental source: CER, embryo fibroblasts
A:Note: sequence extracted from NCBI backbone (NCBIN:134459, NCBI:P.134462)

Query Match 21.8%; Score 17; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 SIKRDH 6
DB 3 SEBQDH 8

RESULT 86
PH1605
Ig H chain V-D-J region (wild-type clone 328) - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C:Accession: PH1605
R:Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A:Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A:Reference number: PH1605; PMID:93301609; PMID:8315387
A:Accession: PH1605
A:Molecule type: DNA
A:Residues: 1-12 <LRV>
A:Cross-references: UNIPARC:UPI000017C6C1

A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 8.4e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KRDNNDY 9
| | |
Db 6 REDAMDY 12

RESULT 87

146794
hypothetical protein [imported] - Haloarcula marismortui (fragment)

C;Species: Haloarcula marismortui
C;Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004
C;Accession: 146794
R;Arndt, E.

PEBS Lett. 267, 193-198, 1990
A;Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and
A;Reference number: S10731; MUID:90336772; PMID:2143141

A;Accession: 146794
A;Status: preliminary; translated from GB/EMBL/DBJ
A;Molecule type: DNA
A;Residues: 1-12 <ARN>
A;Cross-references: UNIPROT:P10971; UNIPARC:UPI0000167C4; EMBL:X5511; NID:643610; PIDD

Query Match 21.8%; Score 17; DB 2; Length 12;
Best Local Similarity 27.3%; Pred. No. 8.4e+03;
Matches 3; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
| | | | |
Db 1 IQGREGDLOEN 11

RESULT 88

PT0331

Ig heavy chain CRD3 region (clone J2-121) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C;Accession: PT0331
R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Catton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991
A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A;Reference number: PT0222; MUID:91108337; PMID:1899102

A;Accession: PT0331
A;Molecule type: DNA
A;Residues: 1-13 <YAM>
A;Cross-references: UNIPARC:UPI000017C219

A;Experimental source: B lymphocyte
C;Keywords: heterotetramer; immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 13;
Best Local Similarity 30.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 4 RDNDYSKNP 13
| | | | |
Db 2 RGRDYNMPP 11

RESULT 89

170075

glycophorin B (miscellaneous) - human (fragment)

C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 14-Aug-1997 #text_change 09-Jul-2004
C;Accession: 170075
R;Rearden, A.; Phan, H.; Dubnicoff, T.; Kudo, S.; Fukuda, M.

J. Biol. Chem. 265, 9259-9263, 1990
A;Title: Identification of the crossing-over point of a hybrid gene encoding human glyco
A;Reference number: I55334; MUID:90264417; PMID:1971625

A;Accession: 170075
A;Status: translated from GB/EMBL/DBJ

A;Molecule type: DNA
A;Residues: 1-13 <REA>
A;Cross-references: UNIPROT:Q14461; UNIPARC:UPI00000730D2; GB:M33505; GB:J05465; NID:91
A;Note: this sequence was not determined in this report; the translation is from an inc
C;Genetics:

A;Gene: GDB:GYPB
A;Cross-references: GDB:118891
A;Map position: 4q28-4q31

Query Match 21.8%; Score 17; DB 4; Length 13;
Best Local Similarity 75.0%; Pred. No. 9.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDN 6
| | |
Db 2 KRDN 5

RESULT 90

PT0029

karataasin - karatas (fragment)

C;Species: Bromelia plumieri (karatas)
C;Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C;Accession: PT0029
R;Montes, C.; Amador, M.; Cuevas, D.; Cordoba, F.

Agric. Biol. Chem. 54, 17-24, 1990
A;Title: Subunit structure of karataasin, the proteinase isolated from Bromelia plumieri
A;Reference number: PT0029; MUID:90344224; PMID:1368518

A;Accession: PT0029
A;Molecule type: protein
A;Residues: 1-14 <MON>

A;Cross-references: UNIPROT:P22442; UNIPARC:UPI000012DC38
A;Note: the amino terminal sequence shows similarity with papain and stem bromelain
C;Comment: This enzyme is composed of two small subunits linked by disulfide bonds.

Query Match 21.8%; Score 17; DB 2; Length 14;
Best Local Similarity 60.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 DNDXY 9
| | | | |
Db 6 DXXDY 10

RESULT 91

A58945

anti-neoplastic urinary protein - human (fragment)

N;Alternate names: ANUP
C;Species: Homo sapiens (man)
C;Date: 09-Apr-1999 #sequence_revision 09-Apr-1999 #text_change 09-Apr-1999
C;Accession: A58945
R;Ridge, R.J.; Sloane, N.H.

Cytokine 8, 1-5, 1996
A;Title: Partial N-terminal amino acid sequence of the anti-neoplastic urinary protein
A;Reference number: A58945; MUID:96351837; PMID:8742060

A;Accession: A58945
A;Molecule type: protein
A;Residues: 1-15 <RID>
A;Cross-references: UNIPARC:UPI000017C089

A;Note: 13-Thr was also seen; residues 4 and 7 are assumed to be Cys; the authors report
the terminal is blocked
C;Keywords: cytokine; pyroglutamic acid
F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status predicted

Query Match 21.8%; Score 17; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 KNPM 14
| | | | |

Db 8 KPM 11

RESULT 92

PH1631

Ig H chain V-D-J region (clone B-lees 202) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1631

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-lees mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1631

A/Molecule type: DNA

A/Residues: 1-15 <LEV>

A/Cross-references: UNIPARC:UPI000017C699

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 11 KPM 14

Db 2 KPM 5

RESULT 93

B26501

Lipoprotein lipase (BC 3.1.1.34) - guinea pig (fragment)

C/Species: Cavia porcellus (guinea pig)

C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 28-Apr-1993

C/Accession: B26501

R/Bergstrom-Olivera, G.; Oliveira, T.; Jornvall, H.

Eur. J. Biochem. 161, 281-288, 1986

A/Title: Lipoprotein lipases from cow, guinea-pig and man. Structural characterization

A/Reference number: A31178; MUID:87054027; PMID:3536511

A/Accession: B26501

A/Molecule type: protein

A/Residues: 1-15 <BEN>

A/Cross-references: UNIPARC:UPI000017CA2B

C/Keywords: carboxylic ester hydrolase

Query Match 21.8%; Score 17; DB 2; Length 15;

Best Local Similarity 40.0%; Pred. No. 1.1e+04;

Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 4 RDND 8

Db 5 KDYD 9

RESULT 94

PA0059

Protein QP200021 - fungus (Fusarium sporotrichioides) (fragment)

C/Species: Fusarium sporotrichioides

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004

C/Accession: PA0059

R/Chow, L.P.; Fukaya, N.; Sugita, Y.; Ueno, Y.; Tabuchi, K.; Tsugita, A.

submitted to JFPI, October 1994

A/Description: Two dimensional polyacrylamide gel electrophoresis of Fusarium sporotrichioides

A/Reference number: PA0059

A/Accession: PA0059

A/Molecule type: protein

A/Residues: 1-15 <CHO>

A/Cross-references: UNIPROT:Q7M4Y3; UNIPARC:UPI000017B410

Query Match

Best Local Similarity 21.8%; Score 17; DB 2; Length 15;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 IKRDH 6

Db 4 LEEDH 8

RESULT 95

C45133

casein kinase II (BC 2.7.1.1-) alpha chain - dog (fragment)

C/Species: Canis lupus familiaris (dog)

C/Date: 30-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C/Accession: C45133

R/Ou, W.J.; Thomas, D.Y.; Bell, A.W.; Bergeron, J.J.

J. Biol. Chem. 267, 23789-23796, 1992

A/Title: Casein kinase II phosphorylation of signal sequence receptor alpha and the ass

A/Reference number: A45133; MUID:93054738; PMID:1331100

A/Accession: C45133

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <OU>

A/Cross-references: UNIPROT:Q9TRK9; UNIPARC:UPI0000088890

A/Experimental source: endoplasmic reticulum, pancreas

A/Note: sequence extracted from NCBI backbone (NCBI:118799)

C/Superfamily: kinase-related transforming protein; protein kinase homology

C/Keywords: ATP; heterotrimer; phosphotransferase; serine/threonine-specific protein

Query Match

Best Local Similarity 21.8%; Score 17; DB 2; Length 16;

Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HNDY 9

Db 12 HNDY 15

RESULT 96

PT0224

Ig heavy chain CDR3 region (clone 1-91) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0224

R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Catton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0224

A/Molecule type: DNA

A/Residues: 1-16 <YAM>

A/Cross-references: UNIPARC:UPI000017C1D6

A/Experimental source: B lymphocyte

A/Note: the authors translated the stop codon for residue 9 as X

C/Keywords: heterotrimer; immunoglobulin

Query Match 21.8%; Score 17; DB 2; Length 16;

Best Local Similarity 100.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 8 DYS 10

Db 4 DYS 6

RESULT 97

S48655

glutathione dehydrogenase (ascorbate) (BC 1.8.5.1) - spinach (fragment)

N/Alternate names: dehydroascorbate reductase; DHA reductase; tryptan inhibitor (Kunitz

C/Species: Spinacia oleracea (spinach)

C/Date: 15-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004

C/Accession: S48655

R/Tuempert, S.; Pollmann, H.; Haeblerlein, I.

FEBS Lett. 352, 159-162, 1994

A/Title: A novel dehydroascorbate reductase from spinach chloroplasts homologous to pla

A/Reference number: S48655; MUID:95010699; PMID:7925967

A/Accession: S48655

A:Molecule type: protein
A:Residues: 1-17 <TRU>
A:Cross-references: UNIPROT:Q9T2H6, UNIPARC:UPI000093AAAF
A:Superfamily: plant kunitz-type proteinase inhibitor
C:Keywords: chloroplast; oxidoreductase

Query Match 21.8%; Score 17; DB 2; Length 17;
Best Local Similarity 42.9%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 DYSKNPM 14
| :
| :
Db 5 DNEGNPL 11

RESULT 98

B44923
carboxypeptidase 3 - Rhizomucor circinelloides f. lusitanicus (fragment)
C:Species: Rhizomucor circinelloides f. lusitanicus
C>Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 04-Dec-1994
C:Accession: B44923
R:DiSanto, M.E.; Li, Q.H.; Logan, D.A.
J. Bacteriol. 174, 447-455, 1992
A>Title: Purification and characterization of a developmentally regulated carboxypeptidase
A:Reference number: A44923; MUID:92105011; PMID:1729237
A:Accession: B44923
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <Dis>
A:Cross-references: UNIPARC:UPI000017B1C0
A>Note: sequence extracted from NCBI backbone (NCBIP:75616)

Query Match 21.8%; Score 17; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.2e+04;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HNDYS 10
| :
| :
Db 11 HERS 15

RESULT 99

A46592
lactase-phlorizin hydrolase, 200K isoform - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 16-Feb-1994 #sequence_revision 18-Nov-1994 #text_change 01-Nov-1996
C:Accession: A46592
R:Dudley, M.A.; Hachey, D.L.; Quaroni, A.; Hutches, T.W.; Nichols, B.L.; Rosenberger, J.
J. Biol. Chem. 268, 13609-13616, 1993
A>Title: In vivo sucrose-isomaltase and lactase-phlorizin hydrolase turnover in the fed
A:Reference number: A46592; MUID:93293888; PMID:8514793
A:Accession: A46592
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-17 <DUD>
A:Cross-references: UNIPARC:UPI0000067CC
A>Note: sequence extracted from NCBI backbone (NCBIP:134559)
C:Keywords: carbohydrate digestion; intestine

Query Match 21.8%; Score 17; DB 2; Length 17;
Best Local Similarity 30.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKNPM 14
| :
| :
Db 4 DRNPIAAGPL 13

RESULT 100

S24780
protein-tyrosine kinase (EC 2.7.1.112) lck - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C>Date: 19-Feb-1994 #sequence_revision 26-Jul-1996 #text_change 05-Oct-2004

C:Accession: I58370; S24780
R:Shin, S.; Steffen, D.L.
Oncogene 8, 141-149, 1993
A>Title: Frequent activation of the lck gene by promoter insertion and aberrant splicing
A:Reference number: I58370; MUID:93141260; PMID:8423992
A:Accession: I58370
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-18 <RES>
A:Cross-references: UNIPROT:Q01621; UNIPARC:UPI00001709FB; EMBL:Z15029; NID:956567; PDB:
C:Genetics:
A:Gene: lck
C:Superfamily: Tyrosine-protein kinase, proto-oncogene SRC type; protein kinase homolog
C:Keywords: ATP; blocked amino end; lipoprotein; myristylation; phosphoryltransferase; thl
P;2/Modified site: myristylated amino end (Gly) (in mature form) #status predicted
F;3/Binding site: palmitate (Cys) (covalent) #status predicted

Query Match 21.8%; Score 17; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 10 SKNP 13
| :
| :
Db 6 SSNP 9

Search completed: January 20, 2006, 19:12:09
Job time : 8.94231 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 46.5769 Seconds
(without alignments)
212.066 Million cell updates/sec

Title: US-09-662-293-1

Perfect score: 78

Sequence: 1 SIKRDNDYKNPM 14

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : UniProt_05.80.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	35	44.9	20	2	Q9PR55 ONCMY
2	28	35.9	15	1	AVP2 CAVPO
3	28	35.9	20	2	C711V5 GRHIZ
4	27	34.6	13	2	Q53KLI ORISA
5	27	34.6	14	2	Q8W1T7 BOSCA
6	26	33.3	11	2	Q9UNL8 HUMAN
7	26	33.3	20	2	Q9UCB5 HUMAN
8	25.5	32.7	20	2	Q9S8H1 HORVU
9	25	32.1	19	2	Q4X3T4 PLACH
10	25	32.1	20	1	SPAZ_ARTOL
11	25	31.4	20	2	Q9QUM2 SMURI
12	24.5	31.4	17	2	Q4XBK6 PLACH
13	24.5	31.4	19	2	Q7M0Q1 PSBPU
14	24	30.8	19	2	Q9S8G9 PSOTB
15	24	30.8	19	2	Q90510 SHIV1
16	24	30.8	20	2	Q9S8H0 PSOTB
17	23.5	30.1	13	2	Q4YHVI PLABE
18	23	29.5	13	2	Q83171 GVIRU
19	23	29.5	15	1	TXZB_BUNCA
20	23	29.5	18	2	C711V7 GRHIZ
21	23	29.5	18	2	Q90M82 RAT
22	23	29.5	19	2	Q90514 SHIV1
23	23	29.5	20	2	Q4XKID PLACH
24	23	29.5	20	2	Q6V0Z6 MUSSP
25	22.5	28.8	18	2	Q7YXH4 CAEBL
26	22.5	28.8	19	2	Q905G4 SHIV1
27	22.5	28.8	19	2	Q90RGS SHIV1
28	22	28.2	14	2	Q90UN9 HUMAN
29	22	28.2	16	2	Q9R4Z5 STRSU
30	22	28.2	16	2	Q5DJ22 SOLSO
31	22	28.2	17	1	BMTID_BOOMI

32	22	28.2	17	2	Q34216 96PHN	Q34216 sphingomona
33	22	28.2	18	2	Q4XK28 PLACH	Q4XK28 plasmidium
34	22	28.2	18	2	Q64134 SMURI	Q64134 ractus sp.
35	22	28.2	18	2	Q6DUU4 RAT	Q6DUU4 ractus norv
36	22	28.2	19	2	Q4XGA8 PLACH	Q4XGA8 plasmidium
37	22	28.2	20	2	Q7JNH9 DROME	Q7JNH9 drosophila
38	22	28.2	20	2	Q4Y3Y1 PLACH	Q4Y3Y1 plasmidium
39	22	28.2	20	2	Q9PS15 ONCKI	Q9PS15 oncoctrymchu
40	21.5	27.6	19	2	Q4NSW7 THEPA	Q4NSW7 theileria p
41	21.5	27.6	19	2	Q905G8 SHIV1	Q905G8 human immun
42	21.5	27.6	19	2	Q905J6 SHIV1	Q905J6 human immun
43	21	26.9	11	2	Q7M0L3 BACCI	Q7M0L3 bacillus ci
44	21	26.9	12	2	Q4XW72 PLACH	Q4XW72 plasmidium
45	21	26.9	12	2	Q4YET5 PLABE	Q4YET5 plasmidium
46	21	26.9	13	2	Q9QCK3 BVV	Q9QCK3 borna disea
47	21	26.9	13	2	Q9QCK6 BVV	Q9QCK6 borna disea
48	21	26.9	13	2	Q9QCK9 BVV	Q9QCK9 borna disea
49	21	26.9	13	2	Q9QCL2 BVV	Q9QCL2 borna disea
50	21	26.9	13	2	Q9QCL5 BVV	Q9QCL5 borna disea
51	21	26.9	13	2	Q9QCL8 BVV	Q9QCL8 borna disea
52	21	26.9	13	2	Q9QCM1 BVV	Q9QCM1 borna disea
53	21	26.9	13	2	Q9QCM4 BVV	Q9QCM4 borna disea
54	21	26.9	14	2	Q69Z00 HUMAN	Q69Z00 homo sapien
55	21	26.9	14	2	Q9TWX8 MANSE	Q9TWX8 manduca sex
56	21	26.9	14	2	Q54394 STRLI	Q54394 streptomyce
57	21	26.9	14	2	Q9RSR5 STRAU	Q9RSR5 straphylococ
58	21	26.9	15	1	MK1_PALPR	Q80408 palomona pr
59	21	26.9	15	1	MK2A_PALPR	Q80409 palomona pr
60	21	26.9	15	1	TX12B_BUNCA	Q84473 bungarus ca
61	21	26.9	15	1	UP02_MERAN	Q84439 metarhizium
62	21	26.9	15	2	Q9UC17 HUMAN	Q9UC17 homo sapien
63	21	26.9	15	2	Q7M0C8 SMURI	Q7M0C8 mus sp. cd3
64	21	26.9	15	2	Q9PXC5 TEV	Q9PXC5 tobacco etc
65	21	26.9	16	1	MK2B_PALPR	Q80410 palomona pr
66	21	26.9	16	1	Q61EJ3 MOUSE	Q61EJ3 palomona pr
67	21	26.9	16	2	Q9RSR6 STRAU	Q9RSR6 mus musculu
68	21	26.9	18	2	Q26062 HELPY	Q26062 helicobacte
69	21	26.9	18	2	Q4X617 PLACH	Q4X617 plasmidium
70	21	26.9	19	2	Q9QW83 RAT	Q9QW83 ractus norv
71	21	26.9	19	2	Q905F6 SHIV1	Q905F6 human immun
72	21	26.9	19	2	MEPP_MYTEB	Q83146 mytilus edu
73	21	26.9	20	2	Q9UCF0 HUMAN	Q9UCF0 homo sapien
74	21	26.9	20	2	Q9TPW8 NABGR	Q9TPW8 neogleria g
75	21	26.9	20	2	Q4YQV7 PLABE	Q4YQV7 plasmidium
76	21	26.9	20	2	Q9RSB1 ABRHY	Q9RSB1 aeromonas h
77	21	26.9	20	2	Q9QVC1 SMURI	Q9QVC1 ractus norv
78	21	26.9	20	2	Q34694 HOMAN	Q34694 homarus ame
79	20.5	26.3	8	2	Q15893 HUMAN	Q15893 homo sapien
80	20	25.6	8	2	Q9UDZ4 HUMAN	Q9UDZ4 homo sapien
81	20	25.6	8	2	Q5RLS1 PIG	Q5RLS1 sus scrofa
82	20	25.6	8	2	Q93SR0 STABP	Q93SR0 straphylococ
83	20	25.6	10	2	P82136 SPIOL	Q82136 spincia ol
84	20	25.6	10	2	Q9QVU7 SMURI	Q9QVU7 mus sp. mep
85	20	25.6	11	2	P96319 DBSDS	P96319 deasilfovir
86	20	25.6	11	2	Q6LBU0 MOURS	Q6LBU0 mus musculu
87	20	25.6	11	2	Q7MOD4 RAT	Q7MOD4 ractus norv
88	20	25.6	13	2	Q6LDS1 BPT3	Q6LDS1 bacterioph
89	20	25.6	13	2	Q51605 92ZZZ	Q51605 plasmid col
90	20	25.6	14	1	HY14_PIG	Q51605 sus scrofa
91	20	25.6	14	1	Q5XVW8 SMOLU	Q5XVW8 candidatus
92	20	25.6	14	2	Q6XWV1 SMOLU	Q6XWV1 chrysaanthem
93	20	25.6	14	2	Q6XWV4 SMOLU	Q6XWV4 hydrangea p
94	20	25.6	14	2	Q6XWV7 SMOLU	Q6XWV7 plantago vi
95	20	25.6	14	2	Q6WXXV SMOLU	Q6WXXV apicoc ast
96	20	25.6	14	2	Q6WXXK SMOLU	Q6WXXK leafhopper-
97	20	25.6	14	2	Q6WXX6 SMOLU	Q6WXX6 grey dogwo
98	20	25.6	14	2	Q6WXX9 SMOLU	Q6WXX9 blueberry s
99	20	25.6	14	2	Q6WXX8 SMOLU	Q6WXX8 clover phyl
100	20	25.6	14	2	Q6WXX8 SMOLU	Q6WXX8 clover phyl

ALIGNMENTS

RA Buell C., Yuan Q., Ouyang S., Liu J., Wang A., Malet R., Lin H.,
 RA Zhu W., Hamilton J., Jones K., Tallon L., Feldblyum T., Taitlin T.,
 RA Berr J., Kim M., Jin S., Fedorch D., Vuong H., Overton II L.,
 RA Reardon M., Weaver B., John S., Lewis M., Ulteback T., Van Aken S.,
 RA Wortman J., Haas B., Koo H., Zismann V., Hsiao J., Iobst S.,
 RA de Vazaliles A., White O., Salzberg S., Fraser C.,
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AC146328; AAX95034.1; -; Genomic DNA.
 DR EMBL, AC135794; AAX96196.1; -; Genomic DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 13 AA; 1520 MW; 9F1D63397ED5B5A CRC64;

Query Match 34.6%; Score 27; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYSK 11
 DB 6 DYNDSK 12

RESULT 5
 Q8W17_BOSCA PRELIMINARY; PRT; 14 AA.
 ID Q8W17_BOSCA PRELIMINARY; PRT; 14 AA.
 AC Q8W17;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Ribulose-1,5-bisphosphate large subunit (Fragment).
 GN Name=rdcl;
 OS Bosrychia calliptera.
 OC Chloroplast.
 OC Eukaryota; Rhodophyta; Florideophyceae; Ceramiales; Rhodomeleaceae;
 OC Bosrychia.
 OX NCBI_TaxID=161377;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Zuccarello G.C., West J.A.;
 RT "Phylogeography of the Bosrychia calliptera/B. pinna complex
 (Rhodomeleaceae, Rhodophyta) and divergence rates based on nuclear,
 RT mitochondrial and plastid DNA markers."
 RL Phycologia 41:49-60(2002).
 DR EMBL, AF382909; AAL67239.1; -; Genomic DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1484 MW; 93ED4984B765AF05 CRC64;

Query Match 34.6%; Score 27; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 DHNDYSK 13
 DB 2 DTADYSRP 10

RESULT 6
 Q9UNL8_HUMAN PRELIMINARY; PRT; 11 AA.
 ID Q9UNL8_HUMAN PRELIMINARY; PRT; 11 AA.
 AC Q9UNL8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
 DE APC2 protein (Fragment).
 GN Name=APC2;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RA Carr I.M., Markham A.F., Colella P.L., Wei L., Ashkan J., Morrison E.,
 RA Meredith D.M.;
 RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF110338; AAD29275.1; -; Genomic DNA.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 11 AA; 1326 MW; 75881D7BBA41EAB4 CRC64;

Query Match 33.3%; Score 26; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 1.3e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDHN 7
 DB 2 VLKRDHN 7

RESULT 7
 Q9UCB5_HUMAN PRELIMINARY; PRT; 20 AA.
 ID Q9UCB5_HUMAN PRELIMINARY; PRT; 20 AA.
 AC Q9UCB5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Ribonuclease HB-1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.

RA MEDLINE=94107224; PubMed=8280059;
 RA Yasuda T., Nadano D., Takeshita H., Kishi K.;
 RT "Two distinct secretory ribonucleases from human cerebrum:
 RT purification, characterization and relationships to other
 RT ribonucleases."
 RL Biochem. J. 296:617-625(1993).
 DR PIR; S45003; NRH01.
 DR GO; GO:0004519; F:endonuclease activity; IEA.
 DR GO; GO:0016787; F:hydrolyase activity; IEA.
 DR GO; GO:0003676; F:nucleic acid binding; IEA.
 DR GO; GO:0004522; F:pancreatic ribonuclease activity; IEA.
 DR InterPro; IPR001427; RNaseA.
 DR Pfam; PF00074; RNaseA; 1.
 SQ SEQUENCE 20 AA; 2352 MW; D85B5BA27234551 CRC64;

Query Match 33.3%; Score 26; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 2.5e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 KRDNDYSK 13
 DB 9 BRHMDSDSP 19

RESULT 8
 Q9S8H1_HORVU PRELIMINARY; PRT; 20 AA.
 ID Q9S8H1_HORVU PRELIMINARY; PRT; 20 AA.
 AC Q9S8H1;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE BAKER'S ASTHMA allergen BDP (Fragment).
 OS Hordeum vulgare (Barley).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Hordeum.
 OX NCBI_TaxID=4513;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95269763; PubMed=7750539; DOI=10.1016/0014-5793(95)00355-D;
 RA Garcia-Casado G., Armentia A., Sanchez-Monge R., Sanchez L.M.,

RA Lopez-Otin C., Salcedo G.;
 RT "A major baker's asthma allergen from rye flour is considerably more
 active than its barley counterpart.";
 RL FEBS Lett. 364:36-40(1995).
 DR PIR; S65605; S65605.
 SQ SEQUENCE 20 AA; 2307 MW; 28DDC7C002364803 CRC64;
 Query Match 33.7%; Score 25.5; DB 2; Length 20;
 Best Local Similarity 26.3%; Pred. No. 3e+03;
 Matches 5; Conservative 5; Mismatches 2; Indels 7; Gaps 1;
 QY 3 KRDNHYSK-----NPM 14
 DB 1 ERDYGECRVGKSPINPL 19
 RESULT 9
 Q4X3T4 PLACH PRELIMINARY; PRT; 19 AA.
 ID Q4X3T4 PLACH PRELIMINARY; PRT; 19 AA.
 AC Q4X3T4;
 DT 13-SEP-2005 (TRENBLREL. 31, Created)
 DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
 DE Hypoetical protein (Fragment).
 GN ORFNames=PC404988.00.0;
 OS Plasmodium chabaudi;
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5825;
 RN NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett V., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01010317; CAH88659.1; -; Genomic_DNA.
 KM Hypoetical protein. 1
 FT NON TER
 SQ SEQUENCE 19 AA; 2089 MW; F6F5B66FD7348F CRC64;
 Query Match 32.1%; Score 25; DB 2; Length 19;
 Best Local Similarity 62.5%; Pred. No. 3.5e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 1 SIKRDAND 8
 DB 10 SIKRVHNN 17
 RESULT 10
 SPZL ARTOL STANDARD; PRT; 20 AA.
 ID SPZL ARTOL STANDARD; PRT; 20 AA.
 AC P83290;
 DT 25-OCT-2004 (Rel. 45, Created)
 DT 25-OCT-2004 (Rel. 45, Last sequence update)
 DE Serine protease (EC 3.4.21.-) (Aoz) (Fragment).
 OS Arthropoda; Fungi; Ascomycota; Pezizomycotina; Orbiliomycetes;
 CC Orbiliales; Orbiliaceae; Orbilia.
 CC NCBI_TaxID=13349;
 RN [1]
 RP PROTEIN SEQUENCE AND FUNCTION.
 RC STRAIN=807;
 RA Zhao M., Zhang K.;
 RL Submitted (FEB-2002) to Swiss-Prot.

CC -!- FUNCTION: Degrades native collagen. Immobilizes P.redivivus. Seems
 CC to have a role in the infection of nematode cuticle.
 CC -!- SIMILARITY: Belongs to the peptidase S8 family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC DR Interpro; IPR000209; Pept_S8_S53.
 DR PROSITE; PS00136; SUBTILASE_ASP; PARTIAL.
 DR PROSITE; PS00137; SUBTILASE_HIS; PARTIAL.
 DR PROSITE; PS00138; SUBTILASE_SER; PARTIAL.
 KM Collagen degradation, direct protein sequencing; Hydrolyase; Protease;
 KW Serine protease.
 FT NON TER
 SQ SEQUENCE 20 AA; 2281 MW; 1AA7A11CC4EAB73B CRC64;
 Query Match 32.1%; Score 25; DB 1; Length 20;
 Best Local Similarity 80.0%; Pred. No. 3.7e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 6 HNDYS 10
 DB 15 HEDYS 19
 RESULT 11
 Q9QUM2 9MURI PRELIMINARY; PRT; 20 AA.
 ID Q9QUM2 9MURI PRELIMINARY; PRT; 20 AA.
 AC Q9QUM2;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-DEC-2001 (TRENBLREL. 19, Last annotation update)
 DE 22 KDa INTRALYSOSOMAL lipid-transfer protein (Fragment).
 OS Rattus sp.
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Barchontoglires; Glires; Rodentia; Sciurognathi;
 CC Muridae; Murinae; Rattus.
 CC NCBI_TaxID=10118;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=97104296; PubMed=8948454;
 RA Kuwana T., Mullock B.M., Luzzio J.P.;
 RT "Identification of a lysosomal protein causing lipid transfer, using a
 RT fluorescence assay designed to monitor membrane fusion between rat
 RT liver endosomes and lysosomes.";
 RL Biochem. J. 308:937-946(1995).
 DR HSSP; P17900; IGI3.
 SQ SEQUENCE 20 AA; 2211 MW; 3A160591EA542C5 CRC64;
 Query Match 32.1%; Score 25; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 3.7e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 QY 5 DHNDYSNP 13
 DB 4 DNDDEKDP 12
 RESULT 12
 Q4XB8 PLACH PRELIMINARY; PRT; 17 AA.
 ID Q4XB8 PLACH PRELIMINARY; PRT; 17 AA.
 AC Q4XB8;
 DT 13-SEP-2005 (TRENBLREL. 31, Created)
 DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)
 DE Hypoetical protein (Fragment).
 GN ORFNames=PC403652.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 CC NCBI_TaxID=5825;

```

RN [1]
RN NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koof T.W.A.,
RA Bettman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Biddle S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86 (2005).
CC -1 CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, CAAT01007779; CAH85594.1; -; Genomic_DNA.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 17 AA; 2058 MW; 90C8A5A88D2E2082 CRC64;

Query Match 31.4%; Score 24.5; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.8e+03;
Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

OY 1 SIKRDNDND 10
DB 5 SVRR-HQRY 13

RESULT 13
O7M001_PSEPU PRELIMINARY; PRT; 19 AA.
AC O7M001_PSEPU
DT 01-MAR-2004 (TREMBlrel. 26, Created)
DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
DE Dihydrodipicolinate dehydrogenase (EC 1.8.1.4) beta chain B1
DE (Fragment).
OS Pseudomonas putida.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=303;
RN [1]
RP PROTEIN SEQUENCE.
RX PubMed=8521848;
RA Hecker K., Luo J., Burns G., Braewell E.H., Sokatch J.R.,
RT "Purification of active B1 alpha 2 beta 2 of Pseudomonas putida
RT branched-chain-oxoacid dehydrogenase."
RL Eur. J. Biochem. 233:828-836(1995).
DR PIR: S63476; S63476.
DR GO: GO:0004148; P.dihydrodipoyl dehydrogenase activity; IEA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 19 AA; 2075 MW; A1989ED78655376C CRC64;

Query Match 31.4%; Score 24.5; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 4.3e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 5 DHNDYKNP 13
DB 3 DHNN-SIMP 10

RESULT 14
O9S8G9_PSOTE PRELIMINARY; PRT; 19 AA.
AC O9S8G9_PSOTE
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Proline-rich protein (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

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OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucotsids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OC Psophocarpus.
OX NCBI_TaxID=3891;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95277008; PubMed=7757337;
RA Baska M., Hayakawa H.,
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells."
RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 30.8%; Score 24; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 5.3e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 8 DYSKNP 14
DB 1 DYKRPV 7

RESULT 15
O90510_9HIV1 PRELIMINARY; PRT; 19 AA.
AC O90510_9HIV1
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Tat protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroviruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/088922202753394745;
RA Taniuchi Y., Takehisa J., Bikardou B., Moudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, M.Pandi M., W'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo."
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL, AF410444; AAU10242.1; -; Genomic_DNA.
FT NON_TER
FT NON_TER
SQ SEQUENCE 19 AA; 2353 MW; 366929ED4BE69237 CRC64;

Query Match 30.8%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 5.3e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RDNDY 9
DB 11 QDHQDF 16

RESULT 16
O9S8H0_PSOTE PRELIMINARY; PRT; 20 AA.
AC O9S8H0_PSOTE
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE Proline-rich protein (Fragment).
OS Psophocarpus tetragonolobus (Goa bean) (Asparagus bean).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eucotsids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
OX NCBI_TaxID=3891;
RN [1]
RP PROTEIN SEQUENCE.

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RX MEDLINE=95277008; PubMed=7757337;
RA Beaka M., Hayakawa H.;
RT "Specific secretion of proline-rich proteins by salt-adapted winged
RT bean cells."
RL Plant Cell Physiol. 36:441-446(1995).
SQ SEQUENCE 20 AA; 2246 MW; AEE9BD45CAF0F677 CRC64;

Query Match 30.8%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 DYSKNPM 14
   |||
Db 1 DYKRPV 7

RESULT 17
O4YHV1_PLABE PRELIMINARY; PRT; 13 AA.
ID O4YHV1_PLABE PRELIMINARY;
AC O4YHV1_1
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB402765.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OC NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Blwell S.L., Rastandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jase C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01004957; CAI02415.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1539 MW; 1589FC880F5FA444 CRC64;

Query Match 30.1%; Score 23.5; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 4.3e+03;
Matches 5; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 1 SIKRDNDYS 10
   :|||
Db 2 TLKR-NDYN 10

RESULT 18
O83171_9VIRU PRELIMINARY; PRT; 13 AA.
ID O83171_9VIRU PRELIMINARY;
AC O83171_1
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
DE Hypothetical protein (Fragment).
OS Cauliflower mosaic virus.
OC Viruses; Retroviruses; Caulimoviridae; Caulimovirus.
OC NCBI_TaxID=10641;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Newkirk J., Hubler R., Hohn T.;
RA Newkirk J., Hubler R., Hohn T.;
RT "A viable mutation in cauliflower mosaic virus, a retroviruslike plant

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RT virus, separates its capsid protein and polymerase genes."
RL J. Virol. 62:1460-1463(1988).
DR EMBL; M19741; AAA66605.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 13 AA; 1600 MW; 5DD9E7FDC4A5CB13 CRC64;

Query Match 29.5%; Score 23; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KNPM 14
   |||
Db 2 KNPM 5

RESULT 19
TX2B_BUNCA STANDARD; PRT; 15 AA.
ID TX2B_BUNCA STANDARD;
AC P84470;
DT 10-MAY-2005 (Rel. 47, Created)
DT 10-MAY-2005 (Rel. 47, Last sequence update)
DE Neurotoxin T2 B chain (Fragment).
OS Bungarus candidus (Malayan krait).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidosaurs; Squamata; Scleroglossa; Serpentes; Colubroidea;
OC Elapidae; Bungarinae; Bungarus.
OC NCBI_TaxID=92438;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
RP SPECIFICITY, AND LETHAL DOSE.
RC TISSUE=Venom;
RX PubMed=14765867; DOI=10.1093/jb/mwq187;
RA Know O., Chanhome L., Omori-Sato T., Ogawa Y., Yanoshita R.,
RA Semejima Y., Kuch U., Mebs D., Stipijica V.;
RT "Isolation, toxicity and amino terminal sequences of three major
RT neurotoxins in the venom of Malayan krait (Bungarus candidus) from
RT Thailand."
RL J. Biochem. 134:799-804(2003).
CC -1- FUNCTION: Neurotoxin T2 is a presynaptic neurotoxin of the venom
CC that exhibits indirect hemolytic activity against human
CC erythrocytes. The B chain is homologous to venom basic protease
CC inhibitors but has no protease inhibitor activity and is non-
CC toxic.
CC -1- SUBUNIT: Heterodimer; disulfide-linked. The A chains have
CC phospholipase A2 activity and the B chains show homology with the
CC basic protease inhibitors.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- TOXIC DOSE: LD50 is 0.22 mg/kg by intravenous injection in mice.
CC -1- SIMILARITY: Contains 1 BPT1/Kunitz inhibitor domain.
CC -----
CC This Swiss-Prot entry is copyrighted. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR InterPro; IPR002223; Prot inh Kunz-m.
DR PROSITE; PS00280; BPT1_KUNITZ_1; PARTIAL.
DR PROSITE; PSS0279; BPT1_KUNITZ_2; PARTIAL.
KW Direct protein sequencing; Neurotoxin; Presynaptic neurotoxin; Toxin.
FT NON_TER 15
FT NON_TER 15
SQ SEQUENCE 15 AA; 1866 MW; 828AB0FB98A971A0 CRC64;

Query Match 29.5%; Score 23; DB 1; Length 15;
Best Local Similarity 36.4%; Pred. No. 6.1e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 KRNDNDYKNP 13
   :|||
Db 1 KRHRDODKRP 11

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RESULT 20
ID Q711V7_9RHIZ PRELIMINARY; PRT; 18 AA.
AC Q711V7;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE NodB protein (Fragment).
GN Name=nodB;
OS Rhizobium sp. STM251.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
OX NCBI_TaxID=142631;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=STM251;
RA Moulin L.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ300259; CAC82892.1; -, Genomic_DNA.
PT NON TER 18
SQ SEQUENCE 18 AA; 2055 MW; 1BB4F819521E2F9F CRC64;

Query Match 29.5%; Score 23; DB 2; Length 18;
Best Local Similarity 30.0%; Pred. No. 7.5e+03;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDNDYS 10
DB 9 AVRNVYGDVS 18

RESULT 21
ID Q9QW82_RAT PRELIMINARY; PRT; 18 AA.
AC Q9QW82;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE PHOSPHOPHORIN-PEPTIDE fragment 12-45 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91291127; PubMed=2064607;
RA Sabsey B., Stecler-Stevens W.G., Lechner J.H., Veis A.;
RT "Domain structure and sequence distribution in dentin phosphophoryn.";
RL Biochem. J. 276:699-707(1991).
FT NON TER 1
SQ SEQUENCE 18 AA; 1993 MW; 8861C9A93B5A5BA CRC64;

Query Match 29.5%; Score 23; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 7.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10
DB 3 DDDYS 8

RESULT 22
ID Q90514_9HIV1 PRELIMINARY; PRT; 19 AA.
AC Q90514;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).

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OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/088922202753394745;
RA Taniguchi Y., Takehisa J., Bikanoud B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengui, W'Pandi M., W'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H. Joseph.;
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo.";
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL, AF410443; AAL10238.1; -, Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 19 AA; 2151 MW; 2A91C2A4D1167636 CRC64;

Query Match 29.5%; Score 23; DB 2; Length 19;
Best Local Similarity 45.5%; Pred. No. 8e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 4 RDNDYSKNPM 14
DB 11 KDH----KNPV 17

RESULT 23
ID Q4XKU0_PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XKU0;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC400052.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Plorens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Duggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC CCUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL, CAJ01005037; CAH82472.1; -, Genomic_DNA.
KM Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2393 MW; 122DCDB7D1F44AB CRC64;

Query Match 29.5%; Score 23; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 8.4e+03;
Matches 6; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

QY 2 IKRDHN--DYSKNPM 14
DB 5 IKKNMISKYTYNKM 19

RESULT 24
ID Q6V0Z6_MUSSP PRELIMINARY; PRT; 20 AA.
AC Q6V0Z6;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)

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DT 05-JUL-2004 (TREMBlrel. 27, Last annotation update)
DE Glutathione S-transferase omega 1 (Fragment).
GN Name=Gstol;
OS Mus spretus (Western wild mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxId=10096;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Abail N., Ruiz-Laguna J., Pueyo C.;
RA Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY355156; AA055841.1; -; mRNA.
DR GO; GO:0016740; P:transferase activity; IEA.
KM Transferase.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2415 MW; E950E936504895E0 CRC64;

Query Match 29.5%; Score 23; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 8.4e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 YSKNPM 14
DB 13 PEKNPL 18

RESULT 25
Q7YXK4 CAEBL PRELIMINARY; PRT; 18 AA.
ID Q7YXK4 CAEBL PRELIMINARY;
AC Q7YXK4;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Neuropeptide-like protein protein 16, Isoform b.
GN Name=nlp-16; ORFNames=TL3A10.5;
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditodea;
OC Neuropeptide; Peptide; Caenorhabditis.
OX NCBI_TaxId=6239;
RN [1]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE GENOMIC DNA].
RC STRAIN=Bristol N2; PubMed=9851916;
RX MEDLINE=98063613; PubMed=9851916;
RG The C. elegans sequencing consortium;
RT "Genome sequence of the nematode C. elegans: a platform for
RT investigating biology."
RL Science 282:2012-2018(1998).
DR EMBL; U56963; AA001524.1; -; Genomic DNA.
DR EMBL; TL3A10.5; Caenorhabditis elegans.
DR WormBase; WBGene0003754; TL3A10.5.
DR WormPep; TL3A10.5b; CB35009.
DR GO; GO:0007218; P:neuropeptide signaling pathway; IEA.
KM Complete proteome; Neuropeptide.
SQ SEQUENCE 18 AA; 2047 MW; A1176979A6CF773 CRC64;

Query Match 28.8%; Score 22.5; DB 2; Length 18;
Best Local Similarity 35.7%; Pred. No. 9.2e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 1; Gaps 1;

QY 1 SIKRDH-NDYSKNP 13
DB 3 SPSPDHDSHNSP 16

RESULT 26
Q90SG4 9HIV1 PRELIMINARY; PRT; 19 AA.
ID Q90SG4 9HIV1 PRELIMINARY;
AC Q90SG4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)

DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxId=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=2163216; PubMed=11804559; DOI=10.1089/08892202753394745;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengyi, M'Pandi M., M'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.;
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo."
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL; AF410448; AL010258.1; -; Genomic DNA.
KM AIDS Res. Hum. Retroviruses 18:79-83(2002).
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2263 MW; 3E5E64FD66039636 CRC64;

Query Match 28.8%; Score 22.5; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 9.8e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 4 RDHNDYSKNPM 14
DB 8 KSHQDH-QNPV 17

RESULT 27
Q90RG9 9HIV1 PRELIMINARY; PRT; 19 AA.
ID Q90RG9 9HIV1 PRELIMINARY;
AC Q90RG9;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxId=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=96C921;
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08892202753394745;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengyi, M'Pandi M., M'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H.Joseph.;
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT Republic of Congo."
RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL; AF127547; AA04904.1; -; Genomic DNA.
DR FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2281 MW; 367E766D66068236 CRC64;

Query Match 28.8%; Score 22.5; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 9.8e+03;
Matches 4; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 4 RDHNDYSKNPM 14
DB 8 KSHQDH-QNPV 17

RESULT 28
Q90NM9 HUMAN PRELIMINARY; PRT; 14 AA.
ID Q90NM9 HUMAN PRELIMINARY;
AC Q90NM9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)


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DE RING3 protein (Fragment).
GN Name=RING3;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Keddache M., Zhang F., Greenberg D.A.
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Keddache M.
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
FT NON_TER 1
SQ SEQUENCE 14 AA; 1677 MW; 5CDP036680AE22D3 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 8.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 DHNDYSKQPM 14
DB 1 DYHKLKQPM 10

RESULT 29
O9R4Z5_STRSU PRELIMINARY; PRT; 16 AA.
AC O9R4Z5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE SULIYSIN (Fragment).
OS Streptococcus suis.
CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
CC Streptococcus.
OX NCBI_TaxID=1307;
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=94222539; PubMed=8168935;
RA Jacobs A.A., Loeffen P.U., van den Berg A.J., Storm P.K.;
RT "Identification, purification, and characterization of a chlo-
RL infect. Immun. 63:1742-1748(1994).
SO SEQUENCE 16 AA; 1979 MW; 73C2EDD825AB3850 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 9.9e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 3 KRDNHDY 9
DB 3 KQDINQY 9

RESULT 30
O5DJ22_SOLSO PRELIMINARY; PRT; 16 AA.
AC O5DJ22;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Amylase 281 (Amylase 282) (Fragment).
GN Name=amy281; Synonym=amy282;
OS Soles solea (Common sole).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Pleuronectiformes;
OC Soleidae; Soleidae; Soles.

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OX NCBI_TaxID=90069;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Rolland J.-L., Bonhomme F.;
RT "Novel polymorphic exon-primed intron-crossing markers from common
RT sole (Solea solea)".
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY748905; AAX14322.1; -; Genomic DNA.
DR EMBL; AY748907; AAX14324.1; -; Genomic DNA.
DR EMBL; AY748908; AAX14325.1; -; Genomic DNA.
DR EMBL; AY748909; AAX14326.1; -; Genomic DNA.
DR EMBL; AY748910; AAX14327.1; -; Genomic DNA.
DR EMBL; AY748904; AAX14321.1; -; Genomic DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1947 MW; F3E137ABD5E71C16 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 9.9e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 4 RDNDY 9
DB 9 KDQNDW 14

RESULT 31
BMTID_BOOMI STANDARD; PRT; 17 AA.
AC P83607;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Kunitz-type serine protease inhibitor Bmti-D (Fragment).
OS Boophilus microplus (Cattle tick).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.
OX NCBI_TaxID=6941;
RN [1]
RP PROTEIN SEQUENCE, AND FUNCTION.
RC TISSUE=Larva;
RX PubMed=15556274; DOI=10.1016/j.biochi.2004.09.010;
RA Sasaki S.D., Azcolini S.S., Hirata I.Y., Andreotti R., Tanaka A.S.;
RT "Boophilus microplus tick larvae, a rich source of kunitz type serine
RL Biochimie 86:643-649(2004).
CC -!- FUNCTION: Inhibits bovine trypsin and human plasma kallikrein, but
CC not human neutrophil elastase.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- SIMILARITY: Contains 1 BPT/Kunitz inhibitor domain.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR InterPro; IPR02223; Prot_inh_Kunz-m.
DR PROSITE; PS00280; BPTI_KUNITZ_1; PARTIAL.
DR PROSITE; PS50279; BPTI_KUNITZ_2; PARTIAL.
KM Direct protein sequencing; Protease inhibitor;
KW Serine protease inhibitor.
FT SITE 17
FT NON_TER 17
SQ SEQUENCE 17 AA; 1649 MW; 7A151C71899F44BBB CRC64;

Query Match 28.2%; Score 22; DB 1; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 8 DYSNKP 13
DB 3 DFKVP 8

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RESULT 32
O34216_98PHN
ID O34216_98PHN PRELIMINARY; PRT; 17 AA.
AC O34216;
DT 01-JAN-1998 (TREMBlrel. 05, Created)
DT 01-JAN-1998 (TREMBlrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE 2-hydroxymuconic semialdehyde dehydrogenase (Fragment).
GN Name=phng;
OS Sphingomonas chungbokensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxID=561993;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DJ77;
RX MEDLINE=97445124; PubMed=9299451; DOI=10.1006/brc.1997.6959;
RA Kim S., Kwon O.K., Kim Y., Kim C.K., Lee K.S., Kim Y.C.;
RT "Localization and sequence analysis of the phnH gene encoding 2-
hydroxy-pent-2,4-dienoyl hydratase in Pseudomonas sp. strain DJ77.";
RL Biochem. Biophys. Res. Commun. 238:56-60(1997).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DJ77;
RA Kim Y.-C.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U97697; AAB71650.1; -; Genomic_DNA.
DR GO; GO:0019866; C:inner membrane; IEA.
DR GO; GO:0005355; F:glucose transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPRO00803; Gluc transporter.
DR PRINTS; PR00172; GLUCTRNSPORT.
FT NON_TER 1
SQ SEQUENCE 17 AA; 2203 MW; 4E913B3E1212214B CRC64;
Query Match 28.2%; Score 22; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 1.1e+04;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDHNDYK 11
Db 4 LHRDHQHLRK 13

RESULT 33
O4XK28_PLACH
ID O4XK28_PLACH PRELIMINARY; PRT; 18 AA.
AC O4XK28;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC400359.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karra M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Jansen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Jaiswal S.L., Rajandream M.A., Carucci D.J., Yates J.R., Katatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
preliminary data.
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
EMBL; CAJ01005284; CAH82734.1; -; Genomic_DNA.

KM Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2322 MW; DC5241E9253A3411 CRC64;
Query Match 28.2%; Score 22; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.1e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 KRDHNDYK 11
Db 3 KRDHNDYK 11

RESULT 34
O64134_9MURI
ID O64134_9MURI PRELIMINARY; PRT; 18 AA.
AC O64134;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Cyclic adenosine 3',5'-monophosphate response element-binding protein
CRBB (Fragment).
GN Name=CRBB;
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=92110991; PubMed=1723142;
RA Weber G., Meyer T.E., Lesieur M., Hermann H.L., Gerard N.,
RA Habener J.F.;
RT "Developmental stage-specific expression of cyclic adenosine 3',5'-
monophosphate response element-binding protein CRBB during
spermatogenesis involves alternative exon splicing.";
RL Mol. Endocrinol. 5:1418-1430(1991).
DR EMBL; S78641; AAB21253.2; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2058 MW; 00840D65B42ECD6F CRC64;
Query Match 28.2%; Score 22; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 2 IKRDHNDY 9
Db 5 VKQDVSDP 12

RESULT 35
O6DU04_RAT
ID O6DU04_RAT PRELIMINARY; PRT; 18 AA.
AC O6DU04;
DT 25-OCT-2004 (TREMBlrel. 28, Created)
DT 25-OCT-2004 (TREMBlrel. 28, Last sequence update)
DT 25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Glial glutamate transporter GLT1/V4 (Fragment).
GN Name=SLC1A2;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley;
RA Rozyczka J., Engle J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY643517; AAT66430.1; -; mRNA.
FT NON_TER 18
SQ SEQUENCE 18 AA; 2153 MW; CADCA20790427F3 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 SIKDDHNDYSK 11
||:|:
8 SIORSANNMPK 18

RESULT 36
Q4XG8 PLACH

ID Q4XG8 PLACH PRELIMINARY; PRT; 19 AA.

AC Q4XG8;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

GN ORFNames=PC401844.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

OX NCBI_TaxID=5625;

RN [1]

RA Nucleotide sequence.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

transcriptomic, and proteomic analyses."

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAJ01006479; CAH84060.1; -; Genomic_DNA.

KM Hypothetical protein.

FT NON TER 1

SO SEQUENCE 19 AA; 2381 MW; 63D14AB1EC9293B7 CRC64;

QY 6 HNDY 9
||:|:
11 HNNY 14

Db

Query Match 28.2%; Score 22; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 37
Q7JNH9 DROME

ID Q7JNH9 DROME PRELIMINARY; PRT; 20 AA.

AC Q7JNH9;

DT 05-JUN-2004 (TREMBlrel. 27, Created)

DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)

DE Peptide: Glycine-alpha-hydroxylating monooxygenase (Fragment).

GN Name=dPM;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Preygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI_TaxID=7227;

RN [1]

RA Nucleotide sequence.

RX MEDLINE=97160645; PubMed=9006979;

RA Elpiper B.A., Taghert P.H.,

RT "Neuropeptide amidation in Drosophila: separate genes encode the two

RT enzymes catalyzing amidation."

RL J. Neurosci. 17:1363-1376(1997).

DR EMBL; U77431; AAB52571.1; -; Genomic DNA.

GO; GO:0004497; P:monooxygenase activity; IEA.

KW Monooxygenase.
FT NON TER 1
SQ SEQUENCE 20 AA; 2257 MW; 9D1796B8C7E2C68A CRC64;

Query Match 28.2%; Score 22; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 DYKSNP 13
||:|:
11 DYTEEP 16

RESULT 38
Q4Y3Y1 PLACH

ID Q4Y3Y1 PLACH PRELIMINARY; PRT; 20 AA.

AC Q4Y3Y1;

DT 13-SEP-2005 (TREMBlrel. 31, Created)

DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)

DE Hypothetical protein (Fragment).

GN ORFNames=PC102140.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.

OX NCBI_TaxID=5625;

RN [1]

RA Nucleotide sequence.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

transcriptomic, and proteomic analyses."

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

DR EMBL; CAJ01001233; CAH76129.1; -; Genomic_DNA.

KM Hypothetical protein.

FT NON TER 1

SO SEQUENCE 20 AA; 2391 MW; 22256D25639FBD57 CRC64;

QY 6 HNDY 9
||:|:
2 HNNY 5

Db

Query Match 28.2%; Score 22; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 39
Q9PS15 ONCKI

ID Q9PS15 ONCKI PRELIMINARY; PRT; 20 AA.

AC Q9PS15;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DE Creatine kinase (EC 2.7.3.2) (Fragment).

OS Oncorhynchus kisutch (Coho salmon).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;

OC Proteanopterygii; Salmoniformes; Salmonidae; Oncorhynchus.

OX NCBI_TaxID=8013;

RN [1]

RA Nucleotide sequence.

RX MEDLINE=93080727; PubMed=1449598;

RA White K.C., Babbitt P.C., Buechter D.D., Kenyon G.L.,

RT "The principal islet of the Coho salmon (Oncorhynchus kisutch) contains

the BB isoenzyme of creatine kinase."

RL J. Protein Chem. 11:489-494(1992).
 DR PIR; A53875; A53875.
 DR GO; GO:0004111; F:creatine kinase activity; IRA.
 SQ SEQUENCE 20 AA; 2425 MW; BFB71D6D2A86E11 CRC64;

Query Match 28.2%; Score 22; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HNDYSKN 12
 DB 6 HNNFKLN 12

RESULT 40

QANSW7 THEPA PRELIMINARY; PRT; 19 AA.
 ID QANSW7
 AC QANSW7
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=FP02_0175;
 OS Theileria parva.
 OC Eukaryota; Alveolata; Apicomplexa; Piroplasmida; Theileridae;
 OC Theileria.
 OC NCBI_TaxId=5875;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;
 RA Gardner M.J., Bishop R., Shah T., de Villiers E.P., Carlton J.M.,
 RA Hall N., Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M.,
 RA Sato S., Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J.,
 RA Jiang L., Lynn J., Weaver B., Shoabdi A., Wasawo D., Crabtree J.,
 RA Wortman J.R., Haas B., Angiuoli S.V., Creasy T.H., Lu C., Suh B.,
 RA Silva J.C., Utecherback T.R., Feldblum T.V., Perlea M., Allen J.,
 RA Venter J.C., Fraser C.M., Nene V.;
 RT "Genome sequence of Theileria parva, a bovine pathogen that transforms
 lymphocytes.";
 RL Science 309:134-137(2005).
 RU [2]
 RN [2]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Muguga;
 RA Ren Q., Paulsen I.T., Pain A., Berriman M., Wilson R.J.M., Sato S.,
 RA Ralph S.A., Mann D.J., Xiong Z., Shallom S.J., Weidman J., Jiang L.,
 RA Lynn J., Weaver B., Shoabdi A., Wasawo D., Crabtree J., Wortman J.R.,
 RA Haas B., Angiuoli S., Creasy T.H., Lu C., Suh B., Silva J.C.,
 RA Utecherback T., Feldblum T., Perlea M., Allen J., Taracha B.L.,
 RA Salzberg S.L., White O., Fitzhugh H.A., Morzaria S., Venter J.C.,
 RA Fraser C.M., Nene V.;
 RL Submitted (JUN-2005) to the EMBL/GenBank/DBJ databases.
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AAGK0100002; EMBL32456.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 19 AA; 2310 MW; F72C572A54B8EFC CRC64;

Query Match 27.6%; Score 21.5; DB 2; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.5e+04;
 Matches 5; Conservative 3; Mismatches 4; Indels 3; Gaps 1;

QY 3 KRDH---NDYSKNPM 14
 DB 5 RRKHYKSTKYSSDPV 19

RESULT 41
 Q905G8 9HIV1 PRELIMINARY; PRT; 19 AA.
 ID Q905G8 9HIV1
 AC Q905G8;

DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Tat protein (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OC NCBI_TaxId=11676;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/0889220275394745;
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
 RA Ido B., Hayami M., Ichimura H., Parra H.Joseph.;
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
 RT Republic of Congo.";
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
 DR EMBL; AF410447; AL10254.1; -; Genomic_DNA.
 FT NON TER 1 1
 FT NON TER 19 19

SQ SEQUENCE 19 AA; 2366 MW; 367E64E194069237 CRC64;
 Query Match 27.6%; Score 21.5; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 1.5e+04;
 Matches 4; Conservative 4; Mismatches 2; Indels 1; Gaps 1;

QY 4 RDHNDYSKNPM 14
 DB 8 QSHQDH-QNPV 17

RESULT 42

ID Q905J6 9HIV1 PRELIMINARY; PRT; 19 AA.
 AC Q905J6;
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Tat protein (Fragment).
 OS Human immunodeficiency virus 1.
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OC NCBI_TaxId=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/0889220275394745;
 RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
 RA N'Doundou-N'Kodia M.-Y., Obengui, M'Pandi M., M'Pele P., Harada Y.,
 RA Ido B., Hayami M., Ichimura H., Parra H.Joseph.;
 RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
 RT Republic of Congo.";
 RL AIDS Res. Hum. Retroviruses 18:79-83(2002).
 DR EMBL; AF410440; AL10226.1; -; Genomic_DNA.
 FT NON TER 1 1
 FT NON TER 19 19

SQ SEQUENCE 19 AA; 2391 MW; 3E5E7ED9D0038637 CRC64;
 Query Match 27.6%; Score 21.5; DB 2; Length 19;
 Best Local Similarity 40.0%; Pred. No. 1.5e+04;
 Matches 4; Conservative 4; Mismatches 1; Indels 1; Gaps 1;

QY 5 DHNDYSKNPM 14
 DB 9 NHQDH-QNPV 17

RESULT 43
 Q7M0L3 BACCI PRELIMINARY; PRT; 11 AA.
 ID Q7M0L3 BACCI
 AC Q7M0L3;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)

DE Cyclooligoglucosaccharide fructanotransferase (EC 2.4.-.-)
 (Fragment).
 OS Bacillus circulans.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 OX NCBI_TaxID=1397;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95201377; PubMed=7765973;
 RA Kusube S., Mitui K., Yamagishi M., Yamada K., Morimoto Y.,
 RT "Purification and characterization of cyclooligoglucosaccharide
 fructanotransferase (CPTase) from *Bacillus circulans* MCI-2554,"
 RL Biosci. Biotechnol. Biochem. 59:31-34(1995).
 DR PIR; PC2330; PC2330.
 RT NON_TER 1 1
 FT NON_TER 11 11
 SQ SEQUENCE 11 AA; 1398 MW; D841E119466CB59 CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 9.8e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 Oy 6 HNDYSKNP 13
 Db 2 HLPYQNP 9

RESULT 44
 Q4XW72_PLACH PRELIMINARY; PRT; 12 AA.
 AC Q4XW72;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS ORName=PC105378.00.0;
 OS Plasmodium chabaudi.
 OS Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karra M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses,"
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01002684; CAH78839.1; -; Genomic_DNA.
 KM Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1376 MW; 5099241BB0441E3 CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 SIKRDHN 7
 Db 1 SASRKN 7

RESULT 45
 Q4YETS_PLABE PRELIMINARY; PRT; 12 AA.
 AC Q4YETS;
 DT 13-SEP-2005 (TREMBlrel. 31, Created)
 DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
 DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).
 OS ORName=PB405057.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 OX NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karra M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses,"
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01005850; CAI03484.1; -; Genomic_DNA.
 KM Hypothetical protein.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1468 MW; 9A7C7B45DB5B0B5A CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 Oy 6 HNDY 9
 Db 3 YNDY 6

RESULT 46
 Q9QCK3_BDV PRELIMINARY; PRT; 13 AA.
 AC Q9QCK3;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)
 DE P40 ORF (Fragment).
 OS Borna disease virus (BDV).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
 OC Bornavirus.
 OX NCBI_TaxID=12455;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99445641; PubMed=10515835; DOI=10.1096/315068;
 RA Cryan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
 RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
 RA Maillach B., Staeheli P., Hufert F.T., Lieb K.,
 RT "Borna disease virus in human brains with a rare form of hippocampal
 RT degeneration but not in brains of patients with common
 RT neuropsychiatric disorders,"
 RL J. Infect. Dis. 180:1695-1699(1999).
 DR EMBL; AJ246865; CAB52108.1; -; Genomic_RNA.
 FT NON_TER 1 1
 SQ SEQUENCE 13 AA; 1620 MW; 8F80680E4021A40A CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1.2e+04;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 KRDNYSK 11
 Db 4 ENDRCDSK 12

RESULT 47
 Q9QCK6_BDV PRELIMINARY; PRT; 13 AA.
 AC Q9QCK6;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2001 (TREMBlrel. 16, Last annotation update)

DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Cysgan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Meilahn E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychiatric disorders.";
RT J. Infect. Dis. 180:1695-1699(1999).
DR EMBL; AJ246864; CAB52105.1; -; Genomic_RNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 KRPHNDYSK 11
DB 4 ENDRCDWSK 12

RESULT 48
ID Q9QCK9_BDV PRELIMINARY; PRT; 13 AA.
AC Q9QCK9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Cysgan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Meilahn E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychiatric disorders.";
RT J. Infect. Dis. 180:1695-1699(1999).
DR EMBL; AJ246863; CAB52102.1; -; Genomic_RNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 KRPHNDYSK 11
DB 4 ENDRCDWSK 12

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Cysgan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Meilahn E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychiatric disorders.";
RT J. Infect. Dis. 180:1695-1699(1999).
DR EMBL; AJ246862; CAB52099.1; -; Genomic_RNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 KRPHNDYSK 11
DB 4 ENDRCDWSK 12

RESULT 50
ID Q9QCL5_BDV PRELIMINARY; PRT; 13 AA.
AC Q9QCL5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBlrel. 16, Last annotation update)
DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Cysgan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Meilahn E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychiatric disorders.";
RT J. Infect. Dis. 180:1695-1699(1999).
DR EMBL; AJ246861; CAB52096.1; -; Genomic_RNA.
FT NON_TER 1
FT NON_TER 13
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

CY 3 KRPHNDYSK 11
DB 4 ENDRCDWSK 12

RESULT 51
ID Q9QCL8_BDV PRELIMINARY; PRT; 13 AA.
AC Q9QCL8;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Czygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Maillan E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychoiatric disorders."
RL J. Infect. Dis. 180:1695-1699(1999).
DR EMBL/ AJ246860; CAB52093.1; -; Genomic_RNA.
FT NON_TER 1 13
FT NON_TER 1 13
SQ SEQUENCE 13 AA; 1673 MW; 8F80680B534A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 52
ID 090CM1_BDV PRELIMINARY; PRT; 13 AA.
AC 090CM1;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Czygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Maillan E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychoiatric disorders."
RL J. Infect. Dis. 180:1695-1699(1999).
DR EMBL/ AJ246859; CAB52090.1; -; Genomic_RNA.
FT NON_TER 1 13
FT NON_TER 1 13
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 53
ID 090CM4_BDV PRELIMINARY; PRT; 13 AA.
AC 090CM4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)

DE P40 ORF (Fragment).
OS Borna disease virus (BDV).
OC Viruses; ssRNA negative-strand viruses; Mononegavirales; Bornaviridae;
OC Bornavirus.
OX NCBI_TaxID=12455;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99445641; PubMed=10515835; DOI=10.1086/315068;
RA Czygan M., Hallensleben W., Hofer M., Pollak S., Sauder C., Bilzer T.,
RA Blumcke I., Riederer P., Bogerts B., Falkai P., Schwarz M.J.,
RA Maillan E., Staeheli P., Hufert F.T., Lieb K.;
RT "Borna disease virus in human brains with a rare form of hippocampal
degeneration but not in brains of patients with common
neuropsychoiatric disorders."
RL J. Infect. Dis. 180:1695-1699(1999).
DR EMBL/ AJ246858; CAB52087.1; -; Genomic_RNA.
FT NON_TER 1 13
FT NON_TER 1 13
SQ SEQUENCE 13 AA; 1620 MW; 8F80680B4021A40A CRC64;

Query Match 26.9%; Score 21; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

RESULT 54
ID 069200_HUMAN PRELIMINARY; PRT; 14 AA.
AC 069200;
DT 25-OCT-2004 (Tremblrel. 28, Created)
DT 25-OCT-2004 (Tremblrel. 28, Last sequence update)
DT 25-OCT-2004 (Tremblrel. 28, Last annotation update)
DE Hypothetical protein DKFZP564G2272 (Fragment).
GN Name=DKFZP564G2272;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RG TISSUE=Brain;
RC The German cDNA Consortium;
RA Blum H., Bauersachs S., Mewes H.W., Weill B., Amid C., Oanger A.,
RA Fodor G., Han M., Wiemann S.,
RL Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL/ AL080100; CAH10728.1; -; mRNA.
KW Hypothetical protein.
FT NON_TER 1 1
FT NON_TER 1 1
SQ SEQUENCE 14 AA; 1596 MW; 737A4A679F6E1B CRC64;

Query Match 26.9%; Score 21; DB 2; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.3e+04;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

RESULT 55
ID 09TWX8_MANSE PRELIMINARY; PRT; 14 AA.
AC 09TWX8;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Juvenile hormone binding protein, JHBP=5.3 kDa Lys-C peptide
(Fragment).

OS Manduca sexta (Tobacco hawkmoth) (Tobacco hornworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Sphingioidea;
 OC Sphingidae; Sphinginae; Manduca.
 ON NCBI_TaxID=7130;
 RX MEDLINE=92078218; PubMed=1744133;
 RA Pak P.W., Roberts D.D., Groso L.E., Parks W.C., Rosenbloom J.,
 RT "Binding of elastin to *Staphylococcus aureus*.";
 RL J. Biol. Chem. 265:23399-23406(1991).
 DR PIR; A41589; A41589.1
 FT NON_TER 1
 FT TER 14
 SQ SEQUENCE 14 AA; 1754 MW; 96CA358699D1C6A CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 7 NDYSKN 12
 DB 6 DDFEKN 11

QY 8 DYSKNPM 14
 DB 1 DYENHPV 7

RESULT 56
 ID 054394_STRLI PRELIMINARY; PRT; 14 AA.
 AC 054394;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DE 01-NOV-1996 (TREMBlrel. 25, Last annotation update)
 DE S-adenosyl-L-homocysteine hydrolase (Fragment).
 OS Streptomyces lividans
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Streptomycetaceae; Streptomycetaceae; Streptomycetes.
 ON NCBI_TaxID=1916;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=TK21;
 RA Romero N.M., Mellado R.P.;
 RT "Activation of the actinophodol biosynthetic pathway in *Streptomyces lividans*.";
 RL FEMS Microbiol. Lett. 121:79-84(1995).
 DR EMBL; X79814; CA56211.1; -; Genomic DNA.
 DR GO; GO:0004013; F:adenosylhomocysteinease activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 DR GO; GO:0006730; P:one-carbon compound metabolism; IEA.
 DR InterPro; IPR000043; Ad_hcy_hydrolase.
 DR Pfam; PF05221; AdhCysase; 1.
 KM Hydrolase.
 FT NON_TER 1
 FT TER 14
 SQ SEQUENCE 14 AA; 1725 MW; 1303D5023C485D2B CRC64;

Query Match 26.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 1.3e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 3 KRBHNDY 9
 DB 8 KADHYRY 14

RESULT 57
 ID 09R5R5_STAUP PRELIMINARY; PRT; 14 AA.
 AC 09R5R5;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE 25-kDa elastin-binding protein (Fragment).
 OS *Staphylococcus aureus*.
 OC Bacteria; Firmicutes; Bacillales; Staphylococcus.

OX NCBI_TaxID=1280;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92078218; PubMed=1744133;
 RA Pak P.W., Roberts D.D., Groso L.E., Parks W.C., Rosenbloom J.,
 RT "Binding of elastin to *Staphylococcus aureus*.";
 RL J. Biol. Chem. 265:23399-23406(1991).
 DR PIR; A41589; A41589.1
 FT NON_TER 1
 FT TER 14
 SQ SEQUENCE 14 AA; 1754 MW; 96CA358699D1C6A CRC64;
 Query Match 26.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 7 NDYSKN 12
 DB 6 DDFEKN 11

RESULT 58
 ID MK1_PALPR STANDARD; PRT; 15 AA.
 AC P80408;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Metanikowin I.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Heteroptera;
 OC Pentatomidae; Pentatomomorpha; Pentatomidae; Pentatomidae;
 ON NCBI_TaxID=55431;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Cherrysh S., Cociancich S., Briand J.-P., Hetru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect *Palomena prasina*: identification of a unique family of proline-rich peptides and of a novel insect defensin.";
 RL J. Insect Physiol. 42:81-89(1996)
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC CC
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 CC CC
 CC Antiliotic; Antimicrobial; Direct protein sequencing; Immune response;
 KM Innate immunity.
 KM Innate immunity.
 SQ SEQUENCE 15 AA; 1838 MW; 21407B663CE46299 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 15;
 Best Local Similarity 44.4%; Pred. No. 1.4e+04;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5 DHNDYSKNP 13
 DB 2 DKPDYRPRP 10

RESULT 59
 ID MK2A_PALPR STANDARD; PRT; 15 AA.
 AC P80409;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Metalkowin IIA.
 OS Palomona praeina (Green shield bug).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 CC Panheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
 CC Pentatominae; Palomona.
 CC NCBI_TaxID=55431;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Hemolymph.
 RA Chertys S., Coclanich S., Briand J.-P., Hecru C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 Palomona praeina: identification of a unique family of proline-rich
 peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC -----
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 CC removed.
 CC -----
 CC Antibiotic; Antimicrobial; Direct protein sequencing; Immune response;
 KW Innate immunity.
 KW SEQUENCE 15 AA; 1893 MW; 23835D063B946299 CRC64;
 SQ
 Query Match 26.9%; Score 21; DB 1; Length 15;
 Best Local Similarity 44.4%; Pred. No. 1.4e+04;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 5 DHNDYSKNP 13
 Db 2 DKPDYRPRP 10
 RESULT 60
 TX12B_BUNCA STANDARD; PRT; 15 AA.
 AC P84473;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Neurotoxin T1-2 B chain (Fragment).
 OS Bungarus candidus (Malayan krait).
 CC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 CC Lepidodermata; Squamata; Scleroglossa; Serpentes; Colubroidae;
 CC Elapidae; Bungarinae; Bungarus.
 CC NCBI_TaxID=92438;
 RN [1]
 RP PROTEIN SEQUENCE, FUNCTION, SUBUNIT, SUBCELLULAR LOCATION, TISSUE
 RP SPECIFICITY, AND LETHAL DOSE.
 RC TISSUE=Venom.
 RX PubMed=14769667; DOI=10.1093/jb/mwg187;
 RA Know O., Chahome T., Omori-Satch T., Ogawa Y., Yanoshita R.,
 RA Samejima Y., Kuch U., Mobs D., Sitprija V.;
 RT "Isolation, toxicity and amino terminal sequences of three major
 RT neurotoxins in the venom of Malayan krait (Bungarus candidus) from
 RT Thailand."
 RL J. Biochem. 134:799-804(2003).
 CC -1- FUNCTION: Neurotoxin T1-2 is a presynaptic neurotoxin of the venom
 CC that exhibits indirect hemolytic activity against human
 CC erythrocytes. The B chain is homologous to venom basic protease
 CC inhibitors but has no protease inhibitor activity and is non-
 CC toxic.
 CC -1- SUBUNIT: Heterodimer; disulfide-linked. The A chains have
 CC phospholipase A2 activity and the B chains show homology with the
 CC basic protease inhibitors.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.

CC -1- TOXIC DOSE: LD(50) is 0.22 mg/kg by intravenous injection in mice.
 CC -1- SIMILARITY: Contains 1 BPPI/Kunitz inhibitor domain.
 CC -----
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 CC removed.
 CC -----
 CC InterPro; IPR002223; Prot_inh_Kunitz-m.
 DR PROSITE; PS00280; BPPI_KUNITZ_1; PARTIAL.
 DR PROSITE; PS0279; BPPI_KUNITZ_2; PARTIAL.
 KW Direct protein sequencing; Neurotoxin; Presynaptic neurotoxin; Toxin.
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1736 MW; 829370B198A971A0 CRC64;
 Query Match 26.9%; Score 21; DB 1; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.4e+04;
 Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 QY 3 KRHDYSKNP 13
 Db 1 RQRHPDCKRP 11
 RESULT 61
 UP02_METAN STANDARD; PRT; 15 AA.
 ID UP02_METAN
 AC P83439;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Unknown 70 kDa protein (Fragment).
 OS Metarhizium anisopliae.
 CC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 CC Hypocreomycetidae; Hypocreales; Clavicipitaceae;
 CC mitosporic Clavicipitaceae; Metarhizium.
 CC NCBI_TaxID=5530;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC STRAIN=54A-1b;
 RX MEDLINE=2234306; PubMed=12455610; DOI=10.1139/w02-074;
 RA Kamp A.M., Bidochka M.J.;
 RT "Protein analysis in a pleomorphically deteriorated strain of the
 RT insect-pathogenic fungus Metarhizium anisopliae."
 RL Can. J. Microbiol. 48:787-792(2002).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined MW of this unknown
 CC protein is: 70 kDa.
 CC -----
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 CC -----
 CC Direct protein sequencing.
 KW NON_TER 15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1483 MW; 2BD474FD7C6BB153 CRC64;
 Query Match 26.9%; Score 21; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.4e+04;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 7 NDYSKNP 13
 Db 9 NDLSPPP 15
 RESULT 62
 G9UC17_HUMAN PRELIMINARY; PRT; 15 AA.
 ID G9UC17_HUMAN
 AC G9UC17
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE 38 kDa MYELOPEROXIDASE (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93094240; PubMed=1334087;
 RA Taylor K.L., Pohl J., Kinkade J.M.Jr.;
 RT "Unique autocatalytic cleavage of human myeloperoxidase. Implications for
 the involvement of active site MET409".
 RL J. Biol. Chem. 267:25282-25288(1992).
 DR GO:0004601; P:peroxidase activity; IEA.
 DR InterPro: IPR02007; AnIm_peroxidase.
 DR PROSITE: PS50292; PEROXIDASE_3; 1.
 SQ SEQUENCE 15 AA; 1791 MW; 8B76949BD0E7321 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDHN 7
 DB 12 REHN 15

RESULT 63
 ID 07M0G8_9MURI PRELIMINARY; PRT; 15 AA.
 AC 07M0G8_9MURI
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE CD33 antigen homolog (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10095;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=94298870; PubMed=8026526;
 RA Chies J.A., Lembezat M.P., Freitas A.A.;
 RT "Entry of B lymphocytes into the persistent cell pool in non-immunized
 mice is not accompanied by somatic mutation of VH genes."
 RL Eur. J. Immunol. 24:1657-1664(1994).
 DR PIR: I67525; I67525.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1823 MW; 1C9A91068FP27916 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KRDH 6
 DB 4 RRDH 7

RESULT 64
 ID 09PKC5_TEV PRELIMINARY; PRT; 15 AA.
 AC 09PKC5_TEV
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Small nuclear inclusion polypeptide cleavage product.
 OS Tobacco etch virus (TEV).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;

OC Potyvirus.
 OC NCBI_TaxID=12227;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=91306428; PubMed=1853555;
 RA Dougherty W.G., Parks T.D.;
 RT "Post-translational processing of the tobacco etch virus 49-kDa small
 RT nuclear inclusion polypeptide: identification of an internal cleavage
 RT site and delimitation of VPg and proteinase domains."
 RL Virology 183:449-456(1991).
 SQ SEQUENCE 15 AA; 1680 MW; 2273B6E461D0F28C CRC64;

Query Match 26.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.4e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 RDHNDYS 10
 DB 9 RDYNPIS 15

RESULT 65
 ID MK2B_PALPR STANDARD; PRT; 16 AA.
 AC P80410;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Metainikowin IIB.
 OS Palomena prasina (Green shield bug).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
 OC Pentheteroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
 OC Pentatominae; Palomena.
 NCBI_TaxID=55431;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Hemolymph;
 RA Cherrysh S., Cociancich S., Briand J.-P., Hetrin C., Bulet P.;
 RT "The inducible antibacterial peptides of the hemipteran insect
 RT Palomena prasina: identification of a unique family of proline-rich
 RT peptides and of a novel insect defensin."
 RL J. Insect Physiol. 42:81-89(1996).
 CC -1- FUNCTION: Antibacterial peptide active against Gram-negative
 CC bacteria.
 CC -1- INDUCTION: By bacterial infection.
 CC -----
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 CC -----
 CC Antibiotic; Antimicrobial; Direct protein sequencing; Immune response;
 CC Innate immunity.
 KW Innate immunity.
 SQ SEQUENCE 16 AA; 2040 MW; AF21407D063B9462 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 16;
 Best Local Similarity 44.4%; Pred. No. 1.5e+04;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 DHNDYSKNP 13
 DB 2 DKPDYRPRP 10

RESULT 66
 ID MK3_PALPR STANDARD; PRT; 16 AA.
 AC P80411;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)

```

DE Metchnikow III.
OC Palomene prasinus (Green shield bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pserygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Pantheeroptera; Pentatomomorpha; Pentatomidae; Pentatomidae;
OC Pentatominae; Palomene.
OX NCBI_TaxID=55431;
RN [1];
RP PROTEIN SEQUENCE.
RC TISSUE=Hemolymph;
RA Chernysh S., Coccianich S., Briand J.-P., Hetru C., Bulet P.;
RT "The inducible antibacterial peptides of the hemipteran insect
RT Palomene prasinus: identification of a unique family of proline-rich
RT peptides and of a novel insect defensin."
RL J. Insect Physiol. 42:81-89(1996).
CC - FUNCTION: Antibacterial peptide active against Gram-negative
CC bacteria.
CC - INDUCTION: By bacterial infection.
CC -----
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CC
CC Antibiotic; Antimicrobial; Direct protein sequencing; Immune response;
CC Innate immunity.
KM SEQUENCE 16 AA; 2024 MW; A9B3835D063B9462 CRC64;
SQ
Query Match 26.9%; Score 21; DB 1; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.5e+04;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 DHNDYKRP 13
Db 2 DKPDYRPRP 10

RESULT 67
Q6LEL3 MOUSE
ID Q6LEL3 MOUSE PRELIMINARY; PRT; 16 AA.
AC Q6LEL3
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE J1 region (Fragment).
GN Name=Igh;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=8019926; PubMed=6769593; DOI=10.1016/0092-8674(80)90089-6;
RA Early P., Huang H., Davis M., Calame K., Hood L.;
RT "An immunoglobulin heavy chain variable region gene is generated from
RT three segments of DNA: VH, D and JH."
RL Cell 19:981-992(1980).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=8101213; PubMed=6774258;
RA Sakano H., Maki R., Kurosawa Y., Roeder W., Tonegawa S.;
RT "Two types of somatic recombination are necessary for the generation
RT of complete immunoglobulin heavy-chain genes."
RL Nature 286:676-683(1980).
RN [3];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=80258493; PubMed=6250219;
RA Newell N., Richards J.E., Tucker P.W., Blattner F.R.;

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RT "J genes for heavy chain immunoglobulins of mouse."
RL Science 209:1128-1132(1980).
RN [4];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=9335830; PubMed=6101208; DOI=10.1016/0092-8674(81)90399-8;
RA Kim S., Davis M., Sim E., Patten P., Hood L.;
RT "Antibody diversity: somatic hypermutation of rearranged VH genes."
RL Cell 27:573-581(1981).
RN [5];
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BALB/c; TISSUE=Myeloma;
RX MEDLINE=81173073; PubMed=6783961;
RA Sakano H., Kurosawa Y., Weigert M., Tonegawa S.;
RT "Identification and nucleotide sequence of a diversity DNA segment (D)
RT of immunoglobulin heavy-chain genes."
RL Nature 290:562-565(1981).
DR EMBL; J00440; AAB59646.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 16
SQ SEQUENCE 16 AA; 1914 MW; 30AFA12F20B5D464 CRC64;

Qy 3 KRDH 6
Db 8 RRDH 11

Query Match 26.9%; Score 21; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 1.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 7 NDYSKN 12
Db 6 DDFEKN 11

RESULT 69
O26062 HELPY
ID O26062 HELPY PRELIMINARY; PRT; 18 AA.
AC O26062
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein HP1536.
GN OrderedLocustNames=HP1536;
OS Helicobacter pylori (Campylobacter pylori).

```

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacterales;
OC Helicobacteraceae; Helicobacter.
OX NCBI_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=2695 / ATCC 700392;
RX MEDLINE=9739467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kariavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klenk H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness E.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.V., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams M.D.,
RA Hickey E.K., Berg D.E., Gocayne J.D., Utterback T.R., Peterson J.D.,
RA Kelley J.M., Cotton M.D., Weidman J.F., Fujii C., Bowman C.,
RA Matthey L., Wallin E., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.,
RA "The complete genome sequence of the gastric pathogen Helicobacter
RT pylori."
RL Nature 388:539-547(1997).
DR EMBL; AEO00651; AAO08578.1; -; Genomic_DNA.
DR PIR; H64711; H64711.
DR TIGR; Hsp1536; -
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 18 AA; 2236 MW; AC0B5A3DFD9CD482 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 7 NDYSKNP 13
DB 9 NHPSRNP 15

RESULT 70
ID Q4X617_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4X617;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=Pc405777.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Kariya M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Truman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.O., Yates J.R., Kallats F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01009496; CH87489.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2278 MW; FA6AC117648FE8A9 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.8e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 IKRDHNDY 9
DB 11 IKQDMARY 18

RESULT 71
ID Q9QW83_RAT PRELIMINARY; PRT; 19 AA.
AC Q9QW83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE PHOSPHORHORN=PERPIDE fragment 12-44 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OX Muridae; Murinae; Rattus.
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91291127; PubMed=2064607;
RA Sabasy B., Stetler-Stevenson W.G., Lechner J.H., Veis A.,
RT "Domain structure and sequence distribution in dentin phosphophoryn."
RL Biochem. J. 276:699-707(1991).
FT NON_TER 1
SQ SEQUENCE 19 AA; 2195 MW; 744603FE729FDE0C CRC64;

Query Match 26.9%; Score 21; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 3; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 6 HNDYSKNP 14
DB 4 HPSYNSNTL 12

RESULT 72
ID Q9QSF6_9H1V1 PRELIMINARY; PRT; 19 AA.
AC Q9QSF6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Tat protein (Fragment).
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21663216; PubMed=11804559; DOI=10.1089/08922202753394745;
RA Taniguchi Y., Takehisa J., Bikandou B., Mboudjeka I.,
RA N'Doundou-N'Kodia M.-Y., Obengul, M'Pandi M., M'Pele P., Harada Y.,
RA Ido E., Hayami M., Ichimura H., Parra H. Joseph.,
RT "Genetic subtypes of HIV type 1 based on the vpu/env sequences in the
RT AIDS Res. Hum. Retroviruses 18:79-83(2002).
DR EMBL; AF410450; AL10266.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2333 MW; 22A23385A9068236 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 4; Conservative 4; Mismatches 0; Indels 4; Gaps 1;

RESULT 73
ID MEFP_MYTED STANDARD; PRT; 20 AA.
AC P83148;
DT 05-JUL-2004 (Rel. 44, Created)

DT 05-JUN-2004 (Rel. 44, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Major extracellular fluid protein (BP protein) (Fragment).
 OS Mytilus edulis (Blue mussel).
 OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloidea;
 OC Mytiloidea; Mytilidae; Mytilinae; Mytilus.
 NC NCB1_Taxid=6550;
 RN [1]
 RP PROTEIN SEQUENCE, SUBUNIT, GLYCOSYLATION, AND MASS SPECTROMETRY.
 RC TRISU=EXTRACELLULAR FLUID;
 RX MEDLINE=1264951; PubMed=11084027; DOI=10.1074/jbc.M006803200;
 RA Hactan S.J., Laue T.M., Chasteen N.D.;
 RT "Purification and characterization of a novel calcium-binding protein
 from the extracellular fluid of the mussel, Mytilus edulis.";
 RL J. Biol. Chem. 276:4461-4468(2001).
 CC -1- FUNCTION: Appears to be a building block of the soluble organic
 CC matrix of the shell. The protein binds calcium.
 CC -1- SUBUNIT: Homodimer.
 CC -1- PTM: Glycosylated.
 CC -1- MASS SPECTROMETRY: MW=28340; METHOD=MALDI; RANGE=1-7; NOTE=Ref.1.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR GO: GO:0005509; P:calcium ion binding; TAS.
 KW Calcium; Direct protein sequencing; Glycoprotein.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2351 MW; CBB0C9B0D6F7451 CRC64;

Query Match 26.9%; Score 21; DB 1; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1.9e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHND 8
 DB 5 DHND 8
 RESULT 74
 Q9UCUO_HUMAN PRELIMINARY; PRT; 20 AA.
 AC Q9UCUO;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Beta 2 microglobulin pI 5.1 isoform (Fragment).
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NC NCB1_Taxid=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=9315819; PubMed=1336137;
 RA Aggeler A., Derancourt J., Jauregui-Adell J., Mion C., Demaille J.G.;
 RT "Biochemical characterization of serum and urinary beta 2
 microglobulin in end-stage renal disease patients.";
 RL Nephrol. Dial. Transplant. 7:1106-1110(1992).
 DR HSRP; P61769; JGN;
 SQ SEQUENCE 20 AA; 2310 MW; 9D01DE22DB2B283 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 YSKNP 13
 DB 10 YSRHP 14

RESULT 75
 Q9TPB8_NABGR PRELIMINARY; PRT; 20 AA.
 AC Q9TPB8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Cyteine protease (Fragment).
 OS Naegleria gruberi.
 OC Eukaryota; Heterolobosea; Schizopyrenida; Vahlkampfiidae; Naegleria.
 NC NCB1_Taxid=5762;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94164273; PubMed=8119377; DOI=10.1006/expr.1994.1023;
 RA Aldape K., Huizinga H., Bouvier J., McKerrow J.;
 RT "Naegleria fowleri: characterization of a secreted histolytic cysteine
 RT protease.";
 RL Exp. Parasitol. 78:230-241(1994).
 SQ SEQUENCE 20 AA; 2325 MW; 010FC692737EEB0 CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;
 Best Local Similarity 75.0%; Pred. No. 1.9e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 RDHN 7
 DB 8 REHN 11

RESULT 76
 Q4YQUT_PLABR PRELIMINARY; PRT; 20 AA.
 AC Q4YQUT;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB107515.00.0;
 OS Plasmidium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmidium.
 NC NCB1_Taxid=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kooij T.W.A.,
 RA Berrihan M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churche C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmidium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAI01002901; CAH99610.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2444 MW; CSD999B1DB5452CD CRC64;

Query Match 26.9%; Score 21; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.9e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IKRDNDYSKN 12
 DB 9 IYRDSKCKKN 19

RESULT 77
 Q9R5E1_ABRHY PRELIMINARY; PRT; 20 AA.
 AC Q9R5E1;
 Q9R5E1_ABRHY PRELIMINARY; PRT; 20 AA.

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Outer-membrane channel-forming protein IV (Fragment).
OS Aeromonas hydrophila.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Aeromonadales;
OC Aeromonadaceae; Aeromonas.
OX NCBI_TaxID=644;
RP [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9313115; PubMed=1283000;
RA Jeanneau D., Gilette N., Rattus F., Buckley J.T.;
RT "Purification of Aeromonas hydrophila major outer-membrane proteins:
RT N-terminal sequence analysis and channel-forming properties.";
RL Mol. Microbiol. 6:335-363(1992).
SQ SEQUENCE 20 AA; 2458 MW; EEDFCBAEECC66D00 CRC64;

Query Match          26.9%; Score 21; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
DB 10 NDYKR 14

RESULT 78
Q9QVCL_9MURI PRELIMINARY; PRT; 20 AA.
ID Q9QVCL_9MURI PRELIMINARY; PRT; 20 AA.
AC Q9QVCL_9MURI PRELIMINARY; PRT; 20 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Kallikrein heavy chain N terminus (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93329502; PubMed=1320938; DOI=10.1016/0167-4838(92)90162-7;
RA Wang C., Tang C.Q., Zhou G.X., Chao L., Chao J.;
RT "Biochemical characterization and substrate specificity of rat
RT prostatic kallikrein (93): comparison with tissue kallikrein, conin and
RT T-kallinogenase.";
RL Biochim. Biophys. Acta 1121:309-316(1992).
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2282 MW; A2402D52573B2D1D CRC64;

Query Match          26.9%; Score 21; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.9e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 DHND 8
DB 3 DHNN 6

RESULT 79
Q34694_HOMAM PRELIMINARY; PRT; 20 AA.
ID Q34694_HOMAM PRELIMINARY; PRT; 20 AA.
AC Q34694_HOMAM PRELIMINARY; PRT; 20 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Cytochrome oxidase subunit I (Fragment).
GN Name=COI;
OS Homo sapiens (Homo).
OC Eukaryota; Metazoa; Chordata; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Astacidea;

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OC Nephropoidea; Nephropoidea; Homarus.
OX NCBI_TaxID=6706;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95327187; PubMed=7603565; DOI=10.1038/376163a0;
RA Boore J.L., Collins T.M., Stanton D., Daehler L.L., Brown W.M.;
RT "Deducing the pattern of arthropod phylogeny from mitochondrial DNA
RT rearrangements.";
RL Nature 376:163-165 (1995).
DR EMBL; U29717; AAA82245.1; Genomic_DNA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005739; C:mitochondrion; IEA.
DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro; IPR000883; COX1.
DR PANTHER; PTHR10422; COX1; 1.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2379 MW; 1A3FE5395AF32008 CRC64;

Query Match          26.3%; Score 20.5; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.3e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 5 DHNDYSKNPM 14
DB 8 DHS-YMEIPM 16

RESULT 80
Q15893_HUMAN PRELIMINARY; PRT; 8 AA.
ID Q15893_HUMAN PRELIMINARY; PRT; 8 AA.
AC Q15893_HUMAN PRELIMINARY; PRT; 8 AA.
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Homo sapiens (clone XP587A) (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX TISSUE=Placenta;
RA Lee C.-C., Yazdani A., Wehnert M., Bailey J., Couch L., Xiong M.,
RA Caskey C.T.H.;
RT "Isolation of chromosome-specific genes by reciprocal probing of
RT arrayed cDNAs and cosmid libraries.";
RL Hum. Mol. Genet. 0:0-0(1995).
DR EMBL; L32073; AAA73883.1; mRNA.
FT NON_TER 1
FT NON_TER 8
SQ SEQUENCE 8 AA; 874 MW; DAA1B6D7376456C5 CRC64;

Query Match          25.6%; Score 20; DB 2; Length 8;
Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 SKNPM 14
DB 1 SQNPL 5

RESULT 81
Q9UDZ4_HUMAN PRELIMINARY; PRT; 8 AA.
ID Q9UDZ4_HUMAN PRELIMINARY; PRT; 8 AA.
AC Q9UDZ4_HUMAN PRELIMINARY; PRT; 8 AA.
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE RHD protein (Fragment).

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GN Name=RHD;
OC Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=93066356; PubMed=1438298;
RA le van Kim C., Mouru I., Cherif-Zahar B., Raynal V., Cherrier C.,
RA Carton J.-P., Collin Y.;
RT "Molecular cloning and primary structure of the human blood group Rhd
RT polypeptide.";
RL Proc. Natl. Acad. Sci. U.S.A. 89:10925-10929(1992).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RX MEDLINE=97260406; PubMed=9106526;
RA Metasni G., Cherif-Zahar B., Mouru I., Carton J.P.;
RT "Characterization of the recombination hot spot involved in the
RT genomic rearrangement leading to the hybrid D-CE-D gene in the DVI
RT phenotype.";
RL Am. J. Hum. Genet. 60:808-817(1997).
RN [3]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Blood;
RA Fiegel W.A.;
RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; 297031; CAB09727.1; -; Genomic DNA.
DR GO; GO:0016021; C:Integral to membrane; NAS.
FT NON_TER 1
FT SEQUENCE 8 AA; 1042 MW; D296944691PB5AB1 CRC64;
SQ
Query Match 25.6%; Score 20; DB 2; Length 8;
Best Local Similarity 57.1%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 DYKDKPM 14
Db 2 DYKDKPM 8

RESULT 82
Q5RLS1_PIG PRELIMINARY; PRT; 8 AA.
ID Q5RLS1_PIG
AC Q5RLS1;
DT 01-FEB-2005 (Tremblrel. 29, Created)
DT 01-FEB-2005 (Tremblrel. 29, Last sequence update)
DT 01-FEB-2005 (Tremblrel. 29, Last annotation update)
DE S13-domain binding protein 4 (Fragment).
OS Name=S13BP4;
GN S13BP4 (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sub.
OX NCBI_TaxID=9823;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Ear;
RA Du H.L., Chen J., Zhang Y.S., Cui J.X., He C., Zhang X.Q.;
RT "Improving the comparative map of SSC1q21-q26 containing QTL for
RT reproduction in swine.";
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY805698; AAV65974.1; -; Genomic DNA.
DR EMBL; AY805699; AAV65975.1; -; Genomic DNA.
DR EMBL; AY805700; AAV65976.1; -; Genomic DNA.
DR EMBL; AY805697; AAV65973.1; -; Genomic DNA.
FT NON_TER 1
FT SEQUENCE 8 AA; 998 MW; F942DB5AAB6DAA6 CRC64;
SQ
Query Match 25.6%; Score 20; DB 2; Length 8;

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Best Local Similarity 60.0%; Pred. No. 2.2e+06;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDY 9
Db 2 DDDDY 6

RESULT 83
Q93SR0_STAEP PRELIMINARY; PRT; 8 AA.
ID Q93SR0_STAEP
AC Q93SR0;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
DE Beta-lactamase repressor Blat (Fragment).
GN Name=Blat;
OS Staphylococcus epidermidis.
OC Staphylococcus epidermidis.
OC Bacteria; Firmicutes; Bacillales; Staphylococcus.
OX NCBI_TaxID=1282;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21680477; PubMed=11822776; DOI=10.1089/10766290152773374;
RA Sidhu M.S., Heir B., Sorum H., Holck A.;
RT "Genetic linkage between resistance to quaternary ammonium compounds
RT and beta-lactam antibiotics in food-related Staphylococcus spp.";
RL Microb. Drug Resist. 7:363-371(2001).
DR EMBL; AY028779; AAK8453.1; -; Genomic DNA.
KM Plasmid.
FT NON_TER 1
FT SEQUENCE 8 AA; 930 MW; 4E3325B05AA44720 CRC64;
SQ
Query Match 25.6%; Score 20; DB 2; Length 8;
Best Local Similarity 80.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NDYSK 11
Db 3 NDISK 7

RESULT 84
P82136_SPIOL PRELIMINARY; PRT; 10 AA.
ID P82136_SPIOL
AC P82136;
DT 01-JUN-2000 (Tremblrel. 14, Created)
DT 01-JUN-2000 (Tremblrel. 14, Last sequence update)
DT 01-OCT-2003 (Tremblrel. 25, Last annotation update)
DE Chloroplast 30S ribosomal protein S18 beta (Fragment).
OS Spinacia oleracea (Spinach).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=cv. Alvaro; TISSUE=Leaf;
RX MEDLINE=20435797; PubMed=10874039; DOI=10.1074/jbc.M004350200;
RA Yamaguchi K., von Knochlauch K., Sudramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 30S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28455-28465(2000).
CC -1- SUBCELLULAR LOCATION: Chloroplast.
CC -1- TISSUE SPECIFICITY: Expressed in all plant tissues.
CC -1- MISCELLANEOUS: S18 alpha and beta forms differ in pI. Beta is the
CC least basic form.
CC -1- MISCELLANEOUS: ON THE 2D-GEL ITS MW IS: 14 kDa.
CC -1- SIMILARITY: BELONGS TO THE S1P FAMILY OF RIBOSOMAL PROTEINS.
DR GO; GO:0009507; C:Chloroplast; IEA.
DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro; IPR001648; Ribosomal_S18.

```


RT "Cytochrome-c oxidase in developing rat heart. Enzymic properties and
 RT and no-terminal sequences suggest identity of the fetal heart and the
 RL adult liver isoform.";
 DR Bur. J. Biochem. 230:235-241(1995).
 DR PIR; S65377; S65377.
 DR GO; GO:0004129; F:cytochrome-c oxidase activity; IEA.
 FT NON_TER 1 1
 FT SEQUENCE 11 AA, 927 MW, 4F3B57D71EAA873 CRC64;
 SQ
 Query Match 25.6%; Score 20; DB 2; Length 11;
 Best Local Similarity 66.7%; Pred. No. 1.5e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SIKRDH 6
 DB 2 SAKGDH 7

RESULT 89
 Q6LDS1_BPT3 PRELIMINARY; PRT; 13 AA.
 ID Q6LDS1;
 AC Q6LDS1;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE RNA polymerase III (Fragment).
 OS Bacteriophage T3.
 OC Bacteriophage T3.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC T7-like viruses.
 CX NCBI_TaxID=10759;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86221699; PubMed=3011596; DOI=10.1016/0378-1119(86)90098-3;
 RA Morita C.E., Klement J.F., McAllister W.T.;
 RT "Cloning and expression of the bacteriophage T3 RNA polymerase gene.";
 RL Gene 41:193-200(1986).
 DR EMBL; M22609; AAA63781.1; -; Genomic_DNA.
 FT NON_TER 13 13
 FT SEQUENCE 13 AA, 1567 MW, 16F2BD5EAO21054 CRC64;
 SQ
 Query Match 25.6%; Score 20; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 DHNDYS 10
 DB 8 EKNDPS 13

RESULT 90
 Q51605_9222Z PRELIMINARY; PRT; 13 AA.
 ID Q51605_9222Z PRELIMINARY;
 AC Q51605;
 DT 01-NOV-1996 (TReMBLrel. 01, Created)
 DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE C1E7 protein (Fragment).
 GN Name=C1E7;
 OS Plasmid COL7.
 OC Plasmid COL7.
 OC other sequences; plasmids.
 CX NCBI_TaxID=2450;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=92293113; PubMed=1603061;
 RA Soong B.W., Lu F.M., Chak K.-F.;
 RT "Characterization of the cea gene of the COL7 plasmid.";
 RL Mol. Gen. Genet. 233:177-183(1992).
 DR EMBL; M62409; AAA98055.1; -; Genomic DNA.
 DR GO; GO:0015643; F:toxin binding; IEA.
 DR GO; GO:0030153; P:bacteriocin immunity; IEA.
 DR InterPro; IPR000290; Colicin_pycocin.

DR Pfam; PF01320; Colicin_Pycocin; 1.
 KM plasmid.
 FT NON_TER 13 13
 FT SEQUENCE 13 AA, 1501 MW, 9E75F892148CB045 CRC64;
 SQ
 Query Match 25.6%; Score 20; DB 2; Length 13;
 Best Local Similarity 30.0%; Pred. No. 1.8e+04;
 Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 2 IKRDNDYSK 11
 DB 3 LKNSIDYTE 12

RESULT 91
 HY14_PIG STANDARD; PRT; 14 AA.
 ID HY14_PIG
 AC P01155;
 DT 21-JUL-1986 (Rel. 01, Created)
 DT 21-JUL-1986 (Rel. 01, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Hypothalamic tetradecapeptide.
 OS Sus scrofa (Pig).
 OC Bkaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suidae;
 OC Sus.
 CX NCBI_TaxID=9823;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Schleginger D.H., Niall H.D., Linthicum G.L., Dupont A., Schally A.V.;
 RL Submitted (NOV-1976) to the PIR data bank.
 CC -----
 CC "This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC -----
 DR PIR; A01419; NYPG14.
 KM Amidation; Direct protein sequencing.
 FT MOD RES 14 14
 FT SEQUENCE 14 AA, 1648 MW, 3DDF87E2419DB47 CRC64;
 SQ
 Query Match 25.6%; Score 20; DB 1; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 YSRNP 13
 DB 3 YGKSP 7

RESULT 92
 Q5XVM8_9MOLU PRELIMINARY; PRT; 14 AA.
 ID Q5XVM8_9MOLU PRELIMINARY;
 AC Q5XVM8;
 DT 25-OCT-2004 (TReMBLrel. 28, Created)
 DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Candidatus Barley phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma;
 OC Candidatus Phytoplasma asteris.
 CX NCBI_TaxID=297014;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Badel;
 RA Uptonaviciene L., Jomantienė R., Davis R.E.;
 RT "First report of Barley as host of a phytoplasma belonging to group
 RL 16Srl subgroup B ";
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL: AY735448; AAU81712.1; -; Genomic DNA.
 DR GO: GO:0003735; P:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1771 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 Db 2 RGHNKDK 9

RESULT 93
 O6KXW1_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Chryseantheum yellows phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma;
 OC Candidatus Phytoplasma asteris.
 NCBI_TaxID=238674;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CHRYM;
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 associated with aster yellows and related diseases.";
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).
 DR EMBL: AY264869; AAP91867.1; -; Genomic DNA.
 DR GO: GO:0003735; P:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1789 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 Db 2 RGHNKDK 9

RESULT 94
 O6KXW4_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Hydrangea phyllody phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma;
 OC Candidatus Phytoplasma asteris.
 NCBI_TaxID=238673;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=HYDP;
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 associated with aster yellows and related diseases.";

RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).
 DR EMBL: AY264869; AAP91864.1; -; Genomic DNA.
 DR GO: GO:0003735; P:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1789 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 Db 2 RGHNKDK 9

RESULT 95
 O6KXW7_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS plantago virescence phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma;
 OC Candidatus Phytoplasma asteris.
 NCBI_TaxID=238672;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PVM;
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 associated with aster yellows and related diseases.";
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).
 DR EMBL: AY264867; AAP91861.1; -; Genomic DNA.
 DR GO: GO:0003735; P:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1789 MW; 4CC8BBE94FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 Db 2 RGHNKDK 9

RESULT 96
 O6KXW0_9MOLU PRELIMINARY; PRT; 14 AA.

AC O6KXW0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Apricot aster yellows phytoplasma.
 OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 NCBI_TaxID=238671;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=ACLR-AY;
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 associated with aster yellows and related diseases.";

RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).
 DR EMBL: AY264664; AAP91852.1; -; Genomic DNA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1771 MW; 4CC88BB9FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 |||||
 Db 2 RGHNKDK 9

RESULT 97
 Q6WXX3_9MOLU PRELIMINARY; PRT; 14 AA.

AC Q6WXX3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Leifhopfer-borne phytoplasm.

OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 OX NCBI_TaxID=238670;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=CVB,
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 RT associated with aster yellows and related diseases.";
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).
 DR EMBL: AY264665; AAP91855.1; -; Genomic DNA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1771 MW; 4CC88BB9FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 |||||
 Db 2 RGHNKDK 9

RESULT 98
 Q6WXX6_9MOLU PRELIMINARY; PRT; 14 AA.

AC Q6WXX6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Grey dogwood 'witches'-broom phytoplasma.

OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 OX NCBI_TaxID=238669;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=GD1,
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 RT associated with aster yellows and related diseases.";
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).

DR EMBL: AY264664; AAP91852.1; -; Genomic DNA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1789 MW; 4CC88BB9FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 |||||
 Db 2 RGHNKDK 9

RESULT 99
 Q6WXX9_9MOLU PRELIMINARY; PRT; 14 AA.

AC Q6WXX9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Blueberry stunt phytoplasma.

OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 OX NCBI_TaxID=37695;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=BBS3,
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 RT associated with aster yellows and related diseases.";
 RL Int. J. Syst. Evol. Microbiol. 54:1037-1048(2004).
 DR EMBL: AY264663; AAP91849.1; -; Genomic DNA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1789 MW; 4CC88BB9FE747A3 CRC64;

Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 4 RDHNDYSK 11
 |||||
 Db 2 RGHNKDK 9

RESULT 100
 Q6WXX8_9MOLU PRELIMINARY; PRT; 14 AA.

AC Q6WXX8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE Ribosomal protein S19 (Fragment).
 GN Name=rpS19;
 OS Clover phylloidy phytoplasma.

OC Bacteria; Firmicutes; Mollicutes; Acholeplasmatales;
 OC Acholeplasmataceae; Candidatus Phytoplasma.
 OX NCBI_TaxID=35777;
 RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=KVG, KVE, and CPH;
 RA Lee I.-M., Gundersen-Rindal D.E., Davis R.E., Bottner K.D.,
 RA Marcone C., Seemuller E.;
 RT "Candidatus Phytoplasma asteris", a novel phytoplasma taxon
 RT associated with aster yellows and related diseases.";

RL Int. J. Syst. Evol. Microbiol. 54:1037-1048 (2004).
 DR EMBL; AY264860; AAP91840.1; -; Genomic_DNA.
 DR EMBL; AY264861; AAP91843.1; -; Genomic_DNA.
 DR EMBL; AY264862; AAP91846.1; -; Genomic_DNA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 KW Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 14 AA; 1771 MW; 4CC8B8EF8FE747A3 CRC64;
 Query Match 25.6%; Score 20; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 4 RDHNDYSK 11
 DB 2 RGHKKDK 9

Search completed: January 20, 2006, 19:11:01
 Job time : 49.5769 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 75.5769 Seconds
(without alignments)
116.273 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114

Sequence: 1 DYEPGSRGKPKAPLYKRP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 243163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

A_GeneSeq_21:*
1: geneseqp1980s:*
2: geneseqp1980s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*
9: geneseqp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	3	AA552511 House dus
2	114	100.0	20	5	AAU96315 Der HMW-m
3	39	34.2	14	4	AA000360 Human pro
4	38	33.3	10	5	AAU92321 PHOR1-FSD
5	38	33.3	10	5	AAU92517 PHOR1-FSD
6	38	33.3	10	5	AAU92613 PHOR1-FSD
7	37	32.5	16	9	AAW21182 Human ade
8	36	31.6	20	2	AAW71598 Protein t
9	36	31.6	20	3	AAV81932 Peptide f
10	36	31.6	20	3	AA080489 Peptide d
11	35	30.7	9	9	ADM23014 SARS coro
12	35	30.7	15	9	ADM78056 Human inf
13	35	30.7	15	9	ADM77792 Human can
14	34.5	30.3	18	2	AAAR3725 Collagen-
15	34.5	30.3	18	2	AAAR3725 Collagen-
16	34.5	30.3	18	2	AAW57681 Collagen-
17	34	29.8	14	4	AA000359 Human pro
18	34	29.8	15	8	AD571368 Extensin
19	34	29.8	20	7	AD515704 E. coli t
20	34	29.8	20	7	AD515704 E. coli t
21	33.5	29.4	15	9	AAW78278 Rat neuro
22	33	28.9	9	5	AAU92598 PHOR1-FSD
23	33	28.9	10	5	AAU92855 PHOR1-FSD
24	33	28.9	14	8	AD592104 Human odo

25	33	28.9	16	6	ABP55617 Human cyt
26	33	28.9	16	7	ADD24038 Breast ca
27	33	28.9	17	1	AA080012 Sequence
28	33	28.9	17	1	AA080012 Sequence
29	33	28.9	18	2	AAV32877 Fibronect
30	33	28.9	18	2	AAV32865 Fibronect
31	33	28.9	19	4	AA62425 Human SAP
32	33	28.9	19	6	ABP74734 Proteome
33	33	28.9	19	8	AD513312 Human rha
34	33	28.9	19	9	ADY39949 Human pla
35	33	28.9	19	9	AEAA3956 Mass spec
36	32	28.1	14	5	ABJ00309 Human IGR
37	32	28.1	15	2	AAAR4744 SPYR 19b-
38	32	28.1	15	8	AD017459 Different
39	32	28.1	16	7	ADU90073 Human pap
40	32	28.1	17	2	AAW17560 Beta-B2-c
41	32	28.1	17	3	AA080129 Hepatitis
42	32	28.1	17	7	ADJ90086 Human pap
43	32	28.1	17	7	ADJ90087 Human pap
44	32	28.1	17	8	ADP74618 Hmno aci
45	32	28.1	18	7	ADU90100 Human pap
46	32	28.1	18	7	ADU90101 Human pap
47	32	28.1	18	7	ADU90102 Human pap
48	32	28.1	19	7	ADU90115 Human pap
49	32	28.1	19	7	ADU90117 Human pap
50	32	28.1	19	7	ADU90118 Human pap
51	32	28.1	19	7	ADU90116 Human pap
52	32	28.1	20	2	AAW71596 Protein t
53	32	28.1	20	3	AAV81930 Peptide f
54	32	28.1	20	3	AA080487 Peptide d
55	32	28.1	20	7	ADJ90133 Human pap
56	32	28.1	20	7	ADU90135 Human pap
57	32	28.1	20	7	ADU90132 Human pap
58	32	28.1	20	7	ADU90134 Human pap
59	32	28.1	20	7	ADU90131 Human pap
60	31	27.2	9	5	AB874361 Karyophi1
61	31	27.2	9	5	AB874355 Karyophi1
62	31	27.2	9	5	AB874364 Karyophi1
63	31	27.2	12	4	AA661173 Anopheles
64	31	27.2	12	9	ADV62107 S. marcesc
65	31	27.2	13	5	ADZ37873 Human kin
66	31	27.2	14	5	ABP46490 Human Bly
67	31	27.2	14	7	ADG97317 eCFV VHCD
68	31	27.2	15	4	AA080601 Human cyt
69	31	27.2	15	7	ADU90060 Human pap
70	31	27.2	15	9	ADV12192 Human pho
71	31	27.2	15	9	ADW76221 Human cyt
72	31	27.2	15	9	ADX56199 Cardiovaa
73	31	27.2	16	2	AAW25403 p53bp2 SH
74	31	27.2	16	7	ADU90072 Human pap
75	31	27.2	16	9	ADX56200 Cardiovaa
76	31	27.2	16	9	ADX56207 Cardiovaa
77	31	27.2	17	1	AA080011 Sequence
78	31	27.2	17	7	ADP22395 Nuclear 1
79	31	27.2	17	7	ADP17331 Nuclear t
80	31	27.2	17	7	ADP86158 Human NLS
81	31	27.2	17	7	ADU90085 Human pap
82	31	27.2	18	2	AAW66552 HSV-2 g1y
83	31	27.2	18	6	AAW66552 HSV-2 g1y
84	31	27.2	18	7	ADU90099 Human pap
85	31	27.2	18	8	ADK50419 Human pap
86	31	27.2	19	1	AA081357 Sequence
87	31	27.2	19	2	AAW17416 Chicken a
88	31	27.2	19	2	AAW22884 Peptide K
89	31	27.2	19	2	AAW7227 OA-519 pe
90	31	27.2	19	2	AAW71597 Protein t
91	31	27.2	19	2	AAW67551 Peptide f
92	31	27.2	19	3	AAW64378 Peptide f
93	31	27.2	19	3	AAW81931 Peptide f
94	31	27.2	19	3	AAW80488 Peptide d
95	31	27.2	19	7	ADU90114 Human pap
96	31	27.2	19	9	ADV13539 Human pho
97	31	27.2	20	7	AD515767 E. coli t

98	31	27.2	20	7	ADJ90130	Human pap
99	30.5	26.8	13	6	ABR00752	HCV nonet
100	30	26.3	9	9	ADU70749	Human hep

ALIGNMENTS

RESULT 1

AAV52511

ID AAV52511 standard; peptide; 20 AA.

XX AAV52511;

XX 22-FEB-2000 (first entry)

XX House dust mite allergen protein (map) A/B fragment map(1).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

XX house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

XX hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

XX Dermatophagoides farinae.

XX WO954349-A2.

XX 28-OCT-1999.

XX 16-APR-1999; 99WO-US008524.

XX 17-APR-1998; 98US-00062013.

XX 13-MAY-1998; 98US-0085295P.

XX 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER,

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animal's hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

XX Sequences AAV52510-Y52522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGE present in mite-allergic dog

XX antisera. The HMW-map composition comprises mapA (a 109 kd protein) and

XX mapB (98 kd). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX treated include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX Sequence 20 AA;

SQ

Query Match 100.0%; Score 114; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPLYKRP 20

DB 1 DVEYPSRLGNPKAPLYKRP 20

RESULT 2

AAU96315

ID AAU96315 standard; peptide; 20 AA.

XX AAU96315;

XX 15-UTL-2002 (first entry)

XX Der HMW-map polypeptide #2.

XX Der HMW-map; American house dust mite; antiallergic; mite; IGE;

XX mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

XX 21-MAR-2002.

XX 14-SEP-2001; 2001WO-US028730.

XX 14-SEP-2000; 2000US-00622293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic

XX acid. The Der HMW-map protein is useful for eliciting an immune response

XX against Der HMW-map protein. The protein or a reagent comprising a non-

XX proteinaceous epitope is useful for identifying an animal (e.g., dog,

XX cat) susceptible to or having an allergic response to a mite. A

XX therapeutic composition is useful for desensitising a host animal to an

XX allergic response to a mite. The DNA and protein can be used in the

XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

XX of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting

XX binding of proteins to IGE, to prevent immunocomplex formation, thus

XX reducing hypersensitivity responses to mite allergens, and as vaccines

XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

XX represent Der HMW-map polypeptides of the invention

XX Sequence 20 AA;

SQ

Query Match 100.0%; Score 114; DB 5; Length 20;

Best Local Similarity 100.0%; Pred. No. 2.1e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPLYKRP 20

DB 1 DVEYPSRLGNPKAPLYKRP 20

RESULT 3

AAU00360

ID AAU00360 standard; peptide; 14 AA.

XX AAU00360;

XX 01-OCT-2001 (first entry)

XX Human protein fragment SEQ ID NO: 906.

XX Human; single nucleotide polymorphism, SNP; paternity test;
KW forensic test; aberrant protein expression.
XX
XX Homo sapiens.
OS
XX MO200151670-A2.
PN
XX 19-JUL-2001.
PD
XX
XX 05-JAN-2001; 2001WO-US000322.
PP
XX
XX 07-JAN-2000; 2000US-0174962P.
PR
XX (CUBA-) CUBAGEN CORP.
PA
XX
XX Shimkels RA, Leach MD;
PI
XX MPI; 2001-451871/48.
DR
XX N-F5DB; AAH89475.
DR
XX
XX Isolated human polynucleotides containing single nucleotide
PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
PI infection and diabetes.
XX
XX
XX Disclosure; Page 364; 475pp; English.
PS
XX The present invention relates to human nucleic acids containing single
CC nucleotide polymorphisms (SNPs). These can be used in forensic and
CC paternity tests, and to aid in the treatment of diseases associated with
CC aberrant protein expression, including cancer, amyloidosis, diabetes,
CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
CC meningitis, muscular disorders, dementia, neurological diseases, tubercous
CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
CC autoimmunity. The present sequence is a peptide encoded by a
CC polymorphism-containing oligonucleotide fragment of the invention
CC
XX
XX Sequence 14 AA;
SQ
XX
XX Query Match 34.2%; Score 39; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 DYEPGSRIGN 11
|||
Db 4 DYRYPPRLAN 14
|||
RESULT 4
AAU92321
ID AAU92321 standard; peptide; 10 AA.
XX
XX AAU92321;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX PHOR1-F5D6 peptide #59 tested for HLA binding.
DE
XX
XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.
KW
XX
XX Homo sapiens.
OS
XX MO200214501-A2.
PN
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025862.
PP
XX
XX 17-AUG-2000; 2000US-0226241P.
PR
XX (AGEN-) AGENSYS INC.
PA

XX
PI Hubert RS, Raitano AB, Paris M, Challita-Bid PM, Ge W;
PI Jakobovits A;
XX
XX MPI; 2002-269193/31.
DR
XX
XX Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of
PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene
PT products in tissue sample from subject and comparing it to normal sample.
XX
XX
XX Claim 49; Page 177; 250pp; English.
PS
XX
XX The present invention relates to the isolation of novel human genes
CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene
CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-
CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6
CC polynucleotide and polypeptide sequences are useful in diagnostic and
CC therapeutic methods, and compositions for various cancers such as
CC prostate cancer. The sequences are useful for inhibiting the growth of
CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating
CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can
CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-
CC A11 or PHOR1-F5D6 peptides tested for HLA binding
XX
XX
XX Sequence 10 AA;
SQ
XX
XX Query Match 33.3%; Score 38; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 4 YPGSRIGNPK 13
|||
Db 1 YVGRPYGNPK 10
|||
RESULT 5
AAU92517
ID AAU92517 standard; peptide; 10 AA.
XX
XX AAU92517;
AC
XX
XX 02-JUL-2002 (first entry)
DT
XX
XX PHOR1-F5D6 peptide #255 tested for HLA binding.
DE
XX
XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.
KW
XX
XX Homo sapiens.
OS
XX MO200214501-A2.
PN
XX 21-FEB-2002.
PD
XX
XX 17-AUG-2001; 2001WO-US025862.
PP
XX
XX 17-AUG-2000; 2000US-0226241P.
PR
XX (AGEN-) AGENSYS INC.
PA
XX
XX Hubert RS, Raitano AB, Paris M, Challita-Bid PM, Ge W;
PI Jakobovits A;
XX
XX MPI; 2002-269193/31.
DR
XX
XX Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of
PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene
PT products in tissue sample from subject and comparing it to normal sample.
XX
XX
XX Claim 49; Page 185; 250pp; English.
PS
XX
XX The present invention relates to the isolation of novel human genes
CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene
CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-

CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6
CC polynucleotide and polypeptide sequences are useful in diagnostic and
CC therapeutic methods, and compositions for various cancers such as
CC prostate cancer. The sequences are useful for inhibiting the growth of
CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating
CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can
CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-
CC A11 or PHOR1-F5D6 peptides tested for HLA binding
XX
SQ Sequence 10 AA;

Query Match 33.3%; Score 38; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRLGNPK 13
DB 1 YVGPRTYGNPK 10

RESULT 6
AAU92613
ID AAU92613 standard; peptide; 10 AA.

AC AAU92613;
XX
XX 02-JUL-2002 (first entry)

DE PHOR1-F5D6 peptide #351 tested for HLA binding.

XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.

XX Homo sapiens.

XX WO200214501-A2.

XX 21-FEB-2002.

XX 17-AUG-2001; 2001WO-US025862.

XX 17-AUG-2000; 2000US-0226241P.

XX (AGEN-) AGENSYS INC.

XX Hubert RS, Raitano AB, Faris W, Challita-Eid PM, Ge W;
PI Jakubovics A;

XX WPI; 2002-269193/31.

PT Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of
PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene
PT products in tissue sample from subject and comparing it to normal sample.

XX Claim 49; Page 188; 250pp; English.

XX The present invention relates to the isolation of novel human genes
CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene
CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-
CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6
CC polynucleotide and polypeptide sequences are useful in diagnostic and
CC therapeutic methods, and compositions for various cancers such as
CC prostate cancer. The sequences are useful for inhibiting the growth of
CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating
CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can
CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-
CC A11 or PHOR1-F5D6 peptides tested for HLA binding
XX

SQ Sequence 10 AA;

Query Match 33.3%; Score 38; DB 5; Length 10;
Best Local Similarity 70.0%; Pred. No. 64;
Matches 7; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRLGNPK 13
DB 1 YVGPRTYGNPK 10

RESULT 7
ADMW21182
ID ADMW21182 standard; peptide; 16 AA.

XX ADMW21182;

XX 24-MAR-2005 (first entry)

DE Human adenovirus type 37 third beta repeat of the fiber shaft protein.

XX vector; gene therapy; retinopathy; ophthalmological; fiber shaft.

XX Human adenovirus type 37.

XX WO2004111251-A2.

XX 23-DEC-2004.

XX 10-JUN-2004; 2004WO-US018623.

XX 11-JUN-2003; 2003US-0478008P.

XX (SCRI) SCRIPPS RES INST.

XX (REGC) UNIV CALIFORNIA.

XX Nemerow GR, Wu E, Stewart P;

XX WPI; 2005-040114/04.

PT New modified adenovirus fiber that bind to Coxsackie-Adenovirus Receptor
PT (CAR) comprises a modification to the fiber protein shaft, useful for
PT developing targeted adenoviruses for therapeutic uses, e.g. gene therapy
PT of retinal disorders.

XX Claim 12; SEQ ID NO 58; 171pp; English.

XX This invention relates to a novel modified adenovirus fiber that bind to
CC the Coxsackie-Adenovirus Receptor (CAR) in vivo and comprises a
CC modification to the fiber protein shaft. Specifically, it refers to a
CC modified adenovirus fiber that binds to CAR with less than 50%
CC preferably less than 1% of the binding affinity of the unmodified fiber,
CC and furthermore is shorter and more rigid than its unmodified
CC counterpart. As such, the present invention describes recombinant
CC de-targeted adenovirus viral particles and vectors that can be used as a
CC base vectors to develop targeted adenoviruses for specific therapeutic a
CC uses. Accordingly, by addition of a heterologous nucleic acid encoding a
CC therapeutic product and a targeting ligand in the capsid of the
CC adenoviral particle, the modified adenovirus vector can be used in gene
CC therapy in order to treat retinal disorders. As such, these compositions
CC exhibit ophthalmological activity. This peptide sequence is a beta repeat
CC motif of a human adenovirus fiber shaft protein that can be modified to
XX reduce CAR binding, given in an exemplification of the invention.

SQ Sequence 16 AA;

Query Match 32.5%; Score 37; DB 9; Length 16;
Best Local Similarity 72.7%; Pred. No. 1,5e+02;
Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSRLGNPKAPL 16
DB 1 GSLTVNPKAPL 11

RESULT 8
AAW71598
ID AAW71598 standard; peptide; 20 AA.

XX

AC		AAW71598;	
XX			
DT		24-NOV-1998 (first entry)	
XX			
DE		Protein tyrosine phosphatase peptide PTP PEPT.	
XX			
KM		Mouse; tyrosine phosphorylated cleavage furrow-associated protein; PSRIP, PSRT family; Protein Tyrosine Phosphatase; murine; KW polymerisation) actin monomer; eukaryotic cell; identification; antagonist.	
KX			
OS	Synthetic.		
OJ	Mus sp.		
XX		WO9835037-A1.	
XX			
PB		13-AUG-1998.	
PF		30-JAN-1998; 98WO-US001774.	
PR	07-FEB-1997; 97US-00798419. 29-SEP-1997; 97US-00938829.		
PA	(GETH) GENENTECH INC.		
PI	Lasky LA, Dowbenko DJ;		
DR	WPLI, 1998-447234/38.		
PT	New PEPT-type protein tyrosine phosphatase interacting polypeptide - nucleic acids and vectors; for inducing the polymerisation of actin monomers in eukaryotic cells and identifying antagonists.		
PS	Dileclosure; Page 37; 11pp; English.		
XX			
CC	The present sequence represents a peptide from the present invention which describes murine tyrosine phosphorylated cleavage furrow- associated protein (PESTP), which is a PEST-type protein tyrosine phosphatase (PTP)-interacting polypeptide. PESTP induces the polymerisation of actin monomers in a eukaryotic cell, by introducing a vector containing the nucleic acid sequence encoding PESTP into the cell. Assays for identifying (anti)agonists of PESTP comprise contacting actin polymerisation		
CC			
CQ	Sequence 20 AA;		
Query Match	31.6%; Score 36; DB 2; Length 20;		
Best Local Similarity	60.0%; Pred.No. 2.8e+02;		
Matches	6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;		
OY	6 GSRLGNPKAP 15		
	:		
DB	3 GNRCCKPKGP 12		
RESULT 9			
ID	AAY81932 standard; protein; 20 AA.		
AC	AAY81932;		
DT	27-JUN-2000 (first entry)		
DE	Peptide fragment of PKXP-HSCF.		
XX			
KM	PEST phosphatase interacting protein; PESTP, tumour therapy;		
KX	protein tyrosine phosphatase; PTP.		
OS	Unidentified.		
XX			
FN	U96040437-A.		
XX			

PD 21-MAR-2000.
XX
PF 29-SEP-1997; 97US-00938830.
XX
PR 17-APR-1997; 97US-0104590P.
XX
PA (GETH) GENENTECH INC.
XX
PI Dowdenko DJ, Laakky LA;
XX
DR WPI; 2000-282393/24.
XX
PT Novel genes encoding protein tyrosine phosphatase binding proteins useful
PT for isolating homologous genes, e.g. in tumor cells, which provide more
PI specific targets for tumor therapy.
XX
PS Disclosure; Col 35; 65pp; English.

This sequence represents a fragment of a protein tyrosine phosphatase (PTP). It was used to isolate the PST phosphatase interacting protein (PTPIP) sequence of the invention. The protein is a protein tyrosine phosphatase that possesses a non-catalytic domain comprising a proline, serine and threonine rich region and a C-terminal segment of 20 amino acid (aa's) rich in proline, and defines an SH3 binding domain. Nucleic acids encoding native PTPIP molecules can be used to isolate homologous genes specifically expressed in tumour cells, which might provide more specific targets for tumour therapy. The DNA is also useful for the preparation of PTPIP polypeptides by recombinant techniques and as hybridisation probes for searching cDNA and genomic libraries for the coding sequence of other PTPIP polypeptide analogues in other species

Sequence 20 AA;

```

Query Match 31.6%; Score 36; DB 3; Length 20;
Best Local Similarity 60.0%; Pred. NO. 2.8e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 6 GSRIGNPKAP 15
   | | | | |
Db 3 GNRCKPKRP 12

RESULT 10
AAB08489
ID AAB08489 standard; peptide: 20 AA.
XX
AC AAB08489;
XX
DT 20-DEC-2000 (first entry)
XX
DB Peptide derived from a protein tyrosine phosphatase.
XX protein tyrosine phosphatase; PTP; phosphatase interacting protein;
KW PSTPIP; PEST family; protein tyrosine phosphatase; actin monomer;
XX tissue typing; tumour cell; tumour imaging.
XX
OS Synthetic.
XX
PN US611073-A.
XX
PD 29-AUG-2000.
XX
PF 06-FEB-1998; 98US-00020222.
XX
PR 17-APR-1997; 97US-0104590P.
XX
PA (GERTH ) GENENTECH INC.
XX
PI LabKey LA;
XX
DR WPI, 2000-586378/55.
XX
TT Novel PST phosphatase interacting protein useful for inducing

```

PT polymerization of actin monomers and for identifying homolog of PST
 CC phosphatase interacting protein.
 XX
 PS Disclosure; Col 34; 48pp; English.
 XX
 CC AAB08487-90 represent peptides derived from protein tyrosine phosphatase
 CC (PTP). They were used to identify interaction domains of a murine protein
 CC tyrosine phosphatase (PTP) phosphatase interacting protein (PSPIP).
 CC PSPIP polypeptides are bound by and dephosphorylated by the PEST family
 CC of protein tyrosine phosphatases. PSPIP associates with actin. PSPIP is
 CC useful for inducing the polymerisation of actin monomer in eukaryotic
 CC cells by introducing the polypeptide into the cell. The polypeptide is
 CC useful for identifying and isolating PSPIP homologues in another
 CC mammalian species, in screening assays to identify antagonists and
 CC agonists of native PSPIP polypeptide and as molecular weight markers on
 CC protein gels. The PSPIP nucleic acid is useful for tissue typing of
 CC specific mammalian tissues, for preparing PSPIP polypeptides by
 CC recombinant techniques, as hybridisation probes for searching cDNA and
 CC genomic libraries for the coding sequence of other PSPIP analogues and
 CC to isolate homologous genes specifically expressed in tumour cells.
 CC Antagonists of PSPIP peptide are useful for inhibiting biological
 CC activity of the peptide. Antibodies of PSPIP are useful to identify
 CC rapidly dividing cells and are used to image tumours comprising such
 CC rapidly dividing cells
 CC
 SQ Sequence 20 AA;
 Query Match 31.6%; Score 36; DB 3; Length 20;
 Best Local Similarity 60.0%; Pred. No. 2.8e+02;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 6 GSRLGNPKAP 15
 Db 3 GNRCKPKKP 12
 RESULT 11
 ID ADM23014
 XX ADM23014 standard; peptide; 9 AA.
 AC ADM23014;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE SARS coronavirus T-cell epitope SEQ ID 70.
 XX
 KM SARS coronavirus infection; infection; respiratory disease;
 KM epitope mapping; vaccine; diagnosis; t-lymphocyte; virucide.
 XX
 OS SARS coronavirus.
 XX
 PN WO2004110349-A2.
 XX
 PD 23-DEC-2004.
 XX
 PF 14-MAY-2004; 2004WO-US015026.
 XX
 PR 14-MAY-2003; 2003DK-00000725.
 XX
 PA (SIGA-) SIGA TECHNOLOGIES INC.
 XX
 PI Nielsen M, Lund O, Lundegaard C, Worning P, Buus S, Brunak S,
 PI Justesen S, Sylvestre-Hvid C, Roder GA, Lambert K;
 XX
 DR WPI; 2005-048689/05.
 XX
 PT New Severe Acute Respiratory Syndrome (SARS) virus T-cell epitope
 PT comprising 407 peptide sequences, each having 9 amino acids, useful in
 PT preparing a vaccine against SARS infection.
 XX
 PS Claim 1; SEQ ID NO 70; 103pp; English.
 XX
 CC The invention relates to a new Severe Acute Respiratory Syndrome (SARS)

CC virus T-cell epitope comprising 407 peptide sequences appearing as
 CC ADM22945-ADM23351. Also included are predicting peptides that are
 CC epitopes (or that can be used as diagnostic tools) a vaccine using a
 CC limited number of the SARS virus peptides, e.g., 1, 2, 3, 4, 5, 8, 16,
 CC 32, 64, 128, 256 or 512, given in the specification, or a diagnostic tool
 CC using a limited number of the SARS virus peptides, e.g., 1, 2, 3, 4, 5,
 CC 8, 16, 32, 64, 128, 256 or 512, given in the specification. Predicting
 CC peptides that are epitopes or that can be used as diagnostic tools
 CC comprises predicting which peptides bind to a MHC (major
 CC histocompatibility complex) molecule with high affinity using a method
 CC with at least one or two of the following features: using a Gibbs sampler
 CC to derive binding motif weight matrices; using a Gibbs sampler including
 CC sequences weighting to derive binding motif weight matrices; or using a
 CC Gibbs sampler including pseudo counts to correct for low counts to derive
 CC binding motif weight matrices. The prediction of the Gibbs sampler weight
 CC matrix is combined with prediction or measurement of proteasomal cleavage
 CC sites, major histocompatibility complex (MHC) binding, presence or
 CC related sequences in patent databases, TAP binding, gene or protein
 CC expression level, function of the protein, localization of the protein,
 CC similarity to self proteins or sequence conservation. The new Severe
 CC Acute Respiratory Syndrome (SARS) virus T-cell epitope is useful in
 CC preparing a vaccine against SARS infection. The present sequence is a
 CC SARS virus epitope of the invention.
 CC
 SQ Sequence 9 AA;
 Query Match 30.7%; Score 35; DB 9; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 11 NPKAPLYK 18
 Db 1 NPKTPKPK 8
 RESULT 12
 ID ADM78056
 XX ADM78056 standard; peptide; 15 AA.
 AC ADM78056;
 XX
 DT 07-APR-2005 (first entry)
 XX
 DE Human inflammation therapy target peptide CEBA.
 XX
 KM DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;
 KM vasotropic; hypotensive; antiarteriosclerotic; antiinflammatory;
 KM antiallergic; immunosuppressive; antibacterial; antiasthmatic;
 KM dermatologic; antidiabetic; gastrointestinal-gen.; antitumor;
 KM thrombolytic; neuroprotective; ophthalmological; antirheumatic;
 KM antipyretic; uropathic; antiparasitic; hepatotropic; antianemic;
 KM muscular-gen.; thyromimetic; antithyroid; gynecological; nephrotropic;
 KM hepatotropic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 KM endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 KM antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;
 KM antiferility; cancer; cardiovascular disease; inflammation;
 KM metabolic disorder; neuropathy; sleep disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO2005007090-A2.
 XX
 PD 27-JAN-2005.
 XX
 PF 02-JUL-2004; 2004WO-US021514.
 XX
 PR 03-JUL-2003; 2003US-0484761P.
 XX
 PA (HARD) HARVARD COLLEGE.
 XX
 PI Blenis J, Murphy LO;
 PI
 XX
 DR WPI; 2005-112720/12.

XX Identification of compound for treating e.g. cancer by culturing cells
 PT expressing target protein in the presence of growth factor, cytokine,
 PT tumor promoter or oncogene and assessing binding after contacting with
 PT the compound.

XX Claim 12, Page 59, 104pp; English.

XX The invention relates to a novel method for the identification of a
 CC therapeutic compound. The method involves providing test cells that
 CC express a target protein containing a D5F domain and MAP kinase;
 CC culturing the cells in the presence of growth factor, cytokine, tumor
 CC promoter or oncogene, contacting the cells with a candidate compound; and
 CC assessing the binding of the MAP kinase to the D5F domain relative to the
 CC binding in the absence of the candidate compound. The invention further
 CC comprises a method for the identification of a therapeutic compound; a
 CC method for treatment of cancer, which involves administering a compound
 CC that inhibits the binding of a MAP kinase to the D5F domain of a target
 CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
 CC have the following activities: cytostatic, cardiovascular-gen., cardiant,
 CC vasotropic, hypotensive, antiarteriosclerotic, antiinflammatory,
 CC antiallergic, immunosuppressive, antibacterial, antislathmatic,
 CC dermatological, antidiabetic, gastrointestinal-gen., antilicer,
 CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,
 CC antipruritic, uropathic, antiparietic, hepatotropic, antianemic, muscular
 CC -gen., thyromimetic, antichyroid, gynecological, nephrotropic,
 CC hepatocytic, virucide, anti-HIV, anabolic, hypertensive, anorectic,
 CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,
 CC antidiabetic, antidiabetic, sedative, hypnotic, CNS-gen., and
 CC antifertility. The therapeutic compound may be used in the treatment
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.
 CC This sequence represents a cardiovascular therapy target peptide of the
 CC invention.

XX Sequence 15 AA;

Query Match 30.7%; Score 35; DB 9; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYRYPSRLG 10
 |::|||:|
 Db 4 DFDYPPAPAG 13

RESULT 13

ADW77792
 ID ADW77792 standard; peptide; 15 AA.

AC ADW77792;

DT 07-APR-2005 (first entry)

XX Human cancer therapy target peptide CBRA #2.

XX D5F domain; MAP kinase; cytostatic; cardiovascular-gen.; cardiant;
 KM vasotropic; hypotensive; antiarteriosclerotic; antiinflammatory;
 KM antiallergic; immunosuppressive; antibacterial; antislathmatic;
 KM dermatological; antidiabetic; gastrointestinal-gen.; antilicer;
 KM thrombolytic; neuroprotective; ophthalmological; antirheumatic;
 KM antipruritic; uropathic; antiparietic; hepatotropic; antianemic;
 KM muscular-gen.; thyromimetic; antichyroid; gynecological; nephrotropic;
 KM hepatocytic; virucide; anti-HIV; anabolic; hypertensive; anorectic;
 KM endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anticonvulsant;
 KM antidiabetic; antidiabetic; sedative; hypnotic; CNS-gen.;
 KM antifertility; cancer; cardiovascular disease; inflammation;
 KM metabolic disorder; neuropathy; sleep disorder.

XX Homo sapiens.

XX WO2005007090-A2.

XX 27-JUN-2005.

XX 02-JUL-2004; 2004WO-US021514.

XX 03-JUL-2003; 2003US-0484761P.

XX (HARD) HARVARD COLLEGE.

XX Blenis J, Murphy LO;

XX WPI; 2005-112720/12.

PT Identification of compound for treating e.g. cancer by culturing cells
 PT expressing target protein in the presence of growth factor, cytokine, the
 PT tumor promoter or oncogene and assessing binding after contacting with
 PT the compound.

XX Claim 11, Page 49; 104pp; English.

XX The invention relates to a novel method for the identification of a
 CC therapeutic compound. The method involves providing test cells that
 CC express a target protein containing a D5F domain and MAP kinase;
 CC culturing the cells in the presence of growth factor, cytokine, tumor
 CC promoter or oncogene, contacting the cells with a candidate compound; and
 CC assessing the binding of the MAP kinase to the D5F domain relative to the
 CC binding in the absence of the candidate compound. The invention further
 CC comprises a method for the identification of a therapeutic compound; a
 CC method for treatment of cancer, which involves administering a compound
 CC that inhibits the binding of a MAP kinase to the D5F domain of a target
 CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
 CC have the following activities: cytostatic, cardiovascular-gen., cardiant,
 CC vasotropic, hypotensive, antiarteriosclerotic, antiinflammatory,
 CC antiallergic, immunosuppressive, antibacterial, antislathmatic,
 CC dermatological, antidiabetic, gastrointestinal-gen., antilicer,
 CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,
 CC antipruritic, uropathic, antiparietic, hepatotropic, antianemic, muscular
 CC -gen., thyromimetic, antichyroid, gynecological, nephrotropic,
 CC hepatocytic, virucide, anti-HIV, anabolic, hypertensive, anorectic,
 CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,
 CC antidiabetic, antidiabetic, sedative, hypnotic, CNS-gen., and
 CC antifertility. The therapeutic compound may be used in the treatment
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
 CC disorders, neuropathy or a behavioural disorder, and a sleep disorder.
 CC This sequence represents a cancer therapy target peptide of the
 CC invention.

XX Sequence 15 AA;

Query Match 30.7%; Score 35; DB 9; Length 15;
 Best Local Similarity 50.0%; Pred. No. 2.9e+02;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYRYPSRLG 10
 |::|||:|
 Db 4 DFDYPPAPAG 13

RESULT 14

AAR37725
 ID AAR37725 standard; peptide; 18 AA.

AC AAR37725;

DT 25-MAR-2003 (revised)

DT 07-SEP-1993 (first entry)

XX Collagen-like polymer #8.

XX Recombinant; collagen-like polymer; CRP; tripeptide; helix; membrane;
 KM fibre; film; coating; triad sequence; collagen; mammalian; moulding;
 KM hydrogel; interchain linkage; colloid suspension.

XX OS Synthetic.
XX PN WO9310154-A1.
XX PD 27-MAY-1993.
XX PF 04-NOV-1992; 92WO-US009485.
XX PR 12-NOV-1991; 91US-00791960.
XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
XX PA Cappello J, Ferrari FA;
XX PI Cappello J, Ferrari FA;
XX DR WPI, 1993-182496/22.
XX High mol. wt. collagen-like protein polymers - capable of being produced
PT in unicellular microorganisms.
XX PS Disclosure; Page 11; 82pp; English.
XX CC The sequences given in AAR37718-32 are examples of recombinantly produced
CC collagen-like polymers (CLPs) which consist of repeated tripeptide
CC sequences selected from a wide range of GXY sequences, where X and Y can
CC be any amino acid. These polymers have molecular weights of >30 kD and
CC are able to form helices due to interchain linkages. These polymers pref.
CC contain a proportion of tripeptide triad sequences found in natural
CC collagens, pref. mammalian collagens. The CLPs impart unique
CC characteristics to materials such as fibres, membranes, films, coatings,
CC hydrogels, colloid suspensions and moulded articles. (Updated on 25-MAR-
CC 2003 to correct PN field.)
XX SQ Sequence 18 AA;

Query Match 30.3%; Score 34.5; DB 2; Length 18;
Best Local Similarity 72.7%; Pred. No. 4.3e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 5 PCSRGNPKAP 15
||| | | | | | | | | | | | | | | | |
DB 6 PCSR-GDPGAP 15

RESULT 15
AAR93332
ID AAR93332 standard; peptide; 18 AA.
XX
AC AAR93332;
XX
DT 25-MAR-2003 (revised)
DT 24-FEB-1996 (first entry)

XX DB Collagen-like polymer repetitive motif 8.

XX KM collagen; repetitive triad motif; recombinant production; photographic;
XX medical; structural; fibre.

XX OS Synthetic.

XX PN US5496712-A.

XX PD 05-MAR-1996.

XX PF 05-NOV-1992; 92US-00972032.

XX PR 06-NOV-1990; 90US-00609716.

XX PR 12-NOV-1991; 91US-00791960.

XX PA (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.

XX PI Cappello J, Ferrari FA;
XX

DR WPI, 1996-150728/15.
XX
XX PT Collagen-like polymers comprising repetitive triads - produced in
PT unicellular organisms with improved characteristics, useful in, e.g.
XX photographic and medical fibres.
XX PS Disclosure; Col 5; 43pp; English.

XX CC The invention concerns collagen-like polymers having repetitive triads
CC with reduced proline content, and where glycine is the initial amino acid
CC and the subsequent amino acids are varied. The choice of triads utilised
CC in a recombinant collagen-like polymer are chosen in order to affect
CC properties such as helix stability, hydration, solubility, gel point,
CC biodegradation and immunogenicity. Also considered is the level of
CC guanidine and cytosine nucleotides (due to levels of glycine and proline)
CC present in the genes encoding the polymers. As the gene is synthesised
CC there is opportunity for strands to loop out, single-stranded DNA to be
CC excised, recombination events to occur which can result in loss of
CC segments of the gene, and inefficient transcription and/or translation
CC (due to the presence of self-complementary sequences), hence genes of the
CC invention are designed to provide the advantageous properties of
CC collagen, while at the same time allowing for stable expression of high
CC mol. wt. collagen-like proteins. Triads of particular interest include
CC GAP, GPP, GAS, GPG, GAO, GPR, GPK, GAK, GAR, GBR,
CC GDR, GRP, GDA, GAN and GEA. The collagen-like polymers may impart new
CC characteristics, finding wide use in photographic, medical, structural
CC and fibre applications, and are capable of being produced in unicellular
CC microorganisms at high mol. wts. and in high efficiency. AAR33225-34 are
CC peptides defining a variety of repetitive triad motifs. The peptides are
CC useful as happens, to produce antisera or monoclonal antibodies specific
CC to the sequences which are then used for affinity purification,
CC identification of the polymers, etc. (Updated on 25-MAR-2003 to correct
CC PF field.)
XX SQ Sequence 18 AA;

Query Match 30.3%; Score 34.5; DB 2; Length 18;
Best Local Similarity 72.7%; Pred. No. 4.3e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

QY 5 PCSRGNPKAP 15
||| | | | | | | | | | | | | | | | |
DB 6 PCSR-GDPGAP 15

RESULT 16
AAM57681
ID AAM57681 standard; peptide; 18 AA.
XX
AC AAM57681;
XX
DT 27-AUG-1998 (first entry)

XX DB Collagen-like polymer fragment.

XX KM Collagen-like polymer; synthetic polymer; fibre coating;
XX prosthetic device; catalytic substance.

XX OS Synthetic.

XX PN US5773249-A.

XX PD 30-JUN-1998.

XX PF 02-MAY-1996; 96US-00642255.

XX PR 04-NOV-1986; 86US-00927258.

XX PR 29-OCT-1987; 87US-00114618.

XX PR 09-NOV-1988; 88US-00259429.

XX PR 06-NOV-1990; 90US-00609716.

XX PR 12-NOV-1991; 91US-00791960.

XX PR 05-NOV-1992; 92US-00972032.

XX PR 22-DEC-1995; 95US-00577046.

XX (PROT-) PROTEIN POLYMER TECHNOLOGIES INC.
 PA Ferrari FA, Cappello J;
 PI WPI, 1998-387004/33.
 DR WPI, 1998-387004/33.
 XX Recombinant collagen-like polymers - useful for making gels, films,
 PT fibres, etc.
 PS Disclosure, Col 6, 93pp; English.
 CC This sequence represents a fragment of a unnatural collagen-like polymer
 CC of the invention. The products may be used as films, fibres, moulded
 CC objects and admixed with other natural or synthetic polymers or coatings
 CC on fibres, films, labware or other surfaces, e.g. prosthetic devices. The
 CC polymers may be used for binding a wide variety of specific binding
 CC materials, as catalytic substances (where the amino acid sequence may
 CC specifically chelate a wide variety of elements), as purification media,
 CC composites, laminates or adhesives. They may also be combined with
 CC inorganic or organic materials such as carbon fibres, nylon fibres,
 CC nitrocellulose, etc., as flask coatings or in synthetic matrices for the
 CC growth and study of cells, as affinity columns or as supports for
 CC biological materials. The polymers have collagen-like properties, but may
 CC be easily expressed in micro-organisms in high efficiency. The new
 CC sequences can be tailored to give the desired properties
 SO Sequence 18 AA;
 QY Query Match 30.3%; Score 34.5; DB 2; Length 18;
 Best Local Similarity 72.7%; Pred. No. 4.3e+02;
 Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
 DB 5 PGSR-LGNPKRP 15
 6 PGSR-GDPGAP 15
 QY
 DB
 RESULT 17
 AAM00359
 ID AAM00359 standard; peptide; 14 AA.
 AC AAM00359;
 XX
 DT 01-OCT-2001 (first entry)
 DE Human protein fragment SEQ ID NO: 905.
 XX
 KM Human; single nucleotide polymorphism; SNP, paternity test;
 KM forensic test; aberrant protein expression.
 XX
 OS Homo sapiens.
 XX
 PN WO200151670-A2.
 PD 19-JUL-2001.
 PF 05-JAN-2001, 2001MO-US000322.
 PR 07-JAN-2000, 2000US-0174962P.
 XX
 PA (CURA-) CURAGEN CORP.
 PI Shinketsu RA, Leach MD;
 XX WPI, 2001-451871/48.
 DR N-PSDB, AAH89474.
 XX
 PT Isolated human polynucleotides containing single nucleotide
 PT polymorphisms, useful for the treatment and diagnosis of e.g. cancer,
 PT infection and diabetes.
 PS Disclosure, Page 364, 475pp; English.

XX The present invention relates to human nucleic acids containing single
 CC nucleotide polymorphisms (SNPs). These can be used in forensic and
 CC paternity tests, and to aid in the treatment of diseases associated with
 CC aberrant protein expression, including cancer, amyloidosis, diabetes,
 CC Alzheimer's disease, Down's syndrome, oedema, lupus (SLE), vasculitis,
 CC glomerulonephritis, haemolytic anaemia, thrombocytopenia, arthritis,
 CC meningitis, muscular disorders, dementia, neurological diseases, tuberculous
 CC sclerosis, male infertility, hypercalcaemia, blood pressure disorders,
 CC osteoporosis, pathogenic infections, hypercholesterolaemia, obesity or
 CC autoimmunity. The present sequence is a peptide encoded by a
 CC polymorphism-containing oligonucleotide fragment of the invention
 XX
 SO Sequence 14 AA;
 QY Query Match 29.8%; Score 34; DB 4; Length 14;
 Best Local Similarity 54.5%; Pred. No. 3.9e+02;
 Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 DB 1 DYRPPGSR-LGN 11
 4 DYRHPPEPLAN 14
 QY
 DB
 RESULT 18
 ADS71368
 ID ADS71368 standard; peptide; 15 AA.
 AC ADS71368;
 XX
 DT 02-DEC-2004 (first entry)
 DE Extensin peptide #1.
 XX
 KM Extensin; hydroxyproline-rich glycoprotein; HRGP, infection; cancer;
 KM immune response; synergistic effect; antimicrobial; cytostatic.
 XX
 OS Unidentified.
 XX
 FH Key Location/Qualifiers
 FT Modified-site 2..3 /label= Hyp
 FT /note= "Hydroxyproline"
 FT Modified-site 9..10 /label= Hyp
 FT /note= "Hydroxyproline"
 FT Modified-site 12 /label= Hyp
 FT /note= "Hydroxyproline"
 XX
 PN US6794495-B1.
 PD 21-SEP-2004.
 PP 18-OCT-1999, 99US-00419927.
 PR 19-OCT-1998, 98US-0104720P.
 XX
 PA (NEWN-) NEW NORDIC DANMARK APS.
 PI Sorensen MB;
 XX WPI, 2004-666364/65.
 DR
 PT Composition comprising an extensin and at least one pectin, is useful in
 PT the treatment of cancer.
 XX
 PS Claim 1; Col 8; 5pp; English.
 CC The invention relates to the composition which comprises the protein
 CC extensin [which is a hydroxyproline-rich glycoprotein (HRGP)] or a
 CC combination of pectin or polysaccharides found in the pectic molecule and
 CC extensin. The invention is useful for preventing or treating a broad

CC variety of disorders including infections and cancers that are associated
CC with a modulation of immune responses and has improved synergistic
CC effect. The present sequence is an extensin peptide.
XX

XX Sequence 15 AA;

Query Match 29.8%; Score 34; DB 8; Length 15;
Best Local Similarity 41.2%; Pred. No. 4.2e+02;
Matches 7; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 2 YEPGSRGNPKAPLYK 18
:|||:|:|:
DB 5 HEPY-----PPRPVYK 15

RESULT 19

ADL5704
ID ADE15704 standard; peptide; 20 AA.

XX ADE15704;

XX 29-JAN-2004 (first entry)

DE E. coli tridegin fragment SEQ ID 21.

XX tridegin; anticoagulant; inhibition; thrombin; factor Xa;
XX platelet aggregation; acetylsalicylic acid; heparin; heparinoid; hirudin;
XX bivalirudin; melagatran; eptifibatide; streptokinase; staphylokinase;
XX eminase; hementin; plasmin; tissue plasminogen activator; tPA; urokinase;
XX thrombolytic activity; transglutaminase inhibitor; factor XIII;
XX blood coagulation cascade.

XX Escherichia coli.

XX WO2003054194-A2.

XX 03-JUL-2003.

XX 20-DEC-2002; 2002WO-EP014684.

XX 21-DEC-2001; 2001DE-01063333.

XX 12-DEC-2002; 2002DE-01058159.

XX (CURA-) CURACYTE AG.

XX Gierstefen H, Stoeckel J, Pamp T, Ohlmann M;

XX WPI; 2003-533140/50.

XX New variants of tridegin, useful as anticoagulant and thrombolytic
XX agents, inhibit factor 13a and have e.g. improved stability against
XX aggregation.

XX Example 3; SEQ ID NO 21; 54pp; German.

XX This invention describes novel variants of the tridegin polypeptide which
XX may be formulated with at least one other agent, especially an
XX anticoagulant that acts by inhibition of thrombin, factor Xa and/or
XX platelet aggregation. The agent can be any of the following compounds
XX acetylsalicylic acid, (low-molecular weight) heparin, heparinoid,
XX hirudin, bivalirudin, melagatran, streptokinase, staphylokinase,
XX eminase, hementin, plasmin, tissue plasminogen activator (tPA) and
XX urokinase. The products of the invention have anticoagulant and
XX thrombolytic activity and inhibit transglutaminases, specifically factor
XX XIII, the last enzyme in the blood coagulation cascade. Compared with
XX wild-type tridegin the novel variants may be less prone to form
XX aggregates when expressed in Escherichia coli, form aggregates more
XX slowly when stored at lower temperatures, be protected against
XX proteolysis when expressed in Pichia pastoris, have greater inhibitory
XX activity, be produced in greater yield, have reduced immunogenicity
XX and/or have slower metabolic degradation after infection. Compositions
XX containing tridegin variants and other anticoagulants, specifically
XX tissue plasminogen activator and urokinase, show a synergistic effect for

CC lysis of blood clots. This sequence represents a wild-type tridegin
CC protein fragment used to construct the variants of the invention.
XX

XX Sequence 20 AA;

Query Match 29.8%; Score 34; DB 7; Length 20;
Best Local Similarity 43.8%; Pred. No. 5.8e+02;
Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 PGRSLGNPKAPLYKRP 20
:|||:|:|:
DB 2 PRSELKPKMDIYQRP 17

RESULT 20

ADL5703
ID ADE15703 standard; peptide; 20 AA.

XX ADE15703;

XX 29-JAN-2004 (first entry)

DE E. coli tridegin fragment SEQ ID 20.

XX tridegin; anticoagulant; inhibition; thrombin; factor Xa;
XX platelet aggregation; acetylsalicylic acid; heparin; heparinoid; hirudin;
XX bivalirudin; melagatran; eptifibatide; streptokinase; staphylokinase;
XX eminase; hementin; plasmin; tissue plasminogen activator; tPA; urokinase;
XX thrombolytic activity; transglutaminase inhibitor; factor XIII;
XX blood coagulation cascade.

XX Escherichia coli.

XX WO2003054194-A2.

XX 03-JUL-2003.

XX 20-DEC-2002; 2002WO-EP014684.

XX 21-DEC-2001; 2001DE-01063333.

XX 12-DEC-2002; 2002DE-01058159.

XX (CURA-) CURACYTE AG.

XX Gierstefen H, Stoeckel J, Pamp T, Ohlmann M;

XX WPI; 2003-533140/50.

XX New variants of tridegin, useful as anticoagulant and thrombolytic
XX agents, inhibit factor 13a and have e.g. improved stability against
XX aggregation.

XX Example 3; SEQ ID NO 20; 54pp; German.

XX This invention describes novel variants of the tridegin polypeptide which
XX may be formulated with at least one other agent, especially an
XX anticoagulant that acts by inhibition of thrombin, factor Xa and/or
XX platelet aggregation. The agent can be any of the following compounds
XX acetylsalicylic acid, (low-molecular weight) heparin, heparinoid,
XX hirudin, bivalirudin, melagatran, streptokinase, staphylokinase,
XX eminase, hementin, plasmin, tissue plasminogen activator (tPA) and
XX urokinase. The products of the invention have anticoagulant and
XX thrombolytic activity and inhibit transglutaminases, specifically factor
XX XIII, the last enzyme in the blood coagulation cascade. Compared with
XX wild-type tridegin the novel variants may be less prone to form
XX aggregates when expressed in Escherichia coli, form aggregates more
XX slowly when stored at lower temperatures, be protected against
XX proteolysis when expressed in Pichia pastoris, have greater inhibitory
XX activity, be produced in greater yield, have reduced immunogenicity
XX and/or have slower metabolic degradation after infection. Compositions
XX containing tridegin variants and other anticoagulants, specifically
XX tissue plasminogen activator and urokinase, show a synergistic effect for
XX lysis of blood clots. This sequence represents a wild-type tridegin

CC protein fragment used to construct the variants of the invention.
 XX Sequence 20 AA;
 SQ

Query Match 29.8%; Score 34; DB 7; Length 20;
 Best Local Similarity 43.8%; Pred. No. 5.8e+02;
 Matches 7; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 PGSRGPNKAPLYRKP 20
 DB 4 PRSELKPMDDIYQRP 19

RESULT 21
 ADM78278
 ID ADM78278 standard; peptide; 15 AA.
 AC ADM78278;
 XX
 XX
 DT 07-APR-2005 (first entry)
 DE Rat neuropathic therapy target peptide SHK2.
 XX
 XX DEF domain; MAP kinase; cytosolic; cardiovascular-gen.; cardiac;
 KM vasotrophic; hypotensive; antiarteriosclerotic; antiinflammatory;
 KM antiallergic; immunosuppressive; antibacterial; antitubercular;
 KM dermatological; antidiabetic; gastrointestinal-gen.; antitumor;
 KM thrombolytic; neuroprotective; ophthalmological; antirheumatic;
 KM antipruritic; uropathic; antipsoriatic; hepatotropic; antianemic;
 KM muscular-gen.; thyromimetic; antihypertensive; hepatotropic; antianemic;
 KM hepatotropic; virologic; anti-HIV; anabolic; hypertensive; anorectic;
 KM endocrine-gen.; neuroleptic; nootropic; antiparkinsonian; anorectic;
 KM antidepressant; antidiabetic; sedative; hypnotic; CNS-gen.;
 KM antileptile; cancer; cardiovascular disease; inflammation;
 KM metabolic disorder; neuropathy; sleep disorder.
 XX
 XX Rattus norvegicus.
 OS
 XX
 XX WO2005007090-A2.
 PN
 XX
 XX 27-JAN-2005.
 PD
 XX
 XX 02-JUL-2004; 2004WO-US021514.
 PF
 XX
 XX 03-JUL-2003; 2003US-0484761P.
 PR
 XX
 XX (HARD) HARVARD COLLEGE.
 PA
 XX
 XX Bientle J, Murphy LO;
 PI
 XX
 XX WPI; 2005-112720/12.
 DR
 XX
 XX Identification of compound for treating e.g. cancer by culturing cells
 PT expressing target protein in the presence of growth factor, cytokine,
 PT tumor promoter or oncogene and assessing binding after contacting with
 PT the compound.
 PT
 XX
 XX Claim 15; Page 67; 104pp; English.
 PS
 XX
 XX The invention relates to a novel method for the identification of a
 CC therapeutic compound. The method involves providing test cells that
 CC express a target protein containing a DBF domain and MAP kinase;
 CC culturing the cells in the presence of growth factor, cytokine, tumor
 CC promoter or oncogene; contacting the cells with a candidate compound; and
 CC assessing the binding of the MAP kinase to the DBF domain relative to the
 CC binding in the absence of the candidate compound. The invention further
 CC comprises a method for the identification of a therapeutic compound; a
 CC method for treatment of cancer, which involves administering a compound
 CC that inhibits the binding of a MAP kinase to the DBF domain of a target
 CC protein; and an antibody that specifically binds to phospho-T-325 c-Fos
 CC (preferably polyclonal or monoclonal). The novel therapeutic compounds
 CC have the following activities: cytostatic, cardiovascular-gen., cardiac,
 CC vasotrophic, hypotensive, antiarteriosclerotic, antiinflammatory,

CC antiallergic, immunosuppressive, antibacterial, antitubercular,
 CC dermatological, antidiabetic, gastrointestinal-gen., antitumor,
 CC thrombolytic, neuroprotective, ophthalmological, antirheumatic,
 CC antipruritic, uropathic, antipsoriatic, hepatotropic, antianemic,
 CC -gen., thyromimetic, antihypertensive, hepatotropic, anorectic,
 CC hepatotropic, virologic, anti-HIV, anabolic, hypertensive, anorectic,
 CC endocrine-gen., neuroleptic, nootropic, antiparkinsonian, anticonvulsant,
 CC antidepressant, antidiabetic, sedative, hypnotic, CNS-gen., and
 CC antileptile. The therapeutic compound may be used in the treatment
 CC of: cancer, cardiovascular disorders, inflammatory disorders, metabolic
 CC disorders, neuropathy or a behavioral disorder, and a sleep disorder.
 CC This sequence represents a neuropathic therapy target peptide of the
 CC invention.
 CC
 XX
 XX Sequence 15 AA;
 SQ

Query Match 29.4%; Score 33.5; DB 9; Length 15;
 Best Local Similarity 43.8%; Pred. No. 5e+02;
 Matches 7; Conservative 2; Mismatches 2; Indels 5; Gaps 1;

QY 2 YRPGSRGPNKAPLY 17
 DB 5 FRYPG-----PRKLY 15

RESULT 22
 AAU92598
 ID AAU92598 standard; peptide; 9 AA.
 XX
 XX AAU92598;
 AC
 XX
 XX 02-JUL-2002 (first entry)
 DT
 XX
 XX PHOR1-F5D6 peptide #336 tested for HLA binding.
 DE
 XX
 XX Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.
 KM
 XX
 XX Homo sapiens.
 OS
 XX
 XX WO200214501-A2.
 PN
 XX
 XX 21-FEB-2002.
 PD
 XX
 XX 17-AUG-2001; 2001WO-US025862.
 PF
 XX
 XX 17-AUG-2000; 2000US-0226241P.
 PR
 XX
 XX (AGEN-) AGENSYS INC.
 PA
 XX
 XX Hubert RS, Raitano AB, Paris M, Challita-Bid PM, Ge W,
 PI Jakobovits A;
 PI
 XX
 XX WPI; 2002-269193/31.
 DR
 XX
 XX Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of
 PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene
 PT products in tissue sample from subject and comparing it to normal sample.
 PT
 XX
 XX Claim 49; Page 189; 250pp; English.
 PS
 XX
 XX The present invention relates to the isolation of novel human genes
 CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene
 CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-
 CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6
 CC polynucleotide and polypeptide sequences are useful in diagnostic and
 CC therapeutic methods, and compositions for various cancers such as
 CC prostate cancer. The sequences are useful for inhibiting the growth of
 CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating
 CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can
 CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-
 CC A11 or PHOR1-F5D6 peptides tested for HLA binding
 CC
 XX
 XX Sequence 9 AA;
 SQ

Query Match 28.9%; Score 33; DB 5; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNPK 13
 | | | | |
 DB 2 GPRYGNPK 9

RESULT 23
 AAU92855
 ID AAU92855 standard; peptide; 10 AA.
 XX
 AC AAU92855;
 XX
 DT 02-JUL-2002 (first entry)
 XX
 DE PHOR1-F5D6 peptide #593 tested for HLA binding.
 XX
 KW Human; PHOR1-A11; PHOR1-F5D6; prostate cancer; cytostatic.
 XX
 OS Homo sapiens.
 XX
 PN WO200214501-A2.
 XX
 PD 21-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025862.
 XX
 PR 17-AUG-2000; 2000US-0226241P.
 XX
 PA (AGEN-) AGENSYS INC.
 XX
 PI Hubert RS, Raitano AB, Farris M, Challita-Bid PM, Ge W;
 PI Jakobovits A;
 XX
 DR WPI; 2002-269193/31.
 XX
 PT Monitoring PHOR1-A11/PHOR1-F5D6 gene products for monitoring presence of
 PT cancer in subject, by determining status of PHOR1-A11/PHOR1-F5D6 gene
 PT products in tissue sample from subject and comparing it to normal sample.
 XX
 PS Claim 49; Page 198; 250pp; English.
 XX
 CC The present invention relates to the isolation of novel human genes
 CC designated PHOR1-A11 and PHOR1-F5D6 and their encoded proteins. The gene
 CC encoding PHOR1-A11 maps to chromosome 1q23, and the gene encoding PHOR1-
 CC F5D6 maps to chromosome 7q33-q35. The PHOR1-A11 and PHOR1-F5D6
 CC polynucleotide and polypeptide sequences are useful in diagnostic and
 CC therapeutic methods, and compositions for various cancers such as
 CC prostate cancer. The sequences are useful for inhibiting the growth of
 CC cancer cells that express PHOR1-A11 or PHOR1-F5D6 and for treating
 CC cancer. The PHOR1-A11 or PHOR1-F5D6 polypeptide or a fragment thereof can
 CC be used to elicit an immune response. AAU91563-AAU92962 represent PHOR1-
 CC A11 or PHOR1-F5D6 peptides tested for HLA binding
 XX
 SQ Sequence 10 AA;
 XX

Query Match 28.9%; Score 33; DB 5; Length 10;
 Best Local Similarity 75.0%; Pred. No. 3.8e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNPK 13
 | | | | |
 DB 1 GPRYGNPK 8

RESULT 24
 ADS92104
 ID ADS92104 standard; peptide; 14 AA.
 XX
 AC ADS92104;

XX 02-DEC-2004 (first entry)
 DT
 XX
 DE Human odorant receptor (OR) peptide fragment SeqID9.
 XX
 KW antibody; antibody complex; modulating chemosensation; transgenic animal;
 KW antigenic site; chemosensation enhancement; taste sensation;
 KW smell sensation; OR; odorant receptor; human.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 1
 FT /note= "Optionally absent"
 XX
 PN WO2003102030-A1.
 XX
 PD 11-DEC-2003.
 XX
 PF 20-MAY-2003; 2003WO-IL000409.
 XX
 PR 20-MAY-2002; 2002US-0382059P.
 XX
 PR 04-MAR-2003; 2003US-0451639P.
 XX
 PA (TVPDT-) TWD TASTE VIRTUAL DIMENSIONS INC.
 XX
 PI Ben-Sasson S;
 XX
 DR WPI; 2004-053430/05.
 XX
 PT New antibody or complex of two or more antibodies, useful for preparing a
 PT composition for modulating chemosensation.
 XX
 PS Disclosure; SEQ ID NO 9; 48pp; English.
 XX
 CC This invention relates to a novel antibody or complex of two or more
 CC antibodies for modulating chemosensation. Claims were also included for a
 CC composition comprising the antibody or complex of antibodies; making an
 CC antibody or complex of antibodies; a transgenic non-human animal that is
 CC genetically engineered to produce an antibody that modulates
 CC chemosensation; selecting a candidate antigenic site; and enhancing
 CC chemosensation. The antibody or complex of two or more antibodies is
 CC useful for preparing a composition for modulating chemosensation, in
 CC particular for use in modulating taste sensation or smell sensation. The
 CC present sequence is that of a human peptide which is related to the
 CC invention.
 XX
 SQ Sequence 14 AA;
 XX

Query Match 28.9%; Score 33; DB 8; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.6e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNPK 13
 | | | | |
 DB 2 GPRYGNPK 9

RESULT 25
 ABP55617
 ID ABP55617 standard; peptide; 16 AA.
 XX
 AC ABP55617;
 XX
 DT 20-FEB-2003 (first entry)
 XX
 DE Human cytokine peptide IL17beta.
 XX
 KW DPP10; dipeptidyl peptidase; prolyl oligopeptidase; enzyme; asthma;
 KW antiinflammatory; antiaesthetic; antipsoriatic; antiarthritic;
 KW antirheumatic; vaccine; gene therapy; inflammatory disease;
 KW inflammatory bowel disease; atopy; rheumatoid arthritis; psoriasis;
 KW chromosome 2q14.

XX Homo sapiens.
 OS
 XX
 PN MO200286113-A2.
 PD
 XX 31-OCT-2002.
 PF
 XX 24-APR-2002; 2002MO-GB001887.
 PR
 XX 24-APR-2001; 2001GB-00010044.
 PR 24-APR-2001; 2001GB-00010046.
 PR 12-OCT-2001; 2001GB-00024575.
 PR 12-OCT-2001; 2001GB-00024594.
 XX
 PA (ISIS-) ISIS INNOVATIONS LTD.
 PI
 XX Cookson WOCM, Moffat MF, Allen M, Iench N;
 DR MPI; 2003-093132/08.
 XX
 PT New nucleic acid sequence comprising DPP10 mRNA, useful for the
 PT manufacture of a medicament for regulating DPP10 protein expression or
 PT for preventing or treating inflammatory disease e.g., inflammatory bowel
 PT disease.
 XX
 XX Example 2; Fig 19; 321pp; English.
 PS
 XX The present invention describes a new isolated nucleic acid sequence (I)
 CC comprising a DPP10 mRNA sequence. DPP10 is a dipeptidyl peptidase (also
 CC known as prolyl oligopeptidase). (I) has antiinflammatory, antiasthmatic,
 CC antihistatic, antiallergic and antirheumatic activities, and can be
 CC used in vaccines and gene therapy. A composition comprising (I) can be
 CC used for the manufacture of a medicament for regulating DPP10 expression
 CC or for preventing or treating inflammatory disease e.g., inflammatory
 CC bowel disease, asthma, atopy, rheumatoid arthritis or psoriasis. (I) can
 CC also be used in an assay for detecting or measuring DPP10 in a sample. A
 CC host cell comprising (I) can be used for producing recombinant DPP10 gene
 CC products, or in drug screening systems to identify agents for diagnosis
 CC or treatment of individuals having or susceptible to inflammatory
 CC disease. Human DPP10 is located on chromosome 2, more specifically
 CC chromosome 2q14. ABQ84254 to ABQ84612 and ABP55569 to ABP55629 represent
 CC sequences used in the exemplification of the present invention
 CC
 XX Sequence 16 AA:
 SQ
 Query Match 28.9%; Score 33; DB 6; Length 16;
 Best Local Similarity 54.5%; Pred. No. 6.5e+02;
 Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 9 LGNPKAPLYKR 19
 DB 5 LGQPRSPKSKR 15
 RESULT 26
 ADD24038
 ID ADD24038 standard; peptide; 16 AA.
 AC
 XX ADD24038;
 DT 15-JAN-2004 (first entry)
 XX
 DE Breast cancer membrane protein (BCMP) peptide SEQ ID NO:1004.
 XX
 KW breast cancer; screening; diagnosis; breast cancer therapy;
 KW breast cancer membrane protein; BCMP; cytosolic; vaccine; human.
 XX
 OS Homo sapiens.
 XX
 KW WO2003087831-A2.
 PN
 XX 23-OCT-2003.
 PD
 XX

PF 10-APR-2003; 2003MO-GB001559.
 XX
 XX 11-APR-2002; 2002GB-00008331.
 PR
 XX (OXFO-) OXFORD GLYCOSCIENCES UK LTD.
 PA
 XX Hudson LJ, Stamps AC, Terrett JA;
 PI
 XX MPI; 2003-845381/78.
 DR
 XX
 XX Screening, diagnosing and/or treating breast cancer by detecting a change
 PT in expression or activity of a breast cancer membrane protein (BCMP)
 PT polypeptide or encoding nucleic acid molecule.
 PS
 XX Example; SEQ ID NO 1004; 81pp; English.
 XX
 XX The present invention describes a method of screening for and/or
 CC diagnosing breast cancer in a subject, and/or monitoring the
 CC effectiveness of breast cancer therapy. The method comprises detecting
 CC and/or quantifying in a biological sample obtained from the subject a
 CC breast cancer membrane protein (BCMP) polypeptide and a nucleic acid
 CC molecule. Also described: (1) an antibody, its functionally-active
 CC fragment, derivative or analogue, that specifically binds to one or more
 CC of the BCMP polypeptide; (2) a diagnostic kit comprising a capture
 CC reagent specific for an BCMP polypeptide, reagents and instructions for
 CC use; (3) a method for screening for anti-breast cancer agents that
 CC interact with the BCMP polypeptide, comprising contacting the polypeptide
 CC with a candidate agent, and determining whether or not the candidate
 CC agent interacts with the polypeptide; (4) a method for screening for anti-
 CC breast cancer agents that modulate the expression or activity of an BCMP
 CC polypeptide or the nucleic acid molecule cited above, comprising
 CC comparing the expression or activity of the polypeptide or nucleic acid
 CC molecule, in the presence and absence of a candidate agent or in the
 CC presence of a control agent, and determining whether the candidate agent
 CC causes the expression or activity of the polypeptide or nucleic acid
 CC molecule to change; and (5) an agent identified by the method of (3) or
 CC (4), which interacts with the polypeptide or causes the expression or
 CC activity of the polypeptide, or the expression of the nucleic acid
 CC molecule to change. BCMPs have cytostatic activities, and can be used in
 CC vaccines. The BCMP polypeptide, nucleic acid molecule, antibody, agent or
 CC their derivatives, are useful in the manufacture of a medicament for the
 CC treatment of breast cancer, where the composition is a vaccine. The
 CC present sequence represents a BCMP peptide which is used in the
 CC exemplification of the present invention.
 CC
 XX Sequence 16 AA:
 SQ
 Query Match 28.9%; Score 33; DB 7; Length 16;
 Best Local Similarity 50.0%; Pred. No. 6.5e+02;
 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 5 PCSRLGNPKAPL 16
 DB 4 PCGMAGTFLRPL 15
 RESULT 27
 AAP80012
 ID AAP80012 standard; protein; 17 AA.
 AC
 XX AAP80012;
 DT 25-MAR-2003 (revised)
 DT 19-SEP-1990 (first entry)
 XX
 DE Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of
 DE herpes simplex virus type 1 (HSV1) glycoprotein B (gB).
 XX
 XX Herpes simplex virus type 1 glycoprotein B; vaccines;
 KW immunogenic synthetic peptide.
 XX
 OS Herpes simplex virus type 1.
 XX

```

FH Key Location/Qualifiers
FT Misc-difference 1 /label= OTHER
FT /note= "Ac-Lys"
FT Misc-difference 2 /label= Nle
FT /label= Nle
FT Misc-difference 16 /label= Nle
FT /label= Nle
FT Misc-difference 17 /label= OTHER
FT /note= "L-NH2"
XX
XX US4761470-A.
XX
XX 02-AUG-1988.
XX
XX 10-APR-1987; 87US-00036651.
XX
XX 16-DEC-1985; 85US-00809452.
XX
XX (MERI ) MERCK & CO INC.
XX
XX PA
XX PI Emini EA, Larson VM, Boger JS;
XX DR WPI; 1988-234840/33.
XX
XX New synthetic oligopeptide immunogens and their conjugates - used for
XX inducing prodn. of antibodies against herpes simplex virus type 1.
XX
XX Claim 3; Page 10; 6pp; English.
XX
XX Immunogenic synthetic peptides of this formula and their salts are new.
XX Also new are conjugates of the peptides covalently bonded to a carrier
XX protein or synthetic polymer. The peptides are immunogens for inducing
XX prodn. of HSV1 neutralising antibodies and so are useful in vaccines.
XX (Updated on 25-MAR-2003 to correct PD field.)
XX
XX SQ Sequence 17 AA;

Query Match 28.9%; Score 33; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 6.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
Db 1 KLGDPRKKNKRP 13

RESULT 28
AAP80013
ID AAP80013 standard; protein; 17 AA.
XX
XX AAP80013;
XX
XX 25-MAR-2003 (revised)
XX 19-SBP-1990 (first entry)
XX
XX Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of
XX herpes simplex virus type 1 (HSV1) glycoprotein B (gB).
XX
XX Herpes simplex virus type 1 glycoprotein B; vaccines;
XX immunogenic synthetic peptide.
XX
XX Herpes simplex virus type 1.
XX
XX Key Location/Qualifiers
XX Misc-difference 1 /label= OTHER
XX /note= "Ac-Lys"
XX Misc-difference 2 /label= Nle
XX /label= Nle
XX Misc-difference 2 /label= OTHER
XX /label= OTHER

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```

FT /note= "p-DenzyIbenzoYL-L"
FT Misc-difference 16 /label= Nle
FT /label= Nle
FT Misc-difference 17 /label= OTHER
FT /note= "L-NH2"
XX
XX US4761470-A.
XX
XX 02-AUG-1988.
XX
XX 10-APR-1987; 87US-00036651.
XX
XX 16-DEC-1985; 85US-00809452.
XX
XX (MERI ) MERCK & CO INC.
XX
XX PA
XX PI Emini EA, Larson VM, Boger JS;
XX DR WPI; 1988-234840/33.
XX
XX New synthetic oligopeptide immunogens and their conjugates - used for
XX inducing prodn. of antibodies against herpes simplex virus type 1.
XX
XX Claim 3; Page 10; 6pp; English.
XX
XX Immunogenic synthetic peptides of this formula and their salts are new.
XX Also new are conjugates of the peptides covalently bonded to a carrier
XX protein or synthetic polymer. The peptides are immunogens for inducing
XX prodn. of HSV1 neutralising antibodies and so are useful in vaccines.
XX (Updated on 25-MAR-2003 to correct PD field.)
XX
XX SQ Sequence 17 AA;

Query Match 28.9%; Score 33; DB 1; Length 17;
Best Local Similarity 46.2%; Pred. No. 6.9e+02;
Matches 6; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
Db 1 KLGDPRKKNKRP 13

RESULT 29
AAV32877
ID AAV32877 standard; peptide; 18 AA.
XX
XX AAV32877;
XX
XX 02-NOV-1999 (first entry)
XX
XX Fibronectin protein heparin II binding domain peptide H-1.
XX
XX Fibronectin; extracellular matrix. Open wound healing; IIRCS domain;
XX acute gaping cutaneous wound; chronic cutaneous ulcer; therapy;
XX wound healing promoter; cell binding domain; heparin II binding domain.
XX
XX Homo sapiens.
XX
XX WO9942117-A1.
XX
XX 26-AUG-1999.
XX
XX 10-FEB-1999; 99WO-US002872.
XX
XX 18-FEB-1998; 98US-00025622.
XX
XX (UWNY ) UNIV NEW YORK STATE RES FOUND.
XX
XX Clark RA, Greiling D;
XX
XX WPI; 1999-527415/44.
XX

```

PT New extracellular matrix used to accelerate healing of acute gaping
 CC cutaneous wounds and chronic cutaneous ulcers.
 XX
 XX
 PS Claim 10; Page 19; 43pp; English.
 CC This sequence represents a fibronectin protein fragment used in the
 CC extracellular matrix of the invention. The extracellular matrix comprises
 CC two or more fibronectin domains in a backbone matrix, and is used to
 CC enhance wound healing. The fibronectin domain peptides used are
 CC preferably from the IICS domain, the cell binding domain, or the heparin
 CC II binding domain of human fibronectin. The matrix facilitates wound
 CC healing by providing an environment that intrinsically recruits new
 CC tissue cells to the wound site. The new matrix is useful for facilitating
 CC wound healing, especially useful for treating open wounds such as acute
 CC gaping cutaneous wounds and chronic cutaneous ulcers. The problem of
 CC chronic, non-healing wounds is severe. These open wounds require long-
 CC term care and procedures that are costly and labour intensive.
 CC Furthermore, these wounds have a severe impact on the patients' quality of
 CC life. Prior compositions and matrices have not been useful or cost
 CC effective. The present invention provides a matrix for wound healing that
 CC meets these requirements, and overcomes the deficiencies of the prior
 CC matrices
 CC
 SQ Sequence 18 AA;
 Query Match 28.9%; Score 33; DB 2; Length 18;
 Best Local Similarity 42.1%; Pred. No. 7.4e+02;
 Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;
 QY 2 YEYSGRLGNPKAPLYKRP 20
 DB 1 YEKRGs----PRREVPRP 15
 RESULT 30
 ID AAY32865
 AAY32865 standard; peptide; 18 AA.
 AC AAY32865;
 DT 02-NOV-1999 (first entry)
 XX
 DE Fibronectin protein heparin II binding domain peptide H-I.
 XX
 KM Fibronectin; extracellular matrix; wound healing promoter; IICS domain;
 KM cell binding domain; heparin II binding domain; haemostasis; therapy;
 KM surgical incisional wound; traumatic wound; radiation wound;
 KM cancer extirpation; venous leg ulcer; diabetic ulcer; pressure ulcer.
 XX
 OS Homo sapiens.
 XX
 PN WO942126-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 10-FEB-1999; 99WO-US002873.
 XX
 PR 18-FEB-1998; 98US-00025706.
 XX
 PA (UNYNY) UNIV NEW YORK STATE RES FOUND.
 XX
 PI Clark RA, Grelling D, Gallit J;
 XX
 DR WPI; 1999-527421/44.
 XX
 PT Extracellular matrix for promoting wound healing containing recombinant
 PT fibronectin-derived peptide and backbone matrix.
 XX
 PS Claim 10; Page 21; 48pp; English.
 XX
 CC This sequence represents a fibronectin protein fragment used in the
 CC extracellular matrix (A) of the invention. (A) is used for promoting
 CC wound healing, and comprises a recombinant fibronectin peptide.

CC containing peptide fragments from at least two fibronectin domains, and a
 CC backbone matrix. The fibronectin domain peptides used are preferably from
 CC the IICS domain, the cell binding domain, or the heparin II binding
 CC domain of human fibronectin. (A) provides haemostasis and an environment
 CC that recruits new tissue cells to the site of the wound. (A) is used to
 CC promote healing of acute or chronic wounds, e.g. surgical incisional
 CC wounds, traumatic wounds, radiation wounds, cancer extirpations, venous
 CC leg ulcers, diabetic ulcers and pressure ulcers
 XX
 SQ Sequence 18 AA;
 Query Match 28.9%; Score 33; DB 2; Length 18;
 Best Local Similarity 42.1%; Pred. No. 7.4e+02;
 Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;
 QY 2 YEYSGRLGNPKAPLYKRP 20
 DB 1 YEKRGs----PRREVPRP 15
 RESULT 31
 ID AAB62425
 AAB62425 standard; peptide; 19 AA.
 AC AAB62425;
 DT 09-JUL-2001 (first entry)
 XX
 DE Human SAPL peptide fragment.
 XX
 KM SAPL; SIT4; SIT4 associated proteins like; human; antidiabetic;
 KM sporulation-induced transcript 4; SAPL; SAPL; gene therapy; IDDM;
 KM insulin-dependent diabetes mellitus; epitope.
 XX
 OS Homo sapiens.
 XX
 PN WO200129213-A1.
 XX
 PD 26-APR-2001.
 XX
 PF 19-OCT-2000; 2000WO-GB004027.
 XX
 PR 19-OCT-1999; 99US-0160400P.
 XX
 PA (WELL) WELLCOME TRUST LTD.
 PA (MERI) MERCK & CO INC.
 XX
 PI Todd JA, Twells RCJ, Hess JW, Hey P, Hey P, Caskey CT;
 PI Hammond H, Metzker ML;
 XX
 DR WPI; 2001-300338/31.
 XX
 PT Isoforms of novel gene arising from alternative splicing and encoding
 PT highly related proteins termed as SAPL and SAPLb, from the IDDM locus
 PT on human chromosome 11q13, useful for treating IDDM and other diseases.
 XX
 PS Claim 22; Page 106; 129pp; English.
 XX
 CC The invention relates to SAPL (SIT4-(sporulation-induced transcript4)
 CC associated proteins-like) polypeptide, selected from SAPL polypeptide
 CC isoforms and SAPLb polypeptide isoforms. The SAPL polynucleotides are
 CC useful in gene therapy for treating and preventing insulin-dependent
 CC diabetes mellitus (IDDM). Fragments of the SAPL DNA are useful as primers
 CC and probes. The SAPL polypeptides are useful in screening for a substance
 CC e.g., a peptide or chemical compound, which interacts and/or binds with
 CC them. The present sequence represents a fragment of the SAPL protein,
 CC that can act as an epitope for raising antibodies
 XX
 SQ Sequence 19 AA;
 Query Match 28.9%; Score 33; DB 4; Length 19;
 Best Local Similarity 54.5%; Pred. No. 7.8e+02;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15
 | | | | |
 DB 5 PEORTCQPSAP 15

RESULT 32

ABP74734
 ID ABP74734 standard; peptide; 19 AA.
 XX

AC ABP74734;
 XX

DT 03-FEB-2003 (first entry)
 XX

DE Proteome analysis related peptide #19.
 XX

KW Proteome analysis; isolation; determination; diagnostic assay; detection;
 KW protein marker; identification; metastatic; invasive cancer;
 KW differential expression; signalling pathway; chromatography.
 XX

OS Homo sapiens.
 OS Synthetic.
 XX

PN WO200277016-A2.
 XX

PD 03-OCT-2002.
 XX

PF 22-MAR-2002; 2002WO-EP003368.
 XX

PR 22-MAR-2001; 2001US-0278171P.
 XX

PR 12-SEP-2001; 2001US-0318749P.
 XX

PR 20-SEP-2001; 2001US-0323999P.
 XX

(VLA-) VLAAMS INTERNUNIVERSITAIR INST BIOTECHNOG.

PI Vandekerckhove J, Gevaert K;
 XX

DR WPI; 2003-067379/06.
 XX

PT Method for isolation of peptides from complex mixture of peptides
 PT involves specific chemical and/or enzymatic alteration of at least one
 PT type of peptide.
 XX

PS Example 19; Page 138; 193pp; English.
 XX

CC The present invention describes a method (M1) for the isolation of a
 CC subset of peptides from a protein peptide mixture (P1). M1 involves: (a)
 CC separating the protein peptide mixture into fractions of peptides via
 CC chromatography; (b) chemically, or enzymatically, or chemically and
 CC enzymatically, altering at least one amino acid of at least one of the
 CC peptides in each fraction, thereby generating a subset of altered
 CC peptides; and (c) isolating the altered (flagged) peptides out of each
 CC fraction via chromatography, where the chromatography of steps (a) and
 CC (c) is performed with the same type of chromatography. M1 can be used for
 CC the isolation and determination of peptides from protein peptide
 CC mixtures. M1 can also be used in diagnostic assays for detection of the
 CC presence, the absence or a variation in expression level of at least one
 CC protein marker or a specific set of proteins indicative of a disease
 CC state. M1 can be used for identifying target proteins present in
 CC metastatic and invasive cancers, in differential expression of proteins
 CC in transgenic mice, identification of proteins that are upregulated or
 CC down regulated in disease tissues, in identification of intracellular
 CC changes in cells with physiological changes such as metabolic shift, in
 CC the identification of biomarkers in cancers and in the identification of
 CC signalling pathways. The method is gel-free methodology for qualitative
 CC and quantitative proteome analysis without the need for multidimensional
 CC chromatography and without the use of affinity tags. ABP74714 to ABP75190
 CC represent peptide sequences used in the exemplification of the present
 CC invention
 XX

SO Sequence 19 AA;
 XX

Query Match 28.9%; Score 33; DB 6; Length 19;

Best Local Similarity 46.2%; Pred. No. 7.8e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DYEPGSRGNPK 13
 | | | | |
 DB 7 DLSTPDVAVGNPK 19

RESULT 33

AD513312
 ID AD513312 standard; peptide; 19 AA.
 XX

AC AD513312;
 XX

DT 16-DEC-2004 (first entry)
 XX

DE Human rheumatoid arthritis marker peptide - SEQ ID 103.
 XX
 KW Rheumatoid arthritis; marker; antiinflammatory; antiarthritic.
 XX

OS Homo sapiens.
 OS WO2004082617-A2.
 XX

PN WO2004082617-A2.
 XX

PD 30-SEP-2004.
 XX

PF 15-MAR-2004; 2004WO-US007880.
 XX

PR 14-MAR-2003; 2003US-0455037P.
 XX

PR (SURRE-) SURREMED INC.
 XX

PI Kantor AB, Becker CH, Schulman H;
 XX

DR WPI; 2004-690929/67.
 XX

PT New isolated marker for rheumatoid arthritis, useful in preparing a
 PT composition for diagnosing or treating rheumatoid arthritis.
 XX

PS Claim 1; SEQ ID NO 103; 184pp; English.
 XX

CC The invention relates to a novel isolated marker for rheumatoid arthritis
 CC selected from one of many (around 400) markers defined in the
 CC specification. Rheumatoid arthritis is a chronic inflammatory disorder of
 CC the small joints which is estimated to affect 2.1 million people in the
 CC United States alone. Current approaches to treat the disease include the
 CC use of non-steroidal antiinflammatory drugs (NSAIDs), which may reduce
 CC pain, swelling and inflammation, and disease-modifying anti-rheumatic
 CC drugs (DMARDs), which act to slow the progression of the disease and
 CC avoid further joint injury. These drugs are associated with a number of
 CC serious side effects and the search for improved therapeutics is a
 CC subject of active research. The marker of the invention demonstrates
 CC antiarthritic activity and may be useful in preparing a composition for
 CC diagnosing or treating rheumatoid arthritis. The current sequence is that
 CC of a human rheumatoid arthritis marker peptide of the invention.
 XX

SO Sequence 19 AA;
 XX

Query Match 28.9%; Score 33; DB 8; Length 19;
 Best Local Similarity 46.2%; Pred. No. 7.8e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 1 DYEPGSRGNPK 13
 | | | | |
 DB 7 DLSTPDVAVGNPK 19

RESULT 34

ADY39949
 ID ADY39949 standard; peptide; 19 AA.
 XX

AC ADY39949;
 XX

DT 19-MAY-2005 (first entry)
 XX
 DE Human plasma polypeptide (HPP) fragment #129.
 XX
 KW Human plasma polypeptide; protein secretion; plasma protein; cancer;
 KW hyperplasia; neurodegeneration; disorder of iron metabolism;
 KW metabolic disorder; fibrosis; prostate hyperplasia;
 KW congenital adrenal hyperplasia; psoriasis; inflammation;
 KW spinal cord injury; Alzheimers disease; Parkinsons disease;
 KW multiple sclerosis; motor neurone disease; peripheral neuropathy;
 KW Guillain Barre syndrome; diabetic neuropathy; demyelinating disease;
 KW hemochromatosis; thalassemia; iron overload; anemia; sickle cell anemia;
 KW diabetes; amyloidosis; cystostatic; antiinflammatory; antiproliferative;
 KW CNS-Gen.; neuroprotective; nootropic; antiparaneonian; antidiabetic;
 KW ophthalmological; hemostatic; antianemic.
 XX
 OS Homo sapiens.
 XX
 PN WO2005019825-A2.
 XX
 PD 03-MAR-2005.
 XX
 PF 19-AUG-2004; 2004WO-EP009323.
 XX
 PR 20-AUG-2003; 2003US-0496966P.
 XX
 PA (XENO-) XENOVA LTD.
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 XX
 PI Argoud-Puy G, Bedere N, Bouguetere L, Cusin I, Mahe B;
 PI Mknjad A, Ruffe S, Rose K, Saudrats C, Scherer A, Papotian R;
 PI Dengler UJ, Croft LJ;
 XX
 DR WPI; 2005-214290/22.
 XX
 PT Detecting a Human Plasma Polypeptide (HPP) comprises contacting a
 PT biological sample with an HPP-binding adsorbent.
 XX
 PS Disclosure, SEQ ID NO 129; 284pp; English.
 XX
 CC The invention relates to a method of detecting a Human Plasma Polypeptide
 CC (HPP) comprising contacting a biological sample with an HPP-binding
 CC adsorbent and detecting and/or quantifying binding of an HPP to the HPP-
 CC binding adsorbent. The invention also relates to a protein array
 CC comprising an adsorbent specific for at least one HPP, a method of
 CC detecting an abnormal concentration of at least one HPP in an individual,
 CC a pharmaceutical composition comprising an amount of HPP-38, HPP-13,
 CC HPP23 or GPR101 polypeptide and a pharmaceutical carrier, a method of
 CC treating cancer, a disease or condition associated with hyperplasia,
 CC neurodegeneration, iron balance or iron transport, a disease associated
 CC with dysregulated serum glucose or a metabolic disorder, a method of
 CC identifying a modulator of a cancer disease, a disease or condition
 CC associated with hyperplasia, neurodegeneration, iron balance or iron
 CC transport or a disease associated with dysregulated serum glucose, a
 CC method of diagnosing or diagnosing a cancer disease, a disease or
 CC condition associated with hyperplasia, neurodegeneration, iron balance or
 CC iron transport or a disease associated with dysregulated serum glucose
 CC and a method of reducing blood glucose levels in a mammal, including a
 CC human. The method is useful for detecting an HPP. The polypeptides,
 CC compositions and methods are useful for diagnosing, diagnosing or
 CC treating a cancer disease, a disease or condition associated with
 CC hyperplasia (e.g. fibrosis, prostate hyperplasia, adrenal hyperplasia or
 CC psoriasis), a disease or condition associated with neurodegeneration
 CC (e.g. spinal cord injuries or CNS injuries, Alzheimers disease,
 CC Parkinsons disease, multiple sclerosis, motor neurone disease,
 CC neuropathy, Guillain Barre syndrome, diabetic neuropathy or demyelinating
 CC disease), a disease or condition associated with iron balance or iron
 CC transport (e.g. hemochromatosis, thalassemia, iron overload, anemia or
 CC sickle cell anemia), a disease associated with dysregulated serum glucose
 CC (e.g. diabetes) or a metabolic disorder (e.g. amyloidosis). This sequence
 CC represents an HPP fragment of the invention.
 XX

SO Sequence 19 AA;
 Query Match 28.9%; Score 33; DB 9; Length 19;
 Best Local Similarity 46.2%; Pred. No. 7.8e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 DB 7 DISTPDVWGNPK 19
 QY 1 DYEPPGSRGNNPK 13
 DB 7 DISTPDVWGNPK 19
 RESULT 35
 AEA33956
 ID AEA33956 standard; peptide; 19 AA.
 XX
 AC AEA33956;
 XX
 DT 11-AUG-2005 (first entry)
 XX
 DE Mass spectrometry peptide, SEQ ID NO:29.
 XX
 KW mass spectrometry; protein sequencing.
 XX
 OS Homo sapiens.
 XX
 PN WO2005052563-A1.
 XX
 PD 09-JUN-2005.
 XX
 PF 19-NOV-2004; 2004WO-US839932.
 XX
 PR 20-NOV-2003; 2003US-0523643P.
 XX
 PA (INDV) UNIV INDIANA RES & TECHNOLOGY CORP.
 PA
 PI Reilly JP, Beardsley RL;
 XX
 DR WPI; 2005-418032/42.
 XX
 PT Preparing derivatized peptides to enhance mass spectral analysis of
 PT peptide by providing composition comprising peptide and labeling N-
 PT terminus of peptide with compound chosen from acetamidine and
 PT propionamide group.
 XX
 PS Example 3; SEQ ID NO 29; 53pp; English.
 XX
 CC The invention relates to a method of preparing (M1) derivatized peptides
 CC to enhance mass spectral analysis of peptide-containing compositions,
 CC comprising providing a composition comprising a peptide and labeling the
 CC N-terminus of the peptide with a compound chosen from an acetamidine group
 CC and a propionamide group. Also disclosed are: a set of modified tryptic
 CC peptides (I) comprising a first and second pool of peptides, where the N-
 CC terminus of the first and second pool peptides are labeled with an
 CC acetamidine group and a propionamide group, respectively; and a method
 CC of identifying a protein or peptide by searching a genomic database using
 CC sequence information derived by directly interpreting mass spectral data.
 CC (M1) further involves blocking lysine residues of the peptide or protein
 CC with guanidiniumurea. The guanidiniumurea is performed with S-
 CC methylisothiourea or O-methylisourea. N-termini are labeled with an
 CC acetamidine group utilizing S-methyl thioacetimidate. N-termini are
 CC labeled with a propionamide group utilizing S-methyl
 CC thiopropionimidate. (M1) further involves dividing the peptide
 CC composition into first and second pool of peptides, where the labeling
 CC step involves labeling the N-terminus of the peptides of the first pool of
 CC peptides with an acetamidine or amide group and labeling the N-terminus
 CC of the peptides of the second pool of peptides with a propionamide or
 CC amide group. The present sequence represents a peptide used to
 CC demonstrate the method of the invention.
 XX
 SO Sequence 19 AA;
 Query Match 28.9%; Score 33; DB 9; Length 19;
 Best Local Similarity 46.2%; Pred. No. 7.8e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
 DB 7 DISTPDVWGNPK 19

Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPK 13
| : : : :
Db 7 DUSTPDVWGNPK 19

RESULT 36
ABJ00309
ID ABJ00309 standard; peptide; 14 AA.
XX AC ABJ00309;
XX DT 02-SEP-2002 (first entry)
XX DE Human IGE immunogenic peptide SEQ ID NO: 93.
XX KW Immunogen; human; IGE; immunoglobulin E; allergy; thio-ether linkage;
XX KW vaccine; anti-allergic.
XX OS Homo sapiens.
XX PN WO200216409-A2.
XX PD 28-FEB-2002.
XX PF 17-AUG-2001; 2001WO-EP009576.
XX PR 22-AUG-2000; 2000GB-00020717.
XX PA (SMIK) SMITHKLINE BEECHAM BIOLOGICALS.
XX PA (PEPT-) PEPTIDE THERAPEUTICS LTD.
XX PI Friede M, Mason S, Turnell WG, Vinals Y Bassolac;
XX DR MPI; 2002-489648/52.
XX PT Conjugate for use in vaccine for treatment of allergy, comprises
XX PT disulfide bridge cyclized peptide and immunogenic carrier.
XX PS Claim 4; Page 11; 45pp; English.
XX CC The present invention relates to conjugates suitable for use in vaccines,
XX CC where the conjugate comprises a disulphide bridge cyclised peptide and an
XX CC immunogenic carrier. The vaccines can be used in the treatment of
XX CC allergies. The present sequence is a peptide immunogen derived from human
XX CC immunoglobulin E (IGE) suitable to be cyclised and used in the invention
XX CC Sequence 14 AA;
XX SQ
Query Match 28.1%; Score 32; DB 5; Length 14;
Best Local Similarity 75.0%; Pred. No. 8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYEYPSR 8
| : : : :
Db 1 DPEWPSR 8

RESULT 37
AAR94744
ID AAR94744 standard; peptide; 15 AA.
XX AC AAR94744;
XX DT 06-NOV-1996 (first entry)
XX DE SPNE 19b-11-715.
XX KW Selected principle neutralisation epitope; SPNE; HIV; Neisseria; antigen;
XX KW monoclonal antibody; HIV; gp120; outer membrane proteosome complex; OMPC;
XX KW SPNE-OMPC conjugate; vaccine; passive immunisation; therapy.

OS Synthetic.
XX PN GB2294047-A.
XX PD 17-APR-1996.
XX PF 10-OCT-1995; 95GB-00020739.
XX PR 14-OCT-1994; 94US-00323338.
XX PA (MERI) MERCK & CO INC.
XX PI Arnold BA, Boots LJ, Conley AJ, Keller PM,
XX DR MPI; 1996-181618/19.
XX PT New antigenic conjugate contg. HIV-specific neutralising epitopes - bound
XX PT to Neisseria outer membrane proteosome, useful in vaccines to treat or
XX PT prevent HIV infection.

PS Claim 1; Page 4; 49pp; English.
XX CC AAR94729-R94746 represent HIV-specific, selected principal neutralisation
XX CC epitopes (SPNE). AAR94739-R94745 are SPNE's identified from phage
XX CC sequences by selection with the monoclonal antibody (MAb) 19b in the
XX CC presence of a competing peptide (see AAR94747 and AAR94748). MAb 19b is a
XX CC neutralising antibody specific for HIV gp120. These sequences are
XX CC covalently bound to the purified outer membrane proteosome complex (OMPC)
XX CC of Neisseria, to form antigenic conjugates. The SPNE-OMPC conjugates are
XX CC used in vaccines for prevention or treatment of HIV infections. The
XX CC conjugates elicit specific HIV-neutralising antibodies which may also be
XX CC used in passive immunisation. The conjugates, or one of these sequences
XX CC can be used to screen blood, or can be used for clinical evaluation and
XX CC diagnosis of AIDS and ARC (AIDS-related complex)
XX SQ Sequence 15 AA;
XX

Query Match 28.1%; Score 32; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 8.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YHYPGSR 8
| : : : :
Db 9 YHYPGSR 15

RESULT 38
ADO17459
ID ADO17459 standard; peptide; 15 AA.
XX AC ADO17459;
XX DT 01-JUL-2004 (first entry)
XX DE Differentially expressed protein lml immunogenic peptide #174.
XX KW Immunostimulant; Cytostatic; Vaccine; Lu1; Lu2; Lu3; Lu4; Lu5;
XX KW lung cancer target protein; lung cancer; hexabrachion; tenascine C;
XX KW cytotoxicin.
XX OS Unidentified.
XX PN WO2004015390-A2.
XX PD 19-FEB-2004.
XX PF 08-AUG-2003; 2003WO-US024698.
XX PR 09-AUG-2002; 2002US-0402057P.
XX PA (APPL-) APPLERA CORP.
XX PI Hoffman S, Wang R, Subramanian G,

XX WPI; 2004-180755/17.
DR
XX
PT Eliciting an immune response, useful in diagnosing, preventing or
PT treating lung cancer, comprises introducing into the subject a
PT composition comprising lung cancer target proteins.
XX
PS Claim 1, Fig 3; 54pp; English.
XX
XX The present invention relates to a method for eliciting an immune
CC response in a subject comprising introducing into the subject a
CC composition comprising purified peptides from differentially expressed
CC proteins lml (AD017766), lml2 (AD017767), lml3 (AD017768), lml4 (AD017769)
CC and lml5 (AD017770). The differentially expressed proteins lml, lml2, lml3,
CC lml4 and lml5 bind to a specific human leukocyte antigen (HLA) allele and
CC are lung cancer target proteins. The method is useful in eliciting an
CC immune response and in diagnosing, preventing or treating lung cancer.
CC The present sequence is an immunogenic peptide from lml. This peptide is
CC a Class I/II overlapping T-cell epitope. lml is hexabrachion (tenascine C
CC or cytotoxicin).
SQ Sequence 15 AA;
Query Match 28.1%; Score 32; DB 8; Length 15;
Best Local Similarity 60.0%; Pred. No. 8.6e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 3 EYFGSRLGNP 12
DB 3 EIPGLRAGTP 12
RESULT 39
ADJ90073 standard; peptide; 16 AA.
XX
XX ADJ90073;
XX
XX 06-MAY-2004 (first entry)
DT
XX
DE Human papillomavirus minor capsid protein L2 peptide #220.
XX
XX transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
KM hepatitis B virus infection; human herpesvirus 1 infection;
KM human herpesvirus 2 infection.
XX
OS Human papillomavirus type 6b.
XX
PN WO2003053332-A2.
XX
PD 03-JUL-2003.
XX
PF 20-AUG-2002; 2002WO-US026549.
XX
PR 20-AUG-2001; 2001US-0313695P.
XX
PA (MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
DR WPI; 2003-586940/55.
XX
PT Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
PS Claim 35; SEQ ID NO 1541; 137pp; English.
XX
CC The invention comprises a composition which contains a peptide associated
CC with a transporter that is capable of increasing the uptake of the
CC peptide by a mammalian cell. The peptide of the invention contains the
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain

CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
SQ Sequence 16 AA;
Query Match 28.1%; Score 32; DB 7; Length 16;
Best Local Similarity 31.2%; Pred. No. 9.2e+02;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYVYFGSRLGNPKAPL 16
DB 1 DTFPTAPMGTPSPV 16
RESULT 40
AAW17560 standard; protein; 17 AA.
XX
XX AAW17560;
XX
XX 27-JAN-1998 (first entry)
DT
XX
DE Beta-B2-crystallin fragment (amino acids 145-161).
XX
XX Beta-A3-crystallin; lens protein; cataract; antigen; autoimmune;
KM epithelial cell; epitope.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX Homo sapiens.
XX
XX EP770398-A2.
XX
PD 02-MAY-1997.
XX
PF 10-OCT-1996; 96EP-00116212.
XX
PR 13-OCT-1995; 95JP-00291993.
XX
PA (SENIP) SENJU PHARM CO LTD.
XX
PI Inoue B;
XX
DR WPI; 1997-237935/22.
XX
XX
PT Composition containing lens antigen or microorganism that expresses it -
PT used to treat or prevent cataract by reducing the level of antibodies
PT directed against lens protein.
XX
PS Example 4; Page 31; 36pp; English.
XX
XX This sequence is an internal fragment of human beta-B2-crystallin. 17
CC peptides constituting beta-B2-crystallin were synthesised and subjected
CC to competitive inhibition assay of beta-B2-crystallins and respective
CC oligopeptides. As a result, only peptide fragment amino acid residues 157
CC -173 showed a strong binding inhibitory effect on beta-B2-crystallin.
CC This suggests that the binding site (epitope) of beta-B2-crystallin to
CC the antibody was present in this region (157-173). Lens antigens of
CC sequence of amino acids numbers 162-166 of beta-B2-crystallin or a
CC microorganism that can express a lens antigen are used in a
CC pharmaceutical composition. The composition can be used to prepare an
CC inhibitor of an increase of anti-lens protein antibodies. The
CC composition, and the inhibitor can be used to treat, prevent or delay the
CC onset of cataract. Cataract is considered to be the result of autoimmune
CC damage to lens epithelial cells induced by lens protein
XX
SQ Sequence 17 AA;
Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 71.4%; Pred. No. 9.9e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 2 YEPYGSR 8
| : | | |
DB 10 YQYFGYR 16

RESULT 41

AAB09129
ID AAB09129 standard; protein; 17 AA.

AC AAB09129;

DT 06-AUG-2003 (revised)

DT 30-AUG-2000 (first entry)

DE Hepatitis GB virus protein sequence SEQ ID NO:251.

KW Hepatitis GB virus; HGBV; diagnosis; therapeutic; immunogenic; infection;
KM detection; characterization; hepatitis.

OS Hepatitis GB virus.

PN US6051374-A.

PD 18-APR-2000.

PF 07-JUN-1995; 95US-00488445.

PR 14-FEB-1994; 94US-00196030.

PR 13-MAY-1994; 94US-00242654.

PR 29-JUL-1994; 94US-00283314.

PR 23-NOV-1994; 94US-00344185.

PR 30-JAN-1995; 94US-00344190.

PT 30-JAN-1995; 95US-00377557.

XX (AABO) ABBOTT LAB.

XX Dawson GJ, Leary TP, Muerhoff AS, Pilot-Matias TJ, Buljk SL;

XX Mushahwar IK, Simons JN, Desai SM, Erker JC, Schlauder GG;

XX WPI; 2000-338307/29.

XX PT Detecting target hepatitis GB virus nucleic acid in a test sample

XX PT suspected of containing HGBV comprises reacting the test sample the HGBV

XX PT polynucleotide probe and detecting the complex that contains target HGBV.

XX Example 9; Col 331-332; 369pp; English.

XX PS The present invention describe a method for detecting target hepatitis GB

XX CC virus (HGBV) nucleic acid (THN) in a test sample (T) suspected of

XX CC containing HGBV. The method involves reacting (T) with a HGBV

XX CC polynucleotide probe (I) containing 15 contiguous nucleotides, and which

XX CC selectively hybridizes to the HGBV genome or its full complement, and

XX CC detecting the complex that contains THN, indicating the presence of

XX CC target HGBV. The method is used for detecting target HGBV nucleic acid in

XX CC the test sample suspected of containing HGBV and for characterization of

XX CC newly ascertained etiological agent of non-A, non-B, non-C, non-D and non

XX CC -B hepatitis causing agents collectively termed as hepatitis GB virus.

XX CC AAB55270 to AAB55489 and AAB08985 to AAB09480 represent nucleotide and

XX CC protein sequences used in the exemplification of the present invention.

XX CC (Updated on 06-AUG-2003 to correct OS field.)

XX SO Sequence 17 AA;

XX Query Match 28.1%; Score 32; DB 3; Length 17;

XX Best Local Similarity 41.7%; Pred. No. 9.9e+02;

XX Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAPL 16

DB 1 PSERFSSPKLPV 12

RESULT 42

ADJ90086
ID ADJ90086 standard; peptide; 17 AA.

AC ADJ90086;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus minor capsid protein L2 peptide #233.

KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;

KW hepatitis B virus infection; human herpesvirus 1 infection;

KW human herpesvirus 2 infection.

OS Human papillomavirus type 6b.

PN WO2003053332-A2.

PD 03-JUL-2003.

PF 20-AUG-2002; 2002WO-US026549.

PR 20-AUG-2001; 2001US-0313695P.

PA (MYRI-) MYRIAD GENETICS INC.

PI Morham S, Zavitz K, Hobden A;

XX WPI; 2003-586940/55.

XX PT Peptides and hybrid polypeptides associated with a transporter that

XX PT increases its uptake by a mammalian cell, useful for inhibiting viral

XX PT budding or propagation, especially for treating e.g. AIDS or hepatitis B

XX PT virus infection.

XX PS Claim 35; SEQ ID NO 1554; 137pp; English.

XX CC The invention comprises a composition which contains a peptide associated

XX CC with a transporter that is capable of increasing the uptake of the

XX CC peptide by a mammalian cell. The peptide of the invention contains the

XX CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain

XX CC of Tsg101. The composition of the invention is useful in the manufacture

XX CC of a medicament for the treatment of viral infections, such as: HIV

XX CC infection (particularly AIDS), hepatitis B virus infection and human

XX CC herpesvirus 1/2 infection. The present amino acid sequence represents a

XX CC peptide of the invention.

XX SQ Sequence 17 AA;

XX Query Match 28.1%; Score 32; DB 7; Length 17;

XX Best Local Similarity 31.2%; Pred. No. 9.9e+02;

XX Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

OY 1 DYEPYGSRLGNPKAPL 16

DB 2 DTFPFPAPMGTFPSV 17

RESULT 43

ADJ90087

ID ADJ90087 standard; peptide; 17 AA.

AC ADJ90087;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus minor capsid protein L2 peptide #234.

KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;

KW hepatitis B virus infection; human herpesvirus 1 infection;

KW human herpesvirus 2 infection.

OS Human papillomavirus type 6b.


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XX  WO2003053332-A2.
PM
PD 03-JUL-2003.
XX
XX 20-AUG-2002; 2002WO-US026549.
PF
XX 20-AUG-2001; 2001US-0313695P.
PR
XX (MYRI-) MYRIAD GENETICS INC.
XX
XX Morham S, Zavitz K, Hobden A;
PI
XX WPI, 2003-586940/55.
XX
XX Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1555; 137pp; English.
PS
XX The invention comprises a composition which contains a peptide associated
CC with a transporter that is capable of increasing the uptake of the
CC peptide by a mammalian cell. The peptide of the invention contains the
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
XX Sequence 17 AA;
SQ
Query Match 28.1%; Score 32; DB 7; Length 17;
Best Local Similarity 31.2%; Pred. NO. 9.9e+02;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
| : : : : :
DB 1 DITPEPTAPMGTPFSPV 16
RESULT 44
ADP74618
ID ADP74618 standard; peptide; 17 AA.
XX
XX ADP74618;
AC
XX 26-AUG-2004 (first entry)
DT
XX
XX Amino acid sequence of a DEP-1 antigen peptide.
DE
XX
XX human; density enhanced phosphatase-1; DEP-1; DEP-1 complex;
XX p120 catenin; adapter protein; Gab 1; hepatocyte growth factor receptor;
XX HGF receptor; scatter factor receptor; SF receptor; Met; plakoglobin;
XX beta-catenin; signal transduction; cell growth; cell proliferation;
XX cell cycle regulation; contact inhibition; cellular differentiation;
XX cellular morphogenesis; cellular motility; cytoskeleton.
XX
XX Homo sapiens.
OS
XX
XX WO2004048549-A2.
PN
XX
XX 10-JUN-2004.
PD
XX
XX 26-NOV-2003; 2003WO-US038089.
PF
XX
XX 26-NOV-2002; 2002US-0429746P.
PR
XX
XX (COLD-) COLD SPRING HARBOR LAB.
PA
XX
XX Palika-Hamblin HL, Tonke NK;
PI

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[illegible]

PT	virus infection.
XX	
PS	Claim 35; SEQ ID NO 1568; 137bp; English.
XX	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UVF domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	herpesvirus 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
SEQ	Sequence 18 AA;
XX	
Query Match	28.1%; Score 32; DB 7; Length 18;
Best Local Similarity	31.2%; Pred. No. 1.1e+03;
Matches	5; Conservative 5; Mismatches 6; Indels 0; Gaps 0
DB	1 DVEYPSRLGNPKAPL 16
	: : : : :
	3 DTFPTAPMGTFPSPV 18
RESULT 46	
ADJ90101	
ID	ADJ90101 standard; peptide; 18 AA.
XX	
AC	ADJ90101;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Human papillomavirus minor capsid protein L2 peptide #248.
XX	
KM	transporter peptide; UVF domain; Tsg101; viral infection; HIV; AIDS;
KM	hepatitis B virus infection; human herpesvirus 1 infection;
XX	human herpesvirus 2 infection.
XX	
OS	Human papillomavirus type 6b.
XX	
PN	WO2003053332-A2.
XX	
PD	03-JUL-2003.
XX	
XX	20-AUG-2002; 2002WO-US026549.
PF	
XX	20-AUG-2001; 2001US-0313695P.
PR	
XX	(MYRI-) MYRIAD GENETICS INC.
PA	
XX	Morham S, Zavitz K, Hobden A;
PI	
XX	WPI, 2003-586940/55.
DR	
XX	
PT	Peptides and hybrid polypeptides associated with a transporter that
PT	increases its uptake by a mammalian cell, useful for inhibiting viral
PT	budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT	virus infection.
XX	
XX	Claim 35; SEQ ID NO 1569; 137bp; English.
PS	
XX	
CC	The invention comprises a composition which contains a peptide associated
CC	with a transporter that is capable of increasing the uptake of the
CC	peptide by a mammalian cell. The peptide of the invention contains the
CC	amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UVF domain
CC	of Tsg101. The composition of the invention is useful in the manufacture
CC	of a medicament for the treatment of viral infections, such as: HIV
CC	infection (particularly AIDS), hepatitis B virus infection and human
CC	herpesvirus 1/2 infection. The present amino acid sequence represents a
CC	peptide of the invention.
XX	
SEQ	Sequence 18 AA;
XX	

Qy		Query Match	28.1%;	Score 32;	DB 7;	Length 18;	
		Best Local Similarity	31.2%;	Pred. No.	1.1e+03;		
		Matches	5;	Conservative	5;	Mismatches	6; Indels 0; Gaps 0;
Db		1 DYEYGSRLGNPKAPL 16	: : : :				
		2 DTPTTAMGTTPSPV 17	: : : :				
<hr/>							
		RESULT 47					
ID		ADJ90102					
xx		ADJ90102 standard; peptide; 18 AA.					
AC		ADJ90102;					
xx		06-MAY-2004 (first entry)					
DT							
xx							
DE		Human papillomavirus minor capsid protein L2 peptide #249.					
xx							
KM		transporter peptide; UBV domain; Tsg101, viral infection; HIV; AIDS;					
KW		hepatitis B virus infection; human herpesvirus 1 infection;					
KM		human herpesvirus 2 infection.					
xx							
OS		Human papillomavirus type 6b.					
xx							
PN		WO2003053332-A2.					
PD							
xx		03-JUL-2003.					
PF							
xx		20-AUG-2002; 2002WO-US026549.					
PR							
xx		20-AUG-2001; 2001US-0333695P.					
PA		(MYRI-) MYRIAD GENETICS INC.					
xx							
PI		Morham S, Zavitz K, Hobden A,					
xx							
DR		WPI; 2003-586940/55.					
xx							
PT		Peptides and hybrid polypeptides associated with a transporter that					
PT		increases its uptake by a mammalian cell, useful for inhibiting viral					
pr		budding or propagation, especially for treating e.g. AIDS or hepatitis B					
xx		virus infection.					
PS		Claim 35; SEQ ID NO 1570; 137pp; English.					
xx							
CC		The invention comprises a composition which contains a peptide associated					
CC		with a transporter that is capable of increasing the uptake of the					
CC		peptide by a mammalian cell. The peptide of the invention contains the					
CC		amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain					
CC		of Tsg101. The composition of the invention is useful in the manufacture					
CC		of a medicament for the treatment of viral infections, such as: HIV					
CC		infection (particularly AIDS), hepatitis B virus infection and human					
CC		herpesvirus 1/2 infection. The present amino acid sequence represents a					
xx		peptide of the invention.					
SQ		Sequence 18 AA;					
<hr/>							
Qy		Query Match	28.1%;	Score 32;	DB 7;	Length 18;	
		Best Local Similarity	31.2%;	Pred. No.	1.1e+03;		
Matches		5;	Conservative	5;	Mismatches	6; Indels	0; Gaps 0;
Db		1 DYEYGSRLGNPKAPL 16	: : : :				
		1 DTPTTAMGTTPSPV 16	: : : :				
<hr/>							
		RESULT 48					
ID		ADJ90115					
xx		ADJ90115 standard; peptide; 19 AA.					
AC		ADJ90115;					

```

XX 06-MAY-2004 (first entry)
DT Human papillomavirus minor capsid protein L2 peptide #262.
DE
XX transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX OS Human papillomavirus type 6b.
XX PN WO2003053332-A2.
XX PD 03-JUL-2003.
XX PF 20-AUG-2002; 2002WO-US026549.
XX PR 20-AUG-2001; 2001US-0313695P.
XX PA (MYRI-) MYRIAD GENETICS INC.
XX PI Morham S, Zavitz K, Hobden A;
XX WPI; 2003-586940/55.
XX DR
XX PT Peptides and hybrid polypeptides associated with a transporter that
XX increases its uptake by a mammalian cell, useful for inhibiting viral
XX budding or propagation, especially for treating e.g. AIDS or hepatitis B
XX virus infection.
XX PS Claim 35; SEQ ID NO 1583; 137bp; English.
XX CC The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
XX amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
XX of Tsg101. The composition of the invention is useful in the manufacture
XX of a medicament for the treatment of viral infections, such as: HIV
XX infection (particularly AIDS), hepatitis B virus infection and human
XX herpesvirus 1/2 infection. The present amino acid sequence represents a
XX peptide of the invention.
XX CC
XX SQ Sequence 19 AA;

Query Match 28.1%; Score 32; DB 7; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.1e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYKPSGRLGNPKAPL 16
   | : : : : :
DB 4 DTFPTAPMGTPSPV 19

RESULT 49
ADJ90117
ID ADJ90117 standard; peptide; 19 AA.
XX
XX AC ADJ90117;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human papillomavirus minor capsid protein L2 peptide #264.
XX
XX KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
XX OS Human papillomavirus type 6b.
XX
XX PN WO2003053332-A2.
XX
XX PD 03-JUL-2003.
XX

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PF 20-AUG-2002; 2002WO-US026549.
XX
XX PR 20-AUG-2001; 2001US-0313695P.
XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX
XX PI Morham S, Zavitz K, Hobden A;
XX WPI; 2003-586940/55.
XX DR
XX PT Peptides and hybrid polypeptides associated with a transporter that
XX increases its uptake by a mammalian cell, useful for inhibiting viral
XX budding or propagation, especially for treating e.g. AIDS or hepatitis B
XX virus infection.
XX PS Claim 35; SEQ ID NO 1585; 137bp; English.
XX
XX CC The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
XX amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
XX of Tsg101. The composition of the invention is useful in the manufacture
XX of a medicament for the treatment of viral infections, such as: HIV
XX infection (particularly AIDS), hepatitis B virus infection and human
XX herpesvirus 1/2 infection. The present amino acid sequence represents a
XX peptide of the invention.
XX CC
XX SQ Sequence 19 AA;

Query Match 28.1%; Score 32; DB 7; Length 19;
Best Local Similarity 31.2%; Pred. No. 1.1e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYKPSGRLGNPKAPL 16
   | : : : : :
DB 2 DTFPTAPMGTPSPV 17

RESULT 50
ADJ90118
ID ADJ90118 standard; peptide; 19 AA.
XX
XX AC ADJ90118;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human papillomavirus minor capsid protein L2 peptide #265.
XX
XX KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
XX OS Human papillomavirus type 6b.
XX
XX PN WO2003053332-A2.
XX
XX PD 03-JUL-2003.
XX
XX PF 20-AUG-2002; 2002WO-US026549.
XX
XX PR 20-AUG-2001; 2001US-0313695P.
XX
XX PA (MYRI-) MYRIAD GENETICS INC.
XX
XX PI Morham S, Zavitz K, Hobden A;
XX WPI; 2003-586940/55.
XX DR
XX PT Peptides and hybrid polypeptides associated with a transporter that
XX increases its uptake by a mammalian cell, useful for inhibiting viral
XX budding or propagation, especially for treating e.g. AIDS or hepatitis B
XX virus infection.
XX

```



```

XX 27-JUN-2000 (first entry)
XX Peptide fragment of PXXP-HSCF.
DB PST phosphatase interacting protein; PSTPIP; tumour therapy;
XX protein tyrosine phosphatase; PTP.
XX Unidentified.
XX US6040437-A.
XX 21-MAR-2000.
XX 29-SEP-1997, 97US-00938830.
XX 17-APR-1997, 97US-0104590P.
XX (GETH ) GENENTECH INC.
XX Dowbenko DJ, Lasky LA;
XX WPI, 2000-282393/24.
XX Novel genes encoding protein tyrosine phosphatase binding proteins useful
XX for isolating homologous genes, e.g. in tumor cells, which provide more
XX specific targets for tumor therapy.
XX Disclosure; Col 35, 65pp; English.
XX This sequence represents a fragment of a protein tyrosine phosphatase
XX (PTP). It was used to isolate the PST phosphatase interacting protein
XX (PSTPIP) sequence of the invention. The protein is a protein tyrosine
XX phosphatase that possesses a non-catalytic domain comprising a proline,
XX serine and threonine rich region and a C-terminal segment of 20 amino
XX acid (aa's) rich in proline, and defines an SH3 binding domain. Nucleic
XX acid encoding native PSTPIP molecules can be used to isolate homologous
XX genes specifically expressed in tumour cells, which might provide more
XX specific targets for tumour therapy. The DNA is also useful for the
XX preparation of PSTPIP polypeptides by recombinant techniques and as
XX hybridisation probes for searching cDNA and genomic libraries for the
XX coding sequence of other PSTPIP polypeptide analogues in other species
XX
SQ Sequence 20 AA;
Query Match 28.1%; Score 32; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 8 RLGPRKAP 15
DB 5 RIGPRKGP 12

```

RESULT 54

AAB08487

ID AAB08487 standard; peptide, 20 AA.

AC AAB08487;

XX 20-DEC-2000 (first entry)

DT Peptide derived from a protein tyrosine phosphatase.

XX protein tyrosine phosphatase; PTP; phosphatase interacting protein;

KW PSTPIP; PEST family; protein tyrosine phosphatase; actin monomer;

XX tissue typing; tumour cell; tumour imaging.

OS Synthetic.

XX US611073-A.

XX 29-AUG-2000.

```

XX 06-FEB-1998; 98US-00020222.
XX 17-APR-1997, 97US-0104590P.
XX (GETH ) GENENTECH INC.
XX Lasky LA;
XX WPI, 2000-586378/55.
XX Novel PST phosphatase interacting protein useful for inducing of PST
XX polymerization of actin monomers and for identifying homolog of PST
XX phosphatase interacting protein.
XX Disclosure; Col 34, 48pp; English.
XX AAB08487-90 represent peptides derived from protein tyrosine phosphatase
XX (PTP). They were used to identify interaction domains of a murine protein
XX tyrosine phosphatase (PTP) phosphatase interacting protein (PSTPIP).
XX PSTPIP polypeptides are bound by and dephosphorylated by the PEST family
XX of protein tyrosine phosphatases. PSTPIP associates with actin. PSTPIP is
XX useful for inducing the polymerisation of actin monomer in eukaryotic
XX cells by introducing the polypeptide into the cell. The polypeptide is
XX useful for identifying and isolating PSTPIP homologues in another
XX mammalian species, in screening assays to identify antagonists and
XX agonists of native PSTPIP polypeptide and as molecular weight markers on
XX protein gels. The PSTPIP nucleic acid is useful for tissue typing of
XX specific mammalian tissues, for preparing PSTPIP polypeptides by
XX recombinant techniques, as hybridisation probes for searching cDNA and
XX genomic libraries for the coding sequence of other PSTPIP analogues and
XX to isolate homologous genes specifically expressed in tumour cells.
XX Antagonists of PSTPIP peptide are useful for inhibiting biological
XX activity of the peptide. Antibodies of PSTPIP are useful to identify
XX rapidly dividing cells and are used to image tumours comprising such
XX rapidly dividing cells
XX
SQ Sequence 20 AA;
Query Match 28.1%; Score 32; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 8 RLGPRKAP 15
DB 5 RIGPRKGP 12

```

RESULT 55

ADJ90133

ID ADJ90133 standard; peptide, 20 AA.

AC ADJ90133;

XX 06-MAY-2004 (first entry)

DT Human papillomavirus minor capsid protein L2 peptide #280.

XX transporter peptide; UVB domain; Tag101; viral infection; HIV; AIDS;

KW hepatitis B virus infection; human herpesvirus 1 infection;

XX human herpesvirus 2 infection.

XX Human papillomavirus type 6b.

OS WO200305332-A2.

XX 03-JUL-2003.

DT 20-AUG-2002; 2002WO-US026549.

XX 20-AUG-2001; 2001US-0313695P.

XX (MYRI-) MYRIAD GENETICS INC.

```
XX Morham S, Zavitz K, Hobden A;
XX WPI; 2003-586940/55.
DR Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1601; 137pp; English.
XX
XX The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
XX amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
XX of Tsg101. The composition of the invention is useful in the manufacture
XX of a medicament for the treatment of viral infections, such as: HIV
XX infection (particularly AIDS), hepatitis B virus infection and human
XX herpesvirus 1/2 infection. The present amino acid sequence represents a
XX peptide of the invention.
XX
XX Sequence 20 AA;
SQ
Query Match      28.1%; Score 32; DB 7; Length 20;
Best Local Similarity 31.2%; Pred. No. 1.2e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
   | : | : | : | :
DB 3 DITFPTAPMGTFPSV 18
RESULT 56
ADJ90135
ID ADJ90135 standard; peptide; 20 AA.
XX
XX ADJ90135;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human papillomavirus minor capsid protein L2 peptide #282.
DE
XX
XX transporter peptide; UBV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
OS
XX
XX WO2003053332-A2.
PN
XX
XX 03-JUL-2003.
PD
XX
XX 20-AUG-2002; 2002WO-US026549.
PF
XX
XX 20-AUG-2001; 2001US-0313695P.
PR
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Morham S, Zavitz K, Hobden A;
PI
XX
XX WPI; 2003-586940/55.
PI
XX
XX Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1603; 137pp; English.
XX
XX The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
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```
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
XX Sequence 20 AA;
SQ
Query Match      28.1%; Score 32; DB 7; Length 20;
Best Local Similarity 31.2%; Pred. No. 1.2e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
   | : | : | : | :
DB 1 DITFPTAPMGTFPSV 16
RESULT 57
ADJ90132
ID ADJ90132 standard; peptide; 20 AA.
XX
XX ADJ90132;
AC
XX
XX 06-MAY-2004 (first entry)
DT
XX
XX Human papillomavirus minor capsid protein L2 peptide #279.
DE
XX
XX transporter peptide; UBV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
XX Human papillomavirus type 6b.
OS
XX
XX WO2003053332-A2.
PN
XX
XX 03-JUL-2003.
PD
XX
XX 20-AUG-2002; 2002WO-US026549.
PF
XX
XX 20-AUG-2001; 2001US-0313695P.
PR
XX
XX (MYRI-) MYRIAD GENETICS INC.
PA
XX
XX Morham S, Zavitz K, Hobden A;
PI
XX
XX WPI; 2003-586940/55.
PI
XX
XX Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
XX Claim 35; SEQ ID NO 1600; 137pp; English.
XX
XX The invention comprises a composition which contains a peptide associated
XX with a transporter that is capable of increasing the uptake of the
XX peptide by a mammalian cell. The peptide of the invention contains the
XX amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UBV domain
XX of Tsg101. The composition of the invention is useful in the manufacture
XX of a medicament for the treatment of viral infections, such as: HIV
XX infection (particularly AIDS), hepatitis B virus infection and human
XX herpesvirus 1/2 infection. The present amino acid sequence represents a
XX peptide of the invention.
XX
XX Sequence 20 AA;
SQ
Query Match      28.1%; Score 32; DB 7; Length 20;
Best Local Similarity 31.2%; Pred. No. 1.2e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;
QY 1 DYEPGSRIGNPKAPL 16
   | : | : | : | :
DB 1 DITFPTAPMGTFPSV 16
```


PI Boulikas T;
XX WPI; 2002-164295/21.
XX
XX
XX Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
XX
PS Claim 14; Page 62; 107pp; English.
XX
XX The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention
XX
SQ Sequence 9 AA;
XX
Query Match 27.2%; Score 31; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. NO. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 EYPSGRLG 10
:::|||||
DB 2 KHPGKRLG 9
XX
RESULT 61
ABB74355
ID ABB74355 standard; peptide; 9 AA.
XX
XX ABB74355;
XX
XX
DT 18-APR-2002 (first entry)
XX
XX Karyophilic peptide SEQ ID NO:119.
XX
XX Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytosstatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
XX Bos taurus.
OS Homo sapiens.
XX
XX WO200193836-A2.
PN
XX
PD 13-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US018657.
PF
XX
PR 09-JUN-2000; 2000US-0210925P.
XX
XX (BOUL/) BOULIKAS T.
PA
XX
XX Boulikas T;
PI
XX

DR WPI; 2002-164295/21.
XX
XX
XX Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
PT nuclear localization signal/fusogenic peptide conjugates into targeted
PT liposome complexes.
XX
XX
PS Claim 14; Page 62; 107pp; English.
XX
XX The present invention describes a method for producing micelles with
CC entrapped therapeutic agents. The method comprises: (1) combining
CC negatively charged agent with a cationic lipid in a ratio where 30-90 %
CC of the negatively charged atoms are neutralised by positive charges on
CC lipid molecules to form an electrostatic micelle complex in 20-80 %
CC ethanol; and (2) combining the micelle complex of (a) with fusogenic-
CC karyophilic peptide conjugates in a 0.0-0.3 ratio, therefore producing
CC micelles with entrapped therapeutic agents. Also described is a method
CC for delivering a therapeutic agent in vivo, comprising the administration
CC of the micelle. ABB74256 to ABB74858 represent specifically claimed
CC nuclear localisation signal (NLS) peptides for use in the method as the
CC fusogenic-karyophilic peptides. The micelles produced can have cytostatic
CC and antitumour activities. The peptide-lipid-polynucleotide complexes
CC produced are useful for inhibiting the progression of neoplastic
CC diseases. The invention relates to the field of gene therapy and is
CC directed toward methods for producing peptide-lipid-polynucleotide
CC complexes suitable for delivery of polynucleotides. The encapsulated
CC molecules display therapeutic efficacy in eradicating solid tumours
CC including but not limited to breast carcinoma or prostate carcinoma.
CC ABB74235 to ABB74255 are used in the exemplification of the present
CC invention
XX
SQ Sequence 9 AA;
XX
Query Match 27.2%; Score 31; DB 5; Length 9;
Best Local Similarity 62.5%; Pred. NO. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 3 EYPSGRLG 10
:::|||||
DB 2 KHPGKRLG 9
XX
RESULT 62
ABB74364
ID ABB74364 standard; peptide; 9 AA.
XX
XX ABB74364;
XX
XX
DT 18-APR-2002 (first entry)
XX
XX Karyophilic peptide SEQ ID NO:128.
XX
XX Fusogenic; nuclear localisation signal; NLS; encapsulation; lipogene;
KW liposome; micelle; karyophilic; cytosstatic; antitumour; solid tumour;
KW peptide-lipid-polynucleotide complex; neoplastic disease; gene therapy;
KW breast carcinoma; prostate carcinoma.
XX
XX Rattus sp.
OS
XX
XX WO200193836-A2.
PN
XX
PD 13-DEC-2001.
XX
XX 08-JUN-2001; 2001WO-US018657.
PF
XX
PR 09-JUN-2000; 2000US-0210925P.
XX
XX (BOUL/) BOULIKAS T.
PA
XX
XX Boulikas T;
PI
XX
XX WPI; 2002-164295/21.
XX
XX Encapsulation of plasmid DNA (lipogenes) and therapeutic agents with
PT

XX Example 4; Page 19; 78pp; English.

XX The present sequence is given in a specification relating to a purified

PS CC or synthetic protein having antopein biological activity. Compositions

CC comprising this protein are useful for inhibiting thrombin activity in

CC humans suffering from a condition such as myocardial infarction, stroke,

CC pulmonary embolism, deep vein thrombosis, peripheral arterial occlusion,

CC disseminated intravascular coagulation, cardiovascular and

CC cerebrovascular thrombosis, thrombosis associated with post-operative

CC trauma, obesity, pregnancy, side effects of oral contraceptives,

CC prolonged immobilisation, and hypercoagulable states associated with

CC haematologic, immunologic or rheumatologic disorders. The protein may

CC also be useful for treating unstable angina, arteriosclerosis, reblockage

CC of vessels after angioplasty with a balloon catheter, or blood clotting

CC in haemodialysis. It is also used as anticoagulant to inhibit thrombin

CC activity by inhibiting platelet aggregation in extracorporeal blood

XX SQ Sequence 12 AA;

OY 5 PGSRLGNPKAP 15
|||
Db 2 PGSRLGSGSKP 12

RESULT 64
ADY62107
ID ADY62107 standard; peptide; 12 AA.
AC ADY62107;
XX
XX 19-MAY-2005 (first entry)
DT
DS S_marcascens chitinase A/ chitobiase proteins consensus peptide Seq 122.
DE
DM combinatorial library; DNA recombination; chitinase;
KM beta-N-acetylhexosaminidase; chitobiase.
XX
OS Serratia marcescens.
XX
PN US2005053989-A1.
PD
XX 10-MAR-2005.
PF
PP 26-AUG-2004; 2004US-00926542.
XX
PR 27-AUG-2003; 2003US-0497924P.
XX
PA (SHAR/) SHARON G.
PA (LABA/) LABAN A.
XX
PI Sharon G, Laban A;
XX WPI; 2005-221920/23.
XX
PT Generating divergent libraries of chimeric proteins, comprises
PT transfecting a host with a polynucleotide obtained by recombination
PT between nucleotides encoding consensus amino acid sequences.
XX
XX Disclosure; SEQ ID NO 122; 60pp; English.

XX This invention relates to a novel method for generating divergent

CC libraries of recombinant chimeric proteins. Specifically, it refers to a

CC method that induces recombination between several distinct, uniform and

CC predefined regions of overlapping polynucleotides encoding sequences with

CC consensus polypeptides that correspond to sequences conserved in several

CC related proteins. As such, this provides a route by which to produce

CC chimeric polynucleotides, which can then be transfected into a host with

CC the polynucleotides. The present invention describes using this method

CC	for generating divergent libraries of several recombinant chimeric
CC	proteins to enable production of recombinant chimeric proteins in a less
CC	expensive, less labor-intensive and more efficient procedure. The
CC	shuffling between variable regions are essentially devoid of sequence
CC	homology, and it maintains the consensus backbone, increases the
CC	production of active enzymes while retaining high diversity and improved
CC	properties, thus, it is more favorable and generates important enzyme
CC	variants. In particular, it refers to the creation of a recombinant
CC	library of chimeric lipase proteins using four parental lipase genes from
CC	various Candida species that share little DNA homology but exhibit
CC	notable protein similarity. A second recombinant library refers to
CC	chimeric chitinase A/ chitinobiose proteins. This peptide sequence is
CC	identified as a conserved region between Serratia marcescens chitinase A
CC	and chitinobiose (beta-N-acetylhexosaminidase) proteins, given in figure 7
CC	of the invention.
XX	
SQ	Sequence 12 AA;
Query Match	27.2%; Score 31; DB 9; Length 12;
Best Local Similarity	50.0%; Pred. No. 9.6e+02;
Matches 4; Conservative	3; Mismatches 1; Indels 0; Gaps 0;
OY	1 DYEPGSR 8 :: :
Db	5 DWEPGRK 12
RESULT 65	
ID	ADZ37873
AC	ADZ37873 standard; peptide; 13 AA.
XX	
DT	ADZ37873;
XX	
DE	30-JUN-2005 (first entry)
XX	
XX	Human kinase substrate peptide SEQ ID 803.
XX	
KW	Kinase; substrate; drug delivery; cancer; restenosis; osteoporosis;
KW	Rheumatoid arthritis; asthma; psoriasis; inflammatory bowel disease;
KW	systemic lupus erythematosus; multiple sclerosis; transplant rejection;
KW	neoplasia; cystostatic; vasotropic; cardiovascular disease; osteopathic;
KW	degeneration; endocrine disease; musculoskeletal disease;
KW	antiinflammation; inflammation; autoimmunity disease; immunosuppressive;
KW	immune disorder; antiarthritic; antirheumatic; antiallergic;
KW	respiratory disease; antiproliferative; dermatological disease;
KW	gastrointestinal-gen.; gastrointestinal disease; neuroprotective;
XX	neurological disease; dermatological; dermatological disease.
XX	
OS	Homo sapiens.
XX	
PN	WO2005035003-A2.
XX	
PD	21-APR-2005.
XX	
PF	22-SEP-2004; 2004WO-US031148.
XX	
PR	22-SEP-2003; 2003US-0505325P.
PR	04-MAY-2004; 2004US-0568340P.
PR	22-JUN-2004; 2004US-0581835P.
XX	
PA	(DIHE-) DIHEDRON CORP.
PI	Ballatore C, Castellino AJ, Desharnais J, Guo Z, Li Q, Newman MJ,
PI	Sun C;
XX	
DR	WPI, 2005-315493/32.
XX	
PT	New conjugate used for treating aberrant cellular activation, migration,
PT	proliferation or survival condition such as cancer, comprises drug and
PT	substrate for protein or lipid kinase linked to protein, optionally by
PT	non-releasable linker.
XX	
PB	Disclosure; SEQ ID NO 803; 407bp; English.

XX	The invention relates to a conjugate (I) comprising a drug and a substrate for a protein kinase or a lipid kinase non-releasably linked to it, optionally by a non-releasable linker. Also included are preparing
CC	pacitaxel C10 carbamate of formula (8a) (which comprises reacting a
CC	pacitaxel compound of formula (5a) with a carboximidamide compound and
CC	reacting the obtained compound of formula (6a) with an amine of formula
CC	X, all formulae given in the specification), a pharmaceutical composition
CC	(PCT) comprising (I) and a carrier, an article (comprising packaging
CC	material, (I) or its derivatives, for treatment/prevention/amelioration
CC	of one or more symptoms (associated with aberrant cellular activation,
CC	migration, proliferation or survival (ACAMPS) and a label that indicates
CC	that (I) is used for treatment, prevention or amelioration of one or more
CC	symptoms associated with ACAMPS), and a peptide comprising an kinase
CC	substrate peptide. The conjugate has improved cytotoxic selectivity index
CC	as compared to an unconjugated drug. The conjugate is useful for treating
CC	conditions caused by ACAMPS characterized by undesirable or aberrant
CC	activation, migration, proliferation or survival of tumor cells,
CC	endothelial cells, B cells, T cells, macrophages, neutrophils,
CC	eosinophils, basophils, monocytes, platelets, fibroblasts, other
CC	connective tissue cells, osteoblasts, osteoclasts and progenitors of
CC	these cell types. The ACAMPS condition is a cancer, coronary arteriosclerosis,
CC	aortic atherosclerosis, chronic inflammation or autoimmunity disease. The
CC	autoimmune disease is rheumatoid arthritis, asthma, psoriasis,
CC	inflammatory bowel disease, systemic lupus erythematosus, systemic
CC	dermatomyositis, inflammatory ophthalmic diseases, autoimmune hematologic
CC	disorders, multiple sclerosis, vasculitis, idiopathic nephrotic syndrome,
CC	transplant rejection or graft versus host disease. The cancer is non-
CC	small cell lung cancer, head squamous cancer, neck squamous cancer,
CC	colorectal cancer, prostate cancer, breast cancer, acute lymphocytic
CC	leukemia, adult acute myeloid leukemia, adult non-Hodgkin's lymphoma,
CC	brain tumor, cervical cancer, childhood cancer, childhood sarcoma,
CC	chronic lymphocytic leukemia, chronic myeloid leukemia, esophageal
CC	cancer, hairy cell leukemia, kidney cancer, liver cancer, multiple
CC	myeloma, neuroblastoma, oral cancer, pancreatic cancer, primary central
CC	nervous system lymphoma, skin cancer or small-cell lung cancer. The
CC	cancer is brain stem glioma, cerebellar astrocytoma, cerebral
CC	astrocytoma, ependyoma, Ewing's sarcoma, germ cell tumor, Hodgkin's
CC	disease, acute myelogenous leukemia, acute lymphoblastic leukemia, liver
CC	cancer, medullablastoma, neuroblastoma, non-Hodgkin's lymphoma,
CC	osteosarcoma, malignant fibrous histiocytoma of bone, retinoblastoma,
CC	rhabdomyo sarcoma, soft tissue sarcoma, supratentorial primitive
CC	neuroectodermal and pineal tumors, visual pathway and hypothalamic
CC	glioma, Wilms' tumor or other childhood kidney tumor. The cancer is
CC	originated from or has metastasized to the bone, brain, breast, digestive
CC	and gastrointestinal system, endocrine system, blood, lung, respiratory
CC	system, thorax, musculoskeletal system, or skin. The cancer is selected
CC	from breast cancer, lung cancer, prostate cancer, ovarian cancer,
CC	esophageal cancer, bladder cancer, hepatoma, neuroblastoma, lymphoma,
CC	testicular cancer, renal cancer, leukemia, colorectal cancer and head and
CC	neck cancer. The conjugate is useful for identifying kinase substrates
CC	capable of selectively accumulating in a target system. The conjugate is
CC	useful for identifying conjugates capable of exhibiting selective
CC	toxicity against a target system. The conjugate is useful for enhancing
CC	drug efficiency. The present sequence is kinase substrate peptide useful
CC	in the conjugate of the invention.
CC	
XX	
SQ	Sequence 13 AA:
Query Match	27.2% Score 31; DB 9; Length 13;
Best Local Similarity	54.5%; Pred. No. 1e+03;
Matches	6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
OY	5 PGRRLGNPKAP 15
DG	2 PGRSRRTTSLP 12
RESULT 66	
ABPa6490	
ID	ABPa6490 standard; peptide; 14 AA.
XX	ABPa6490;

XX 19-AUG-2002 (first entry)
 DT
 XX
 DE Human Blys binding scFv VH CDR3 SEQ ID 2501.
 XX
 KW Blys/ B lymphocyte stimulator; TNF superfamily; human; cytostatic;
 KM tumour necrosis factor; B cell proliferation; B cell differentiation;
 KM immunosuppressive; immunomodulant; immunomodulatory; antineumatic;
 KM arthritis; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
 KM systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS;
 KM common variable immunodeficiency; acquired immunodeficiency syndrome.
 XX
 OS Homo sapiens.
 XX
 PN WO200202641-A1.
 XX
 PD 10-JAN-2002.
 XX
 PF 15-JUN-2001; 2001WO-US019110.
 XX
 PR 16-JUN-2000; 2000US-0212210P.
 PR 17-OCT-2000; 2000US-0240816P.
 PR 16-MAR-2001; 2001US-0276248P.
 PR 21-MAR-2001; 2001US-0277379P.
 PR 25-MAY-2001; 2001US-0293499P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (CMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI, 2002-114799/15.
 XX
 DR Antibodies against B lymphocyte stimulating polypeptides, useful for the
 PT diagnosis and treatment of cancers and immune disorders.
 XX
 PS Claim 2, Page 3001, 3148pp; English.
 XX
 CC This invention describes novel antibodies that immunospecifically bind to
 CC B lymphocyte stimulator (Blys) polypeptides. Blys is a member of the
 CC tumour necrosis factor (TNF) super family and induces B cell
 CC proliferation and differentiation. The antibodies of the invention have
 CC cytostatic, immunosuppressive, immunostimulant, immunomodulatory,
 CC antineumatic and antiAIDS activity and can be used in vaccines to
 CC inhibit the expression and activity of Blys. The antibodies bind to Blys
 CC and so may be used to detect and quantitate the presence of Blys in
 CC biological samples and may be used in this way to diagnose disease
 CC associated with aberrant expression of Blys. They may also be
 CC administered to treat diseases associated with aberrant Blys expression
 CC and activity such as cancer, immune, and autoimmune disorders and
 CC diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis,
 CC immunodeficiency (e.g. common variable immunodeficiency (CVID) and
 CC acquired immunodeficiency syndrome (AIDS)). ABP4390-ABP47228 represent
 CC the antibodies and fragments of the antibodies described in the method of
 CC the invention
 CC
 SO Sequence 14 AA;
 XX
 Query Match 27.2%; Score 31; DB 5; Length 14;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 PKAPLY 17
 |:|||||
 Db 8 PRAPLY 13
 RESULT 67
 ADG97317
 ID ADG97317 standard; peptide, 14 AA.
 XX
 AC ADG97317,
 XX

DT 11-MAR-2004 (first entry)
 XX
 DE scFV VHCDR3 peptide that immunospecifically binds Blys SeqID 2501.
 XX
 KW antibody; B lymphocyte stimulator; Blys; tumour necrosis factor;
 KM B cell proliferation; differentiation; scFv; myasthenia gravis;
 KM multiple sclerosis; asthma; rheumatoid arthritis; AIDS; leukaemia;
 KM carcinoma; lymphoma; antineumatic; antineumatic; neuroprotective;
 KM antiinflammatory; antineumatic; antiallergic; cytostatic.
 XX
 OS unidentified.
 XX
 PN WO2003055979-A2.
 XX
 PD 10-JUL-2003.
 XX
 PF 14-NOV-2002; 2002WO-US036496.
 XX
 PR 16-NOV-2001; 2001US-0331469P.
 PR 19-DEC-2001; 2001US-0340817P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Ruben SM, Barash SC, Choi GH, Vaughan T, Hilbert D;
 PI WPI, 2003-505330/47.
 XX
 DR Novel antibody that immunospecifically binds to a B lymphocyte stimulator
 PT (Blys), useful for detecting and treating diseases or disorders e.g.
 PT rheumatoid arthritis, asthma and leukemia.
 XX
 PS Example 1; SEQ ID NO 2501; 394pp; English.
 XX
 CC This invention relates to novel antibodies that immunospecifically bind
 CC to B lymphocyte stimulator (Blys). The Blys gene has been mapped to
 CC chromosome 13q34 and encodes a protein that is a member of the tumour
 CC necrosis factor superfamily and induces both in vivo and in vitro B cell
 CC proliferation and differentiation. Specifically, it refers to single
 CC chain antibody molecules (scFvs) derived, preferably, from the variable
 CC heavy CDR3 region that immunospecifically bind to a polypeptide, or
 CC fragment thereof, of either human, murine, rat or monkey Blys. The
 CC present invention refers to the use of such antibodies in various methods
 CC for the detection, diagnosis and prognosis of diseases related to the
 CC aberrant expression or inappropriate function of Blys or its receptor. As
 CC such, these compositions are useful for identifying immune disorders
 CC including myasthenia gravis and multiple sclerosis, inflammatory
 CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such
 CC as AIDS and proliferative disorders including leukaemia, carcinoma and
 CC lymphoma. Accordingly, they can be described as exhibiting various
 CC activities such as antineumatic, antineumatic, neuroprotective,
 CC antiinflammatory, antineumatic, antiallergic and cytostatic. This
 CC peptide sequence is a single chain antibody variable heavy CDR3 peptide
 CC that immunospecifically binds Blys of the invention.
 CC
 SO Sequence 14 AA;
 XX

Query Match 27.2%; Score 31; DB 7; Length 14;
 Best Local Similarity 83.3%; Pred. No. 1.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 12 PKAPLY 17
 |:|||||
 Db 8 PRAPLY 13
 RESULT 68
 AAB86601
 ID AAB86601 standard; peptide, 15 AA.
 XX
 AC AAB86601;
 XX
 DT 20-NOV-2001 (first entry)
 XX

DE	Human cytomegalovirus strain AD169 IE1 peptide fragment SEQ ID 58.
XX	
KW	Antigen-specific stimulation; T-lymphocyte; CD8 stimulation; pp65;
KW	CD4 stimulation; immuno-stimulation; IE1, lower matrix phosphoprotein.
XX	
OS	Human cytomegalovirus.
XX	
PN	WO200163286-A2.
XX	
PD	30-AUG-2001.
XX	
XX	
PF	17-FEB-2001; 2001WO-BP001773.
XX	
PR	22-FEB-2000; 2000DE-01009341.
XX	
PA	(KERN/) KERN F.
XX	
PI	Kern F, Volk H, Reinke P, Paulhaber N, Surel I, Khatazmas E;
XX	
DR	WPI, 2001-557718/62.
XX	
PT	Stimulating CD8 or CD4 T cells for the immuno-stimulation of mammals and
PT	the determination of the response to the antigen comprises using a
PT	synthetic peptide library of the specific antigen.
XX	
PS	Example; Fig 1; 85pp; German.
XX	
CC	This sequence represents a novel method for stimulating CD8 or CD4 T
CC	cells for the immuno-stimulation of mammals and the determination of the
CC	response to an antigen (I). The method comprises (i) dividing the amino
CC	acid sequence of the antigen into protein fragments (II) of at least 9
CC	amino acids, whereby adjacent or neighbouring fragments are in the whole
CC	antigen sequence; (ii) synthesizing a peptide library containing (ii);
CC	and (iii) incubating the CD8 and/or CD4 T lymphocytes in a suspension
CC	comprising (II) in a single culture vessel. The method is used to immuno-
CC	stimulate T cells of mammals, particularly humans, and is also useful for
CC	diagnostic purposes to determine if a mammal, especially human, has
CC	previously immunologically responded to a specific protein, and to
CC	determine strength of that response. The method is suitable for in vivo
CC	or in vitro immuno-stimulation of mammalian, more preferably human T
CC	lymphocytes, where the stimulated T lymphocytes are expanded and can be
CC	transfused into a patient. AAB86544-AAB86803 represent fragments of the
CC	human cytomegalovirus IE1 and pp65 lower matrix phosphoprotein which are
CC	used to illustrate the method of the invention
XX	
XX	
SQ	Sequence 15 AA;
Query Match	27.2%; Score 31; DB 4; Length 15;
Best Local Similarity	35.7%; Pred. No. 1.2e+03;
Matches	5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY	5 PGSRLGNPKAPLYK 18
DB	2 PSSKVPREPTVPYTK 15
RESULT 69	
ADJ90060	
ID	ADJ90060 standard; peptide; 15 AA.
XX	
AC	ADJ90060;
XX	
DT	06-MAY-2004 (first entry)
XX	
DE	Human papillomavirus minor capsid protein L2 peptide #207.
XX	
KW	transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
KW	hepatitis B virus infection; human herpesvirus 1 infection;
KW	human herpesvirus 2 infection.
XX	
OS	Human papillomavirus type 6b.
XX	
PN	WO2003053332-A2.

[illegible]

XX 06-AUG-2004; 2004WO-EP008860.
 PF 08-AUG-2003; 2003US-0493599P.
 XX 08-AUG-2003; 2003US-0493836P.
 PR 08-AUG-2003; 2003US-0493867P.
 PR 08-AUG-2003; 2003US-0493985P.
 XX (XENO-) XENOVA LTD.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PA (NOVS) NOVARTIS PHARMA GMBH.
 PI Argoud-Puy G, Beder N, Bougueleret L, Cusin I, Mahe E;
 PI Mkhnejad A, Refas S, Rose K, Saudrais C, Scherer A, Papoian R;
 DR WPI; 2005-195824/20.
 PT Screening and/or diagnosing cardiovascular disorder in subject involves
 PT detecting and/or quantifying level of polypeptide in biological sample
 PT from subject and comparing with control sample.
 XX Claim 1, SEQ ID NO 16; 349pp; English.
 XX The invention relates to a method of screening and/or diagnosing a
 CC cardiovascular disorder (CD) in a subject which comprises detecting
 CC and/or quantifying the level of a polypeptide in a biological sample from
 CC the subject and comparing the level to that of control sample. The method
 CC is useful for screening, diagnosing and treating coronary artery disease,
 CC biliary cirrhosis, gallstones, celiac disease, irritable bowel syndrome,
 CC diabetes, scleroderma, nausea, vomiting, constipation and diarrhea. The
 CC method is rapid and efficient. The present sequence represents a
 CC cardiovascular disorder plasma protein tryptic fragment.
 XX Sequence 15 AA;

Query Match 27.2%; Score 31; DB 9; Length 15;
 Best Local Similarity 85.7%; Pred. No. 1.2e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSRIGNP 12
 DB 6 GSPIGNP 12

RESULT 73
 AAW25403
 ID AAW25403 standard; peptide; 16 AA.
 AC AAW25403;
 XX
 DT 27-MAR-1998 (first entry)
 XX
 DE p53bp2 SH3 domain binding peptide SEQ ID NO:189.
 XX
 KW Cortactin; SH3 domain; binding peptide; Src homology region 3;
 KW tyrosine kinase; immune response; lymphokine; Interleukin 1; Nck; Abl;
 KW PLGamma; p53bp2; Ctk; Yes; Grb2.
 OS Synthetic.
 OS Unidentified.
 XX
 PN WO9730074-A1.
 XX
 PD 21-AUG-1997.
 XX
 PF 14-FEB-1997; 97WO-US002298.
 XX
 PR 16-FEB-1996; 96US-00602999.
 XX
 PA (CYTO-) CYTOGEN CORP.
 PA (UMC-) UNITIV NORTH CAROLINA.
 XX
 PI Sparks AB, Kay BK, Thorn JM, Quilliam LA, Der CJ, Fowlkes DM;

PI Rider JB;
 DR WPI; 1997-424972/39.
 XX
 PT Src homology region 3 binding peptide - used to activate Src tyrosine
 PT kinase(s) and to stimulate immune response by increasing production of
 PT certain lymphokine(s), e.g. interleukin-1.
 XX
 PS Claim 17; Page 99; 131pp; English.

The present sequence represents a Src homology region 3 (SH3) binding
 CC peptide. SH3 binding peptides are selected from: (a) peptides which bind
 CC the SH3 domain of Cortactin, (b) peptides which bind the middle SH3
 CC domain of Nck; (c) peptides which bind the SH3 domain of Abl; (d)
 CC peptides which bind the SH3 domain of Src; (e) peptides which bind the
 CC SH3 domain of PLC gamma; (f) peptides which bind the SH3 domain of p53bp2
 CC ; (g) peptides which bind the amino-terminal SH3 domain of Ctk; (h)
 CC peptides which bind the SH3 domain of Yes; and (i) peptides which bind
 CC the amino-terminal SH3 domain of Grb2. The purified binding peptides can
 CC be used in the method to identify inhibitors of their binding to their
 CC respective SH3 domains, which could be used to modulate the
 CC pharmacological activity of proteins or polypeptide containing the SH3
 CC domain. The peptides can also be used to activate Src or Src-related
 CC protein tyrosine kinases, to stimulate the immune response by increasing
 CC the production of certain lymphokines, e.g. tumour necrosis factor-alpha
 CC and interleukin-1, or to deliver a conjugated molecule to certain
 CC cellular compartments containing Src or Src related proteins

Query Match 27.2%; Score 31; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.3e+03;
 Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPKAPLYK 18
 DB 4 LGRPPIPRK 13

RESULT 74
 ADJ90072
 ID ADJ90072 standard; peptide; 16 AA.
 AC ADJ90072;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human papillomavirus minor capsid protein L2 peptide #219.
 XX
 KW transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
 KW hepatitis B virus infection; human herpesvirus 1 infection;
 KW human herpesvirus 2 infection.
 OS Human papillomavirus type 6b.
 OS
 PN WO2003053332-A2.
 XX
 PD 03-JUL-2003.
 XX
 PF 20-AUG-2002; 2002WO-US026549.
 XX
 PR 20-AUG-2001; 2001US-031695P.
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 XX
 PI Morham S, Zavitz K, Hobden A;
 XX
 DR WPI; 2003-586940/55.
 XX
 PT Peptides and hybrid polypeptides associated with a transporter that
 PT increases its uptake by a mammalian cell, useful for inhibiting viral
 PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
 PT virus infection.

CC method is rapid and efficient. The present sequence represents a
 CC cardiovascular disorder plasma protein tryptic fragment.

XX
 SQ Sequence 16 AA;

Query Match 27.2%; Score 31; DB 9; Length 16;
 Best Local Similarity 85.7%; Pred. No. 1.3e+03;
 Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
 |||||
 DB 6 GSPLGNP 12

RESULT 77

AAP80011
 ID AAP80011 standard; protein; 17 AA.

XX
 AC AAP80011;

XX
 DT 25-MAR-2003 (revised)
 DT 19-SEP-1990 (first entry)

XX
 DE Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of
 DE herpes simplex virus type 1 (HSV1) glycoprotein B (GB).

XX
 KM Herpes simplex virus type 1 glycoprotein B; vaccinees;
 KM immunogenic synthetic peptide.

XX
 OS Herpes simplex virus type 1.

XX
 FH Key Location/Qualifiers

XX
 FT Misc-difference 1 /label= OTHER
 FT /note= "Ac-Tyr"

XX
 FT Misc-difference 2 /label= Nle
 FT /label= OTHER

XX
 FT Misc-difference 17 /label= OTHER
 FT /note= "Cys-NH2"

XX
 PN US4761470-A.

XX
 PD 02-AUG-1988.

XX
 PF 10-APR-1987; 87US-0003651.

XX
 PR 16-DEC-1985; 85US-00809452.

XX
 PA (MERI) MERCK & CO INC.

XX
 PI Emint EA, Larson VM, Boger JS;

XX
 DR WPI; 1988-234840/33.

XX
 PT New synthetic oligopeptide immunogens and their conjugates - used for
 PT inducing prodn. of antibodies against herpes simplex virus type 1.

XX
 PS Claim 3; Page 10; 6pp; English.

XX
 CC Immunogenic synthetic peptides of this formula and their salts are new.
 CC Also new are conjugates of the peptides covalently bonded to a carrier
 CC protein or synthetic polymer. The peptides are immunogens for inducing
 CC prodn. of HSV1 neutralising antibodies and so are useful in vaccinees.
 CC (Updated on 25-MAR-2003 to correct PD field.)

XX
 SQ Sequence 17 AA;

Query Match 27.2%; Score 31; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGNPKAPLYKRP 20

DB
 ||:|:|
 2 LGDPKPKKKKKP 13

RESULT 78

ADCC22395
 ID ADCC22395 standard; peptide; 17 AA.

XX
 AC ADCC22395;

XX
 DT 18-DEC-2003 (first entry)

XX
 DE Nuclear localisation signal motif amino acid sequence SEQ ID NO:244.

XX
 KM recombinant fusion protein; fusion protein; binding; detection;

XX
 KM localisation domain; binding domain;

XX
 OS subcellular compartment localisation.

XX
 PN WO2003012068-A2.

XX
 PD 13-FEB-2003.

XX
 PF 01-AUG-2002; 2002WO-US024572.

XX
 PR 01-AUG-2001; 2001US-0309395P.

XX
 PR 13-DEC-2001; 2001US-0341589P.

XX
 PA (CEBL-) CELLOMICS INC.

XX
 PI Bright G, Premkumar DR, Chen Y;

XX
 DR WPI; 2003-248174/24.

XX
 PT New recombinant fusion protein comprising detection and first
 PT localisation domains and a binding domain for the molecule of interest,
 PT useful for detecting binding of a molecule of interest.

XX
 PS Claim 20; SEQ ID NO 244; 10pp; English.

XX
 CC The present invention describes a recombinant fusion protein (1) for
 CC detecting binding of a molecule of interest. (1) comprises: (a) a
 CC detection domain; (b) a first localisation domain; and (c) a binding
 CC domain for the molecule of interest. The detection domain, the first
 CC localisation domain and the binding domain for the molecule of interest
 CC constituting the recombinant fusion protein for detecting binding of a
 CC molecule of interest are operably linked. The binding domain for the
 CC molecule of interest is separated from the first localisation domain by 0
 CC -20 amino acid residues. The first localisation domain and the binding
 CC domain for the molecule of interest both do not occur in a single non-
 CC recombinant protein with the same spacing as in the recombinant fusion
 CC protein for detecting binding of a molecule of interest. Also described:
 CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
 CC (2) a recombinant expression vector comprising the nucleic acid control
 CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
 CC genetically engineered host cell transfected with the recombinant
 CC expression vector; (4) a kit for detecting binding of the molecule of
 CC interest; and (5) a method for identifying compounds that alter the
 CC binding of the molecule of interest. The recombinant fusion protein is
 CC useful for detecting binding of a molecule of interest. The recombinant
 CC fusion protein eliminates the need to construct two or more chimeric
 CC proteins and enables the monitoring of biochemical events in live, intact
 CC or fixed cells. The present sequence is used in the exemplification of
 CC the present invention.

XX
 SQ Sequence 17 AA;

Query Match 27.2%; Score 31; DB 7; Length 17;
 Best Local Similarity 66.7%; Pred. No. 1.4e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPKAPLYK 18

Db 7 GNPPEPLK 15

RESULT 79

ADP17331 ADF17331 standard; peptide; 17 AA.

AC ADF17331,

DT 12-FEB-2004 (first entry)

DE Nuclear targeting oligopeptide, SEQ ID No 374.

KM cell surface molecule; malignant cell line; cytosolic; immunostimulant;
KW vaccine; gene therapy; premalignant; cancer; nuclear targeting.

OS Unidentified.

PN WO200300928-A2.

PD 03-JUN-2003.

PF 19-JUN-2002; 2002WO-1B003534.

PR 25-JUN-2001; 2001DK-00000992.

PR 02-JUL-2001; 2001US-0301818P.

PA (ODIN-) ODIN MEDICAL AS.

PI Poulsen HS, Pedersen N, Mortensen S, Sorensen SB, Petersen MW,
PI Elsenr HI;

DR WPI; 2003-247897/24.

PT Identifying cell surface molecules with differential expression in
PT malignant cells, by comparing expression of mRNA in malignant cells and
PT normal tissue, and selecting nucleic acid sequences encoding the
PT molecules.

PS Disclosure; SEQ ID NO 374; 223pp; English.

XX The invention relates to a novel method for identifying cell surface
XX molecules expressed at different levels in malignant cells. The method
XX involves providing at least 3 malignant cell lines and 3 total RNA
XX samples derived from normal tissue, comparing expression of mRNA in cell
XX lines and normal tissue, identifying nucleic acid sequences for a
XX difference in amount of mRNA expressed in cell lines and normal tissue,
XX and selecting nucleic acid sequences encoding for the cell surface
XX molecules. The cell surface molecule compositions have cytostatic and
XX immunostimulant activities. The cell surface molecule proteins can be
XX used to create a vaccine and their encoding nucleic acids used in gene
XX therapy. The specific binding partner, capable of associating with the
XX cell surface molecules, is useful for the preparation of a targeting
XX complex, comprising a binding partner capable of binding the cell surface
XX molecules. The targeting complex is useful in the treatment of
XX premalignant and/or malignant conditions in an individual. The condition
XX includes cancer selected from melanoma, brain tumour (e.g. glioblastoma,
XX neuroblastoma, astrocytoma, oligodendroglioma, meningioma,
XX medulloblastoma, neuroma, ependymoma, craniopharyngioma, pineal tumour,
XX germ cell tumour and schwannoma), breast cancer, lung cancer (e.g. small
XX cell lung cancer (SCLC) and non-small cell lung cancer (NSCLC)), prostate
XX cancer, cervix cancer, uterine cancer, ovarian cancer, leukaemia, colon
XX cancer, rectum cancer and bladder cancer. The targeting complex is useful
XX for the preparation of a premalignant and/or malignant conditions in an
XX individual in need of it. This sequence represents a nuclear targeting
XX peptide of the invention.

XX Sequence 17 AA;

Query Match 27.2%; Score 31; DB 7; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPKAPLYK 18

Db 7 GNPPEPLK 15

RESULT 80

ADP86158

ID ADF86158 standard; peptide; 17 AA.

AC ADF86158;

DT 26-FEB-2004 (first entry)

DE Human NLS containing peptide (SeqID 58) derives antimicrobial peptides.

KM antimicrobial; nuclear localisation sequence; NLS; gram positive;

KW gram negative bacteria; human.

OS Homo sapiens.

PN WO2003091429-A1.

PD 06-NOV-2003.

PF 24-APR-2003; 2003WO-1P005225.

PR 25-APR-2002; 2002JP-00124830.

PA (TOAG) TOA GOSEI KK.

PI Yoshida T, Kume M, Yamada Y, Matsuda Y, Kourai H;

DR WPI; 2003-854399/79.

PT Synthetic antimicrobial polypeptides for use as antimicrobials.

PS Disclosure; SEQ ID NO 58; 113pp; Japanese.

XX This invention relates to a novel method of synthesising artificial
XX antimicrobial polypeptides. Specifically, these are peptides that each
XX comprise at least one nuclear localisation sequence (NLS) or modified
XX NLS. Furthermore, each NLS unit consists of at least 5 amino acids and
XX makes up at least 30% of the total amino acids of the peptide. As such,
XX the present invention describes the oligonucleotides encoding these
XX antimicrobial peptides that are effective against a wide range of gram
XX positive and gram negative bacteria including Klebsiella pneumoniae,
XX Bacillus subtilis and Salmonella enteritidis. This peptide sequence
XX represents a peptide from which the novel artificial antimicrobial
XX peptides were derived in an exemplification of the invention.

XX Sequence 17 AA;

Query Match 27.2%; Score 31; DB 7; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPKAPLYK 18

Db 7 GNPPEPLK 15

RESULT 81

ADJ90085

ID ADJ90085 standard; peptide; 17 AA.

AC ADJ90085;

DT 06-MAY-2004 (first entry)

DE Human papillomavirus minor capsid protein L2 peptide #232.

DR WPI; 2003-046718/04.
 XX
 PT New isolated antigenic peptides e.g., for G protein-coupled receptors
 PT (GPCR), useful for diagnosing and designing drugs for treating conditions
 PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
 PT autoimmune diseases.
 XX
 PS Claim 1; Fig 2; 523pp; English.
 XX
 CC The present invention describes antigenic peptides (1) comprising: (a)
 CC any one of 1601 sequences (see ABP82019 to ABP83619) of 12-24 amino
 CC acids. Also described: (1) an assay for the detection of a particular G
 CC protein-coupled receptor (GPCR) or a candidate polypeptide in a sample;
 CC and (2) an isolated antibody having high specificity and high affinity or
 CC avidity for a particular GPCR. (1) can be used as GPCR modulators and in
 CC gene therapy. The antigenic peptides for GPCRs are useful in detecting an
 CC antibody against a particular GPCR, and in the production of specific
 CC antibodies. The peptides and antibodies are also useful for detecting the
 CC presence or absence of corresponding GPCRs. The antigenic peptides for
 CC GPCRs and antibodies are useful for diagnosing and designing drugs for
 CC treating immune-related diseases, growth-related diseases, cell
 CC regeneration-related diseases, immunological-related cell proliferative
 CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
 CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
 CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
 CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
 CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
 CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
 CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
 CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
 CC any other disorder in which GPCRs are involved. The antibodies may be
 CC used in immunoassays and immunodiagnosis. ABZ42523 to ABZ42869 encode
 CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 27.2%; Score 31; DB 6; Length 18;
 Best Local Similarity 71.4%; Pred. No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DYVEPGS 7
 ||:|:
 Db 3 DYGYPKS 9
 XX
 RESULT 84
 ADJ90099
 ID ADJ90099 standard; peptide; 18 AA.
 AC ADJ90099;
 XX
 DT 06-MAY-2004 (first entry)
 XX
 DE Human papillomavirus minor capsid protein L2 peptide #246.
 XX
 KW Transporter peptide; UV domain; Tsg101; viral infection; HIV; AIDS;
 KW hepatitis B virus infection; human herpesvirus 1 infection;
 KW human herpesvirus 2 infection.
 XX
 OS Human papillomavirus type 6b.
 OS
 PN WO2003053332-A2.
 PN
 XX
 PD 03-JUL-2003.
 PD
 XX
 PF 20-AUG-2002; 2002WO-US026549.
 PF
 XX
 PR 20-AUG-2001; 2001US-0313695P.
 PR
 XX
 PA (MYRI-) MYRIAD GENETICS INC.
 PA
 XX
 PI Morhem S, Zavitz K, Hobden A;

XX
 DR WPI; 2003-586940/55.
 XX
 PT Peptides and hybrid polypeptides associated with a transporter that
 PT increases its uptake by a mammalian cell, useful for inhibiting viral
 PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
 PT virus infection.
 XX
 PS Claim 35; SEQ ID NO 1567; 137pp; English.
 XX
 CC The invention comprises a composition which contains a peptide associated
 CC with a transporter that is capable of increasing the uptake of the
 CC peptide by a mammalian cell. The peptide of the invention contains the
 CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UV domain
 CC of Tsg101. The composition of the invention is useful in the manufacture
 CC of a medicament for the treatment of viral infections, such as: HIV
 CC infection (particularly AIDS), hepatitis B virus infection and human
 CC herpesvirus 1/2 infection. The present amino acid sequence represents a
 CC peptide of the invention.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 27.2%; Score 31; DB 7; Length 18;
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DYVEPGSRLLGNPRAP 15
 ||:|:
 Db 4 DIRFPAPMGTPPSP 18
 XX
 RESULT 85
 ADK50419
 ID ADK50419 standard; peptide; 18 AA.
 AC ADK50419;
 XX
 DT 04-NOV-2004 (first entry)
 XX
 DE Human carcinoma-related C35 epitope / gp100 Pmel17 polypeptide 1310.
 XX
 KW C35 epitope; cytostatic; vaccine; tumour; breast; bladder carcinoma;
 KW human; polypeptide; gp100 Pmel17.
 XX
 OS Homo sapiens.
 OS
 OS Unidentified.
 OS
 PN WO2003104428-A2.
 PN
 PD 18-DEC-2003.
 PD
 XX
 PF 10-JUN-2003; 2003WO-US018252.
 PF
 XX
 PR 10-JUN-2002; 2002US-0386738P.
 PR
 XX
 PR 11-DEC-2002; 2002US-0432241P.
 PR
 XX
 PR 23-APR-2003; 2003US-0464650P.
 PR
 XX
 PA (VACC-) VACCINEX INC.
 PA
 XX
 PI (UYRP) UNIV ROCHSTER.
 PI
 XX
 PI Zauderer M, Evans BE, Borrello MA;
 PI
 XX
 DR WPI; 2004-062349/06.
 DR
 XX
 PT Novel C35 polypeptide useful for formulation of immunogenic composition
 PT to induce antibodies and cell-mediated immunity against tumor cells.
 PT
 XX
 PS Disclosure; Page 176; 626pp; English.
 PS
 XX
 CC The invention relates to a novel isolated polypeptide comprising or
 CC consisting of two or more C35 peptide epitopes. The polypeptide of the
 CC invention demonstrates cytostatic activity and may be useful for the
 CC formulation of an immunogenic composition, such as a vaccine, to induce

CC antibodies and cell-mediated immunity against target cells such as tumour
 CC cells. Furthermore, the polypeptide and its analogues may be useful as
 CC prognostic markers for carcinoma, such as human breast or bladder
 CC carcinoma. The current sequence is that of human breast/bladder carcinoma
 CC C35 polypeptide of the invention.

XX
 SQ Sequence 18 AA;

Query Match 27.2%; Score 31; DB 8; Length 18;
 Best Local Similarity 38.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
 ::|||::|
 Db 1 KITNSRPPLYLRP 13

RESULT 86
 AAP81357
 ID AAP81357 standard; protein; 19 AA.

XX
 AC AAP81357;

XX
 DT 25-MAR-2003 (revised)
 DT 19-SEP-1990 (first entry)

XX
 DE Sequence of immunogenic synthetic peptide containing AAs 64 to 77 of
 herpes simplex virus type 1 (HSV1) glycoprotein B (gB).

KW Herpes simplex virus type 1 glycoprotein B; vaccines;
 KW immunogenic synthetic peptide.

XX
 OS Herpes simplex virus type 1.

PH Key Location/Qualifiers

FT Misc-difference 1 /label= Tyr, Lys

FT Misc-difference 1 /note= "or may be absent"

FT Misc-difference 1 /label= OTHER

FT Misc-difference 2 /note= "X-amino, amino-p-benzoylbenzoyl, N-acetyl or
 carboxyl"

FT Misc-difference 2 /label= Nle

FT Misc-difference 17 /note= "or absent"

FT Misc-difference 17 /label= Thr, Cys, Nle

FT Misc-difference 18 /note= "or absent"

FT Misc-difference 18 /label= Pro

FT Misc-difference 19 /note= "or absent"

FT Misc-difference 19 /label= OTHER

FT Misc-difference 19 /note= "P-amino or carboxyl, or a pharmaceutically-
 acceptable salt thereof"

FT Misc-difference 19 /label= Pro

FT Misc-difference 19 /note= "or absent"

XX US4761470-A.

XX PD 02-AUG-1988.

XX PR 10-APR-1987; 87US-00036651.

XX PR 16-DEC-1985; 85US-00809452.

XX PA (MERI) MERCK & CO INC.

XX PI Emint EA, Larson VM, Boger JS;

XX DR WPI; 1988-234840/33.

PT New synthetic oligopeptide immunogens and their conjugates - used for
 PT inducing prodn. of antibodies against herpes simplex virus type 1.

XX
 PS Claim 1; Page 10; 6pp; English.

XX
 CC Immunogenic synthetic peptides of this formula and their salts are new.
 CC Also new are conjugates of the peptides covalently bonded to a carrier
 CC protein or synthetic polymer. The peptides are immunogens for inducing
 CC prodn. of HSV1 neutralising antibodies and so are useful in vaccines.
 CC (Updated on 25-MAR-2003 to correct PD field.)

XX
 SQ Sequence 19 AA;

Query Match 27.2%; Score 31; DB 1; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGDPKPKKKRP 20
 |||::|:
 Db 2 LGDPKPKKKRP 13

RESULT 87
 AAW17416
 ID AAW17416 standard; peptide; 19 AA.

XX
 AC AAW17416;

XX
 DT 17-OCT-2003 (revised)
 DT 18-JUN-1997 (first entry)

XX
 DE Chicken anaemia virus immunogenic peptide #16.

XX
 KW Immunogenic polypeptide; CAV; serum; antibody; diagnosis;

XX
 KW Chicken anaemia virus; vaccine.

XX
 OS Chicken anaemia virus.

XX
 PN JP09071599-A.

XX
 PD 18-MAR-1997.

XX
 PF 06-SEP-1995; 95JP-00229004.

XX
 PR 06-SEP-1995; 95JP-00229004.

XX
 PA (NISK) NIPPON SEIBUTSU KAGAKU KENKYUSHO ZH.

XX
 DR WPI; 1997-231187/21.

XX
 PT Polypeptide(s) highly reactive to chick anaemia virus-infected chicken
 PT serum - are used for antibody and vaccine production for protection
 PT against chicken anaemia virus.

XX
 PS Claim 1; Page 14; 26pp; English.

XX
 CC The sequences given in AAW17401-17 are immunogenic polypeptides which
 CC have a high reactivity to CAV-infected chicken serum. These peptides and
 CC antibodies against them can be used for the diagnosis of chicken anaemia
 CC virus (CAV) infection or in vaccines for preventing CAV infection. The
 CC polypeptides have a high reactivity to CAV-infected chicken serum.
 CC (Updated on 17-OCT-2003 to standardise OS field)

XX
 SQ Sequence 19 AA;

Query Match 27.2%; Score 31; DB 2; Length 19;
 Best Local Similarity 46.7%; Pred. No. 1.6e+03;
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 5 POSRLGNPKAPLYKR 19
 |||::|:
 Db 2 PDLRTDQPKPKKKR 16

```

RESULT 88
AAW32884
XX AAW32884 standard; peptide; 19 AA.
AC
XX AAW32884,
XX
DT 25-MAR-2003 (revised)
DT 16-JAN-1998 (first entry)
XX
DE Peptide K fragment of OA-519.
XX
KM OA-519; cross-reaction; haptoglobin related; hpr; antibody; epitope;
KM haptoglobin 1; haptoglobin 2; cancer; breast cancer; prognosis assay;
KM peptide K.
XX
OS Homo sapiens.
XX
PN US5665874-A.
XX
PD 09-SEP-1997.
XX
PF 05-JUN-1995; 95US-00469005.
XX
PR 17-JAN-1989; 89US-00297722.
PR 04-DEC-1990; 90US-00622407.
PR 26-JUL-1991; 91US-00735522.
PR 24-JUL-1992; 92US-00917716.
PR 26-JUL-1993; 93US-00096908.
PR 24-JAN-1994; 94US-00188426.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Kuhajda FP, Pasternack GR;
XX
DR WPI; 1997-469516/43.
XX
PT DNA encoding protein cross-reactive with hpr gene product - useful to
PT raise antibodies reactive with epitope(s) found on hpr gene product,
PT useful in cancer, especially breast cancer, prognosis assays.
XX
PS Example 12; Col 39-40; 68bp; English.
XX
CC The present sequence is a peptide fragment of a protein (OA-519) cross-
CC reactive with the haptoglobin related (hpr) gene product. OA-519 can be
CC used to raise antibodies reactive with epitopes found on the hpr gene
CC product, but not on haptoglobin 1 or 2, useful in cancer, especially
CC breast cancer, prognosis assays. (Updated on 25-MAR-2003 to correct PF
CC field.)
XX
SQ Sequence 19 AA;

Query Match          27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
   :| | | | |
   :| | | | |
Db 1 HPESPPTNPTRPLF 14

RESULT 89
AAW57227
ID AAW57227 standard; peptide; 19 AA.
XX
AC AAW57227,
XX
XX
DT 25-MAR-2003 (revised)
DT 04-AUG-1998 (first entry)
XX
DE OA-519 peptide fragment SEQ ID NO:3.
XX
KM Human; hpr gene; haptoglobin; solid tumour; cancer; metastasis; breast;

```

```

KM screening; prognosis; prostatic adenocarcinoma.
XX
XX Synthetic.
OS Homo sapiens.
XX
XX US5759791-A.
XX
XX 02-JUN-1998.
XX
PD 24-JAN-1994; 94US-00188426.
XX
PF 17-JAN-1989; 89US-00297722.
PR 04-DEC-1990; 90US-00622407.
PR 26-JUL-1991; 91US-00735522.
PR 24-JUL-1992; 92US-00917716.
PR 26-JUL-1993; 93US-00096908.
XX
PA (UYJO ) UNIV JOHNS HOPKINS.
XX
PI Pasternack GR, Kuhajda FP;
XX
XX WPI; 1998-332128/29.
XX
DR
XX
PT Prognosis of solid tumours e.g. breast carcinoma - based on detection of
PT OA-519 protein or mRNA in histological sections and biological fluids.
XX
PS Example 12; Col 39; 50pp; English.
XX
CC The present sequence represents an OA-519 peptide fragment from an
CC example of the present invention. The present invention describes a
CC method and a kit for screening human samples to aid in determining the
CC prognosis of breast carcinoma. The kit comprises in one or more
CC containers: an antibody which specifically binds to one or more epitopes
CC found on the sequence: Leu Tyr Ser Gly Asn Asp Val Thr Asp Ile Ser Asp
CC Asp Arg Phe Pro Lys Pro Glu Ile Ala Asn Gly Tyr Val Glu Lys Leu Phe
CC Arg Tyr Glu Cys but not found on haptoglobin 1 or 2; and a reagent for
CC detecting the antibody. The method comprises providing a histologic
CC section from the tumour, and contacting the section with an antibody (as
CC described above), and determining whether the antibody specifically binds
CC to the section in cytoplasmic cellular regions, where the presence of the
CC antibody binding correlates with a worsened prognosis of the solid
CC tumour. The method is useful for the prognosis of solid tumours,
CC especially breast carcinomas and prostatic adenocarcinomas. (Updated on
CC 25-MAR-2003 to correct PR field.)
XX
SQ Sequence 19 AA;

Query Match          27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 1.6e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
   :| | | | |
   :| | | | |
Db 1 HPESPPTNPTRPLF 14

RESULT 90
AAW71597
ID AAW71597 standard; peptide; 19 AA.
XX
AC AAW71597,
XX
XX
DT 24-NOV-1998 (first entry)
XX
DE Protein tyrosine phosphatase peptide PTP PEP.
XX
KM Mouse; tyrosine phosphorylated cleavage furrow-associated protein;
KM PSTPIP; PST family; protein tyrosine phosphatase; murine;
KM polymerisation; actin monomer; eukaryotic cell; identification;
KM antagonist.
XX
XX Synthetic.
OS Mus sp.

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XX WO9835037-A1.
 XX 13-AUG-1998.
 PD
 XX 30-JAN-1998; 98WO-US001774.
 PF
 XX 07-FEB-1997; 97US-00798419.
 PR
 XX 29-SEP-1997; 97US-00938829.
 PR
 XX (GENTH) GENENTECH INC.
 PA
 XX Laskey LA, Dowbenko DJ;
 PI
 XX WPI; 1998-447234/38.
 DR
 XX
 XX
 PT New PE8T-type protein tyrosine phosphatase interacting polypeptide -
 PT nucleic acids and vectors; for inducing the polymerisation of actin
 PT monomers in eukaryotic cells and identifying antagonists.
 CC
 PS Disclosure; Page 37; 111pp; English.
 XX
 CC The present sequence represents a peptide from the present invention
 CC which describes murine tyrosine phosphorylated cleavage furrow-
 CC associated protein (PSTRIP), which is a PE8T-type protein tyrosine
 CC phosphatase (PTP)-interacting polypeptide. PSTRIP induces the
 CC polymerisation of actin monomers in a eukaryotic cell, by introducing a
 CC vector containing the nucleic acid sequence encoding PSTRIP into the
 CC cell. Assays for identifying (ant)agonists of PSTRIP comprise contacting
 CC PSTRIP with the agent and monitoring the ability of PSTRIP to induce
 CC actin polymerisation
 CC
 SQ Sequence 19 AA;

Query Match 27.2%; Score 31; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15
 DB 3 GNRFSKPKGP 12

RESULT 91
 AAW96751
 ID AAW96751 standard; peptide; 19 AA.
 XX
 AC AAW96751;
 XX
 DT 14-APR-1999 (first entry)
 XX
 DE Peptide fragment derived from protein OA-519.
 XX
 KW Monoclonal antibody; OA-519; hapctogloblin 1; Hg1, Hg2;
 KW hapctogloblin related protein; hpr; diagnostic marker; human solid tumour;
 KW tumour invasion; early metastasis; breast cancer.
 XX
 OS Homo sapiens.
 XX
 PN US5872217-A.
 XX
 PD 16-FEB-1999.
 XX
 PF 05-JUN-1995; 95US-00469007.
 XX
 PR 17-JAN-1989; 89US-00297722.
 PR 04-DEC-1990; 90US-00622407.
 PR 26-JUL-1991; 91US-00735522.
 PR 24-JUL-1992; 92US-00917716.
 PR 26-JUL-1993; 93US-00096908.
 PR 24-JAN-1994; 94US-00188426.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.

XX KuhaJda FP, Pasternack GR;
 XX
 XX WPI; 1999-166717/14.
 DR
 XX
 XX
 PT New anti-OA-519 antibodies - useful as diagnostic and prognostic markers
 PT for human solid tumours, particularly breast cancers.
 CC
 PS Example 12; Col 25; 51pp; English.

XX Peptides AAW96750-53 are derived from the OA-519 protein. The
 CC specification describes monoclonal antibodies which specifically bind an
 CC epitope found on OA-519 but not on hapctogloblin 1 (Hg1) or Hg2 or,
 CC optionally hapctogloblin related protein (hpr) gene product. The antibodies
 CC can be used to detect OA-519 which is useful as a diagnostic marker in
 CC human solid tumours and for predicting the propensity for tumour invasion
 CC and early metastasis, particularly with breast cancers. They can detect
 CC aggressive tumour cells which result in decreased survival, increased
 CC metastasis, increased rates of clinical recurrence and overall worsened
 CC prognosis. The antibodies can also be used to purify hapctogloblin related
 CC (hpr) proteins
 CC

SQ Sequence 19 AA;

Query Match 27.2%; Score 31; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.6e+03;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPSRLGNPKAPLY 17
 DB 1 HPSEPTPMTEPLP 14

RESULT 92
 AAW84378
 ID AAW84378 standard; peptide; 19 AA.
 XX
 AC AAW84378;
 XX
 DT 26-MAR-1999 (first entry)
 XX
 DE Peptide K from a protein cross-reactive with the hpr gene product.
 XX
 KW Hapctogloblin related gene; hpr gene; hapctogloblin 1; hapctogloblin 2;
 KW antibody; breast carcinoma; diagnostic marker; human solid tumour.
 XX
 OS Synthetic.
 OS Homo sapiens.
 OS
 PN US5864011-A.
 XX
 PD 26-JAN-1999.
 XX
 PF 05-JUN-1995; 95US-00469009.
 XX
 PR 17-JAN-1989; 89US-00297722.
 PR 04-DEC-1990; 90US-00622407.
 PR 26-JUL-1991; 91US-00735522.
 PR 24-JUL-1992; 92US-00917716.
 PR 26-JUL-1993; 93US-00096908.
 PR 24-JAN-1994; 94US-00188426.
 XX
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX
 PI KuhaJda FP, Pasternack GR;
 XX
 DR WPI; 1999-131358/11.
 XX
 PT Polypeptide comprising epitope of hpr gene product - useful for producing
 PT antibodies for cancer prognosis.
 XX
 PS Example 12; Col 25; 51pp; English.
 XX

CC The present sequence represents a peptide derived from a protein that is
 CC immunologically cross-reactive with the haptoglobin related (hpr) gene
 CC product from breast cancer cells. The specificfication also describes a
 CC peptide that is immunologically cross-reactive with polyclonal antibodies
 CC that specifically bind the hpr gene product. The peptide can be used to
 CC raise antibodies specific for a protein that is immunologically cross-
 CC reactive with the hpr gene product but not with haptoglobin 1 or
 CC haptoglobin 2. The peptide is found in the cytoplasm of breast carcinoma
 CC cells and is a useful diagnostic marker in human solid tumours for
 CC predicting the propensity for tumour invasion and early metastasis

XX Sequence 19 AA;

Query Match 27.2%; Score 31; DB 2; Length 19;
 Best Local Similarity 42.9%; Pred. No. 1.6e+03;
 Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPSRLGNPKAPLY 17
 Db 1 HPBSPTNPTEPLF 14

RESULT 93

AAV81931

ID AAV81931 standard; protein; 19 AA.

AC AAV81931;

DT 27-JUN-2000 (first entry)

DE Peptide fragment of PXXP-HSCF.

KM PST phosphatase interacting protein; PSTPIP; tumour therapy;

KM protein tyrosine phosphatase; PTP.

XX Unidentified.

OS US6040437-A.

PN 21-MAR-2000.

PF 29-SEP-1997; 97US-00938830.

PR 17-APR-1997; 97US-0104590P.

XX (GETH) GENENTECH INC.

PI Dowbenko DJ, Lasky LA;

DR WPI; 2000-282393/24.

PT Novel genes encoding protein tyrosine phosphatase binding proteins useful
 PT for isolating homologous genes, e.g. in tumor cells, which provide more
 PT specific targets for tumor therapy.

PS Disclosure; Col 35; 65pp; English.

XX This sequence represents a fragment of a protein tyrosine phosphatase
 CC (PTP). It was used to isolate the PTP phosphatase interacting protein
 CC (PSTPIP) sequence of the invention. The protein is a protein tyrosine
 CC phosphatase that possesses a non-catalytic domain comprising a proline,
 CC serine and threonine rich region and a C-terminal segment of 20 amino
 CC acid (aa 8) rich in proline, and defines an SH3 binding domain. Nucleic
 CC acids encoding native PSTPIP molecules can be used to isolate homologous
 CC genes specifically expressed in tumour cells, which might provide more
 CC specific targets for tumour therapy. The DNA is also useful for the
 CC preparation of PSTPIP polypeptides by recombinant techniques and as
 CC hybridisation probes for searching cDNA and genomic libraries for the
 CC coding sequence of other PSTPIP polypeptide analogues in other species

XX Sequence 19 AA;

Query Match 27.2%; Score 31; DB 3; Length 19;

Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15
 Db 3 GNRFSKPKGP 12

RESULT 94

AAV81931

ID AAV81931 standard; peptide; 19 AA.

AC AAV81931;

DT 20-DEC-2000 (first entry)

DE Peptide derived from a protein tyrosine phosphatase.

KM protein tyrosine phosphatase; PTP; phosphatase interacting protein;

KM PSTPIP; PST family; protein tyrosine phosphatase; actin monomer;

KM tissue typing; tumour cell; tumour imaging.

XX Synthetic.

OS US611073-A.

PN 29-AUG-2000.

PF 06-FEB-1998; 98US-00020222.

PR 17-APR-1997; 97US-0104590P.

XX (GETH) GENENTECH INC.

PI Lasky LA;

DR WPI; 2000-586378/55.

PT Novel PST phosphatase interacting protein useful for inducing
 PT polymerization of actin monomers and for identifying homolog of PST
 PT phosphatase interacting protein.

PS Disclosure; Col 34; 48pp; English.

XX AAB08487-90 represent peptides derived from protein tyrosine phosphatase
 CC (PTP). They were used to identify interaction domains of a murine protein
 CC tyrosine phosphatase (PTP) phosphatase interacting protein (PSTPIP).
 CC PSTPIP polypeptides are bound by and dephosphorylated by the PST family
 CC of protein tyrosine phosphatases. PSTPIP associates with actin. PSTPIP is
 CC useful for inducing the polymerisation of actin monomer in eukaryotic
 CC cells by introducing the polypeptide into the cell. The polypeptide is
 CC useful for identifying and isolating PSTPIP homologues in another
 CC mammalian species, in screening assays to identify antagonists and
 CC agonists of native PSTPIP polypeptide and as molecular weight markers on
 CC protein gels. The PSTPIP nucleic acid is useful for tissue typing of
 CC specific mammalian tissues, for preparing PSTPIP polypeptides by
 CC recombinant techniques, as hybridisation probes for searching cDNA and
 CC genomic libraries for the coding sequence of other PSTPIP analogues and
 CC to isolate homologous genes specifically expressed in tumour cells.
 CC Antagonists of PSTPIP peptide are useful for inhibiting biological
 CC activity of the peptide. Antibodies of PSTPIP are useful to identify
 CC rapidly dividing cells and are used to image tumours comprising such
 CC rapidly dividing cells

XX Sequence 19 AA;

Query Match 27.2%; Score 31; DB 3; Length 19;
 Best Local Similarity 50.0%; Pred. No. 1.6e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15
 Db 3 GNRFSKPKGP 12

```

RESULT 95
ADJ90114
ID ADJ90114 standard; peptide; 19 AA.
XX
AC ADJ90114;
XX
XX 06-MAY-2004 (first entry)
XX
DE Human papillomavirus minor capsid protein L2 peptide #261.
XX
XX transporter peptide; UEV domain; Tsg101; viral infection; HIV; AIDS;
XX hepatitis B virus infection; human herpesvirus 1 infection;
XX human herpesvirus 2 infection.
XX
OS Human papillomavirus type 6b.
XX
PN WO2003053332-A2.
XX
XX 03-JUL-2003.
XX
PF 20-AUG-2002; 2002WO-US026549.
XX
PR 20-AUG-2001; 2001US-0313695P.
XX
PA (MYRI-) MYRIAD GENETICS INC.
XX
PI Morham S, Zavitz K, Hobden A;
XX
DR WPI; 2003-586940/55.
XX
PT Peptides and hybrid polypeptides associated with a transporter that
PT increases its uptake by a mammalian cell, useful for inhibiting viral
PT budding or propagation, especially for treating e.g. AIDS or hepatitis B
PT virus infection.
XX
PS Claim 35; SEQ ID NO 1582; 137pp; English.
XX
CC The invention comprises a composition which contains a peptide associated
CC with a transporter that is capable of increasing the uptake of the
CC peptide by a mammalian cell. The peptide of the invention contains the
CC amino acid motif Pro-Xaa-Xaa-Pro and is capable of binding the UEV domain
CC of Tsg101. The composition of the invention is useful in the manufacture
CC of a medicament for the treatment of viral infections, such as: HIV
CC infection (particularly AIDS), hepatitis B virus infection and human
CC herpesvirus 1/2 infection. The present amino acid sequence represents a
CC peptide of the invention.
XX
SQ Sequence 19 AA;
XX
Query Match 27.2%; Score 31; DB 7; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
XX
QY 1 DYEYPSRLGNPKAP 15
DB 5 DITFPYRWKTPSP 19
XX
RESULT 96
ADV13539
ID ADV13539 standard; peptide; 19 AA.
XX
AC ADV13539;
XX
XX 10-MAR-2005 (first entry)
XX
DE Human phosphorylated peptide from phosphoprotein #1477.
XX
XX Alzheimer's disease; neuroprotective; nootropic; degeneration; tumor;
XX neoplasm; neurological disease; phosphorylation; protein sequencing;
XX phosphoprotein.
XX

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XX
OS Homo sapiens.
XX
XX WO2004108948-A2.
XX
XX 16-DEC-2004.
XX
XX 04-JUN-2004; 2004WO-US017613.
XX
XX 04-JUN-2003; 2003US-0476010P.
XX
XX (HARD ) HARVARD COLLEGE.
XX
XX Gyl SP;
XX
DR WPI; 2005-031720/03.
XX
PT Characterizing phosphorylated polypeptides in a sample comprises
PT digesting the polypeptides with a protease thus generating test peptides,
PT and collecting a fraction of test peptides that enriched for positively
PT charged peptides.
XX
PS Claim 16; Page 87; 123pp; English.
XX
XX The invention relates to characterizing phosphorylated polypeptides in a
XX sample comprising digesting the polypeptides with a protease thus
XX generating test peptides, and collecting a fraction of test peptides that
XX enriched for positively charged peptides. Also included are a method
XX (comprising determining the presence, absence or level of one or more
XX phosphorylated peptides as identified above in cells having a cell state
XX and determining the degree of correlation between the presence, absence
XX or level of phosphorylated polypeptide with the cell state), an isolated
XX peptide of 5-50 amino acids comprising an amino acid sequence that is a
XX subsequence of any of the protein sequences given in the specification
XX (and which comprise a phosphorylation site within the subsequence), an
XX isolated polypeptide selected from any of the polypeptides listed in the
XX specification and is modified at a modification site, an isolated peptide
XX comprising a mass spectral peak signatures, a method for identifying a
XX treatment that modulates phosphorylation of an amino acid in a target
XX polypeptide, a method for generating a peptide standard, a pair of
XX peptide standards comprising the peptide obtained (where the peptide is
XX phosphorylated and a corresponding peptide comprising an identical amino
XX acid sequence but which is not phosphorylated), a system (comprising a
XX computer memory comprising data files storing information relating to the
XX identifying characteristics of positively charged peptides, and a data
XX analysis module capable of executing instructions for organizing and/or
XX searching the data files), a computer program product (comprising data
XX relating to the identifying characteristics of positively charged
XX peptides and comprising instructions for organizing and/or searching the
XX data), and a method for identifying N-terminal peptides in a sample. The
XX method is useful for characterizing phosphorylated polypeptides in a
XX sample. The present sequence is a peptide from a human phosphoprotein,
XX containing a phosphorylation site, identified by the method of the
XX invention.
XX
SQ Sequence 19 AA;
XX
Query Match 27.2%; Score 31; DB 9; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
XX
QY 11 NPKAPLYKRP 20
DB 1 NPKMPQYSSP 10
XX
RESULT 97
ADE15767
ID ADE15767 standard; peptide; 20 AA.
XX
AC ADE15767;
XX
XX 29-JAN-2004 (first entry)
XX

```


PR 31-AUG-2001; 2001US-0316805P.
 XX (STRD) UNIV STANFORD.
 PA (ELIL) LILLY & CO ELI.
 XX
 XX Glenn JS, Myers TM, Glass JI,
 DR WPI; 2003-201229/19.
 XX
 XX Identifying a compound for treating Hepatitis C virus (HCV) infection by
 PT assessing the ability of a compound to interfere the binding of an
 PT amphipathic helix of an HCV nonstructural protein with cytoplasmic
 PT membranes of eukaryotic cell.
 XX
 PS Claim 44; Page 17; 43pp; English.
 XX
 XX The invention relates to a novel method for identifying a compound useful
 CC for treating Hepatitis C virus (HCV) infection. The method comprises
 CC assessing the ability of a candidate compound to interfere with the
 CC binding of an amphipathic helix present in the N-terminal region of an
 CC HCV non-structural protein with cytoplasmic membranes of a eukaryotic
 CC cell, where a compound that interferes with the binding is useful for
 CC treating the infection. The compounds of the invention have virucide, and
 CC hepatotropic activity. The peptides may have a use in gene therapy. The
 CC methods and compounds are useful for treating Hepatitis C virus (HCV)
 CC infection. The composition is useful for eliciting an immunological
 CC response against HCV. The peptides are useful for the preparation of a
 CC medicament for the prevention or treatment of HCV infection in a human.
 CC The sequences shown in ABR00747-ABR00754 represent ligands of the
 CC amphipathic helix of the HCV nonstructural protein NS5A
 XX
 SQ Sequence 13 AA;

Query Match 26.8%; Score 30.5; DB 6; Length 13;
 Best Local Similarity 64.3%; Pred. No. 1.3e+03;
 Matches 9; Conservative 1; Mismatches 1; Indels 3; Gaps 2;

OY 4 YPGSR LGN--PKAP 15
 ||| |||
 Db 1 YP-SKPGNTPKAP 13

RESULT 100
 ADU70749
 XX ID ADU70749 standard; peptide; 9 AA.
 XX
 XX AC ADU70749;
 XX
 XX 10-FEB-2005 (first entry)
 XX
 XX Human heparanase peptide SEQ ID NO:434.
 DE
 XX Human heparanase; vaccine; human leukocyte antigen; HLA;
 KM enzyme; heparinase; cytostatic; immune disorder; metastasis.
 KW Immunostimulant; cytostatic; immune disorder; metastasis.
 XX
 OS Homo sapiens.
 XX
 XX EPI479764-A1.
 PN
 XX 24-NOV-2004.
 PD
 XX 19-MAY-2003; 2003BP-00011038.
 PF
 XX 19-MAY-2003; 2003BP-00011038.
 PR
 XX (DEKR-) DEUT KREBSFORSCHUNGSZENTRUM.
 PA (UYHE-) UNIV HEIDELBERG RUPRECHT-KARLS.
 XX
 XX Schlirmacher V, Beckhove P, Sommerfeldt N;
 PI WPI; 2005-014847/02.
 DR
 XX New heparanase nonapeptide that binds to a human leukocyte antigen (HLA)
 PT

PT molecule or its functional derivative, useful for preparing a medicament
 PT for inducing an immune response or for treating metastatic tumors.
 XX
 XX
 PS Claim 3; SEQ ID NO 434; 269pp; English.
 XX

CC The invention relates to a novel heparanase peptide that binds to a human
 CC leukocyte antigen (HLA) molecule, where the peptide is a nonapeptide, or
 CC its functional derivative. A peptide of the invention has immunostimulant
 CC and cytostatic activity, and is used in a vaccine. The heparinase peptide
 CC is useful for preparing a medicament which induces an immune response or
 CC for treating metastatic tumors. The present sequence represents a
 CC heparinase peptide of the invention.
 XX

SQ Sequence 9 AA;

Query Match 26.3%; Score 30; DB 9; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 5 PGRSLGNP 12
 ||| |||
 Db 2 PGSSILGP 9

Search completed: January 20, 2006, 19:05:10
 Job time : 79.5769 secs

ALIGNMENTS

RESULT 1

US-09-292-225-2

Sequence 2, Application US/09292225

Patent No. 6455686

GENERAL INFORMATION:

APPLICANT: McCall, Catherine A.

APPLICANT: Hunter, Shirley Wu

APPLICANT: Weber, Eric R.

TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS

FILE REFERENCE: AL-2-C3

CURRENT APPLICATION NUMBER: US/09/292,225

EARLIER FILING DATE: 1999-04-15

EARLIER APPLICATION NUMBER: 60/098,909

EARLIER FILING DATE: 1998-09-02

EARLIER APPLICATION NUMBER: 60/085,295

EARLIER FILING DATE: 1998-05-13

EARLIER APPLICATION NUMBER: 60/098,565

EARLIER FILING DATE: 1998-04-17

EARLIER APPLICATION NUMBER: 09/062,013

EARLIER FILING DATE: 1998-04-17

NUMBER OF SEQ ID NOS: 49

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 2

LENGTH: 20

TYPE: PR

ORGANISM: Dermatophagoides farinae

US-09-292-225-2

Query Match 100.0%; Score 114; DB 2; Length 20;

Best Local Similarity 100.0%; Pred. No. 1.5e-10;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPKAPLYKRP 20

Db 1 DYEYPSRLGNPKAPLYKRP 20

RESULT 2

US-08-179-557-37

Sequence 37, Application US/08179557

Patent No. 5837509

GENERAL INFORMATION:

APPLICANT: ISRAELSEN, Hans

APPLICANT: BECH HANSEN, Egon

APPLICANT: MADSEN, Soeren Michael

APPLICANT: JOHANSEN, Eric

APPLICANT: NILSSON, Dan

APPLICANT: VRANG, Astrid

TITLE OF INVENTION: Recombinant Lactic Acid Bacterium

TITLE OF INVENTION: Containing an Inserted Promoter and Method of Constructing

NUMBER OF SEQUENCES: 39

CORRESPONDENCE ADDRESS:

ADDRESSER: Foley & Lardner

STREET: 3000 K Street, N.W.

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/179,557

FILING DATE: 07-JAN-1994

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 1579/92

FILING DATE: 30-DEC-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: DK 0988/93

FILING DATE: 01-SEP-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/DK94/00004

FILING DATE: 03-JAN-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/036,681

FILING DATE: 25-MAR-1993

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30307/140/PLVI

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202 672 5300

TELEFAX: 202 672 5399

TELEX: 904136

INFORMATION FOR SEQ ID NO: 37:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-179-557-37

Query Match 31.6%; Score 36; DB 1; Length 16;

Best Local Similarity 70.0%; Pred. No. 59;

Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYPSRLG 10

Db 7 DLQDPGSRIG 16

RESULT 3

US-08-981-601-12

Sequence 12, Application US/08981601

Patent No. 6133023

GENERAL INFORMATION:

APPLICANT: MADSEN, Soeren Michael

APPLICANT: VRANG, Astrid

APPLICANT: ARNAU, Jose

APPLICANT: RAVN, Peter

APPLICANT: GROENVAALD JOHNSEN, Mads

TITLE OF INVENTION: A LACTIC ACID BACTERIAL REGULATABLE

TITLE OF INVENTION: EXPRESSION SYSTEM

NUMBER OF SEQUENCES: 30

CORRESPONDENCE ADDRESS:

ADDRESSER: FOLEY & LARDNER

STREET: 3000 K Street, N.W.

CITY: Washington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/981,601

FILING DATE: 29-DEC-1997

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/DK97/00341

FILING DATE: 22-AUG-1997

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/711,434

FILING DATE: 06-SEP-1996

ATTORNEY/AGENT INFORMATION:

NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 030307/0158
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-981-601-12

Query Match 31.6%; Score 36; DB 2; Length 16;
Best Local Similarity 70.0%; Pred. No. 59;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEPGSRIG 10
DB 7 DLDPGSRIG 16

RESULT 4

US-08-938-830-22
Sequence 22, Application US/08938830
Patent No. 6040437
GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
APPLICANT: Dowbenko, Donald J.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,830
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-938-830-22

Query Match 31.6%; Score 36; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 6 GSRIGPKAP 15
DB 6 GSRIGPKAP 15

DB 3 GNRGKPKP 12

RESULT 5

US-09-020-222-22
Sequence 22, Application US/09020222
Patent No. 611073
GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPs)
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,222
FILING DATE: 06-Feb-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 02/07/1997
ATTORNEY/AGENT INFORMATION:
NAME: Dregler, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-020-222-22

Query Match 31.6%; Score 36; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 GSRIGPKAP 15
DB 3 GNRGKPKP 12

RESULT 6

US-09-068-377-22
Sequence 22, Application US/09068377
Patent No. 688705
GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
APPLICANT: Dowbenko, Donald J.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
TITLE OF INVENTION: Proteins (PSTPIPs)
FILE REFERENCES: P1066P2
CURRENT APPLICATION NUMBER: US/09/068,377
CURRENT FILING DATE: 1999-05-08
EARLIER APPLICATION NUMBER: US 08/938,300
EARLIER FILING DATE: 1997-09-29
EARLIER APPLICATION NUMBER: US 08/798,419
EARLIER FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 73
SEQ ID NO 22
LENGTH: 20

;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; NAME/KEY: Artificial Sequence
;; LOCATION: 1-20
;; OTHER INFORMATION: Synthetic oligopeptide
US-09-068-377-22

Query Match 31.6%; Score 36; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 75;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 6 GSRLGNPKAP 15
Db 3 GNRCKGPKGP 12

RESULT 7
US-07-972-032-8
; Sequence 8, Application US/07972032
; Patent No. 5496712
; GENERAL INFORMATION:
; APPLICANT: Cappello, Joseph
; APPLICANT: Ferrari, Franco A.
; TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
; TITLE OF INVENTION: PROTEIN POLYMERS
; NUMBER OF SEQUENCES: 85
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bertam I. Rowland
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: CA 94111
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/972,032
; FILING DATE: 19921105
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/791,960
; FILING DATE: 12-NOV-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Rowland, Bertam I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A-55556-1/BIR,PROP-08-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-07-972-032-8

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PGSRLGNPKAP 15
Db 6 PCSR-GDPCAP 15

RESULT 8
US-08-642-255-8
; Sequence 8, Application US/08642255

; Patent No. 5773249
; GENERAL INFORMATION:
; APPLICANT: CAPPELLO, Joseph
; APPLICANT: FERRARI, Franco A.
; TITLE OF INVENTION: High Molecular Weight Collagen-Like
; TITLE OF INVENTION: Protein Polymers
; NUMBER OF SEQUENCES: 135
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/642,255
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: ROWLAND, Bertam I.
; REGISTRATION NUMBER: 20,015
; REFERENCE/DOCKET NUMBER: A55556-3/BIR
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 494-8700
; TELEFAX: (415) 494-8771
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 8:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-642-255-8

Query Match 30.3%; Score 34.5; DB 1; Length 18;
Best Local Similarity 72.7%; Pred. No. 1.1e+02;
Matches 8; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

Qy 5 PGSRLGNPKAP 15
Db 6 PCSR-GDPCAP 15

RESULT 9
US-07-955-905A-3
; Sequence 3, Application US/07955905A
; Patent No. 5770433
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: RECOMBINANT 47 AND 31 KD COCOA PROTEINS AND
; TITLE OF INVENTION: PRECURSOR
; NUMBER OF SEQUENCES: 28
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/955,905A
; FILING DATE: 21-JAN-1993
; CLASSIFICATION: 435
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

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; ORIGINAL SOURCE:
; ORGANISM: Theobroma cacao
; FEATURE:
; NAME/KEY: Region
; LOCATION: 1..14
; OTHER INFORMATION: /note="Tentative N-terminal
; OTHER INFORMATION: sequence of 47kD mature protein"
US-07-955-905A-3

Query Match      29.8%; Score 34; DB 1; Length 14;
Best Local Similarity 60.0%; Pred. NO. 1e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      3 EYPSGRUGNP 12
DB      1 EEPGSGPAMP 10

RESULT 10
US-09-025-706-6
; Sequence 6, Application US/09025706
; Patent No. 5958874
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Gelling, Doris
; APPLICANT: Gailit, James
; TITLE OF INVENTION: RECOMBINANT FIBRONECTIN-BASED
; TITLE OF INVENTION: EXTRACELLULAR MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,706
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R263
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-706-6

Query Match      28.9%; Score 33; DB 1; Length 18;
Best Local Similarity 42.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY      2 YEYPSGRUGNP 20
DB      1 YEKPGS----PREVPRP 15

RESULT 11
US-09-025-622-6
; Sequence 6, Application US/09025622
```

```

; Patent No. 6194378
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A
; APPLICANT: Gelling, Doris
; APPLICANT: Gailit, James
; TITLE OF INVENTION: FIBRONECTIN PEPTIDES-BASED EXTRACELLULAR
; TITLE OF INVENTION: MATRIX FOR WOUND HEALING
; NUMBER OF SEQUENCES: 12
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Jaeckle Fleischmann & Mugel, LLP
; STREET: 39 State Street
; CITY: Rochester
; STATE: New York
; COUNTRY: USA
; ZIP: 14614-1310
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/025,622
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Braham, Susan J
; REGISTRATION NUMBER: 34,103
; REFERENCE/DOCKET NUMBER: 87653.97R270
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 716-262-3640
; TELEFAX: 716-262-4133
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-025-622-6

Query Match      28.9%; Score 33; DB 2; Length 18;
Best Local Similarity 42.1%; Pred. No. 1.9e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY      2 YEYPSGRUGNP 20
DB      1 YEKPGS----PREVPRP 15

RESULT 12
US-10-394-980-17
; Sequence 17, Application US/10394980
; Patent No. 6908740
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCES: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
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ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: part of HBB_HUMAN ((P02023) hemoglobin beta chain)
US-10-394-980-17

Query Match 28.9%; Score 33; DB 2; Length 19;
Best Local Similarity 46.2%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DYEPGSRIGNPK 13
| : |||||
Db 7 DLSTPDVAVGNPK 19

RESULT 13
US-08-233-203-4
Sequence 4, Application US/08233203
Patent No. 5409898
GENERAL INFORMATION:
APPLICANT: Darveau, Richard P.
APPLICANT: Blake, James J.
APPLICANT: Coband, Wesley L.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
TITLE OF INVENTION: INFECTIONS CAUSED BY ORGANISM SENSITIVE TO BETA-LACTAM
TITLE OF INVENTION: ANTIBIOTICS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bristol-Myers Squibb Company, Patent
ADDRESSEE: Department
STREET: 3005 First Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98121
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/233,203
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/655,321
FILING DATE: 19-FEB-1991
APPLICATION NUMBER: US 07/484,020
FILING DATE: 23-FEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: Poor, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: ON0063A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206/728-4800
TELEFAX: 206/448-4775
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: YES
US-08-233-203-4

Query Match 28.1%; Score 32; DB 1; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 15 PLYKRP 20
| : |||||
Db 1 PLYKRP 6

RESULT 14
US-08-625-691-15
Sequence 15, Application US/08625691
Patent No. 5763574
GENERAL INFORMATION:
APPLICANT: Conley, Anthony J.
APPLICANT: Boots, Lynn J.
APPLICANT: Arnold, Beth A.
APPLICANT: Keller, Paul M.
TITLE OF INVENTION: HIV-SPECIFIC SYNTHETIC ANTIGENS AND
TITLE OF INVENTION: THEIR USE
NUMBER OF SEQUENCES: 33
CORRESPONDENCE ADDRESS:
ADDRESSEE: Joanne M. Gieser
STREET: 126 E. Lincoln Avenue, P.O. Box 2000
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065

COMPUTER READABLE FORM:
MEDIUM TYPE: Tape
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,691
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Gieser, Joanne M.
REGISTRATION NUMBER: 32,838
REFERENCE/DOCKET NUMBER: 19270
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3046
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-08-625-691-15

Query Match 28.1%; Score 32; DB 1; Length 15;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 YEYPSGR 8
| : |||||
Db 9 YHYPSGR 15

RESULT 15
US-08-729-152-43
Sequence 43, Application US/08729152
Patent No. 5871739
GENERAL INFORMATION:
APPLICANT: Inoue, Brl
TITLE OF INVENTION: Pharmaceutical Composition
NUMBER OF SEQUENCES: 47
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Iland & Ponack
STREET: Southern Building, Suite 700, 805 Fifteenth
CITY: Street, N.W.
STATE: D.C.
COUNTRY: USA

ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.5 inch, 1.44 Mb storage
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/729,152
FILING DATE: 11-OCT-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 291993/1995
FILING DATE: 13-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
TELEX:
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
US-08-729-152-43

Query Match 28.1%; Score 32; DB 1; Length 17;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 2 YKPGSR 8
DB 10 YKPGSR 16

RESULT 16
US-08-630-915A-226
Sequence 226, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
TITLE OF INVENTION: DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872

REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-630-915A-226

Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 63.6%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 GSRLENPXAPL 16
DB 2 GSGIAPPKPL 12

RESULT 17
US-08-469-260A-251
Sequence 251, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESSES:
ADDRESSER: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: POREMSKI, PRISCILLA B.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-938-2623
TELEFAX: 708-937-6365
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-469-260A-251

Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPL 16
DB 1 PSERFSSPKLPV 12

RESULT 18
US-08-488-446-251

Sequence 251, Application US/08488446
Patent No. 6558898

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMJ. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRES:
ADDRESS: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: POBEMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623

INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-488-446-251

Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPL 16
DB 1 PSERFSSPKLPV 12

RESULT 19
US-08-467-344A-251

Sequence 251, Application US/08467344A
Patent No. 6586568

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMJ. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHRHOF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESS: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <Unknown>

ATTORNEY/AGENT INFORMATION:
NAME: POBEMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 251:

US-08-467-344A-251

Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPL 16
DB 1 PSERFSSPKLPV 12

RESULT 20
US-09-879-957-226

Sequence 226, Application US/09879957
Patent No. 6709821

GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6709821h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLES, Dana M.
APPLICANT: MCCONNELL, Stephen J.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mastrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-879-957-226
Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 63.6%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 6 GSRIGNPKAPL 16
Db 2 GSGIAPKPP 12
RESULT 21
US-08-424-550B-251
Sequence 251, Application US/08424550B
Patent No. 6720166
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: JOHN J. PILOT-MATIAS
APPLICANT: GEORGE J. DAWSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEBHOFF
APPLICANT: JAMES C. ENKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/APed
STREET: 100 ABBOTT PARK ROAD

CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-251
Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 2.5e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 5 PSRRFSPKLPV 12
Db 1 PSRRFSPKLPV 12
RESULT 22
US-08-938-830-20
Sequence 20, Application US/08938830
Patent No. 6040437
GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
APPLICANT: Dowbenko, Donald J.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
TITLE OF INVENTION: Furrow-Associated Proteins (PSTPfs)
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 Inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,830
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreyer, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881

; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-08-938-830-20

Query Match 28.1%; Score 32; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLGNPKAP 15
|:|:|:|:
Db 5 RIGRPKGP 12

RESULT 23
US-09-020-222-20
; Sequence 20, Application US/09020222
; Patent No. 6111073
; GENERAL INFORMATION:

; APPLICANT: Laesky, Laurence A.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
; TITLE OF INVENTION: Furrow-Associated Proteins (PSTPIPS)
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Genentech, Inc.
; STREET: 1 DNA Way
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080

; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/020,222
; FILING DATE: 06-Feb-1998
; CLASSIFICATION:

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/798419
; FILING DATE: 02/07/1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: P1066r1

; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 650/225-3216
; TELEFAX: 650/952-9881
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
US-09-020-222-20

Query Match 28.1%; Score 32; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLGNPKAP 15
|:|:|:|:
Db 5 RIGRPKGP 12

RESULT 24
US-09-068-377-20
; Sequence 20, Application US/09068377
; Patent No. 6887705
; GENERAL INFORMATION:
; APPLICANT: Laesky, Laurence A.

; APPLICANT: Dowbenko, Donald J.
; TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage Furrow-Associated
; TITLE OF INVENTION: Proteins (PSTPIPS)
; FILE REFERENCE: P1066r2
; CURRENT APPLICATION NUMBER: US/09/068,377
; CURRENT FILING DATE: 1999-05-08
; EARLIER APPLICATION NUMBER: US 08/938,300
; EARLIER FILING DATE: 1997-09-29
; EARLIER APPLICATION NUMBER: US 08/798,419
; EARLIER FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 73
; SEQ ID NO 20
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: Artificial Sequence
; LOCATION: 1-20
; OTHER INFORMATION: Synthetic oligopeptide
US-09-068-377-20

Query Match 28.1%; Score 32; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 RLGNPKAP 15
|:|:|:|:
Db 5 RIGRPKGP 12

RESULT 25
US-08-211-070A-1
; Sequence 1, Application US/08211070A
; Patent No. 5585350
; GENERAL INFORMATION:

; APPLICANT: Friedrich, Thomas
; APPLICANT: Koewer, Wolfgang
; APPLICANT: Kroege, Burkhard
; APPLICANT: Bialojan, Siegfried
; TITLE OF INVENTION: No. 5585350e1 thrombin-inhibitory protein from ticks.
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Keil & Weinkauff
; STREET: 1101 Connecticut Avenue
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20036

; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette, 5.25 inch, 360 Kb storage
; COMPUTER: IBM AT-compatible, 80486 processor
; OPERATING SYSTEM: MS-DOS version 6.0
; SOFTWARE: WordPerfect version 5.1
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/211,070A
; FILING DATE: 18-MAR-1994
; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: A6IK 37/64
; APPLICATION NUMBER: PCT/EP92/02198
; FILING DATE: 23-SEP-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-211-070A-1

Query Match 27.2%; Score 31; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEPGSRGPNP 12
|||:|:|
Db 2 DYEPGPKKCRP 13

RESULT 26

US-08-859-183-8
Sequence 8, Application US/08859183
Patent No. 5827731
GENERAL INFORMATION:
APPLICANT: Friedrich, Thomas
APPLICANT: Bialojan, Siegfried
APPLICANT: Bollschweiler, Claus
APPLICANT: Kuensat, Christoph
TITLE OF INVENTION: No. 5827731el thrombin-inhibitory protein
TITLE OF INVENTION: from ticks
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Keil & Weinkauff
STREET: 1101 Connecticut Avenue
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.2 Mb storage
COMPUTER: IBM AT-compatible, 80486 processor
OPERATING SYSTEM: MS-DOS version 6.0
SOFTWARE: WordPerfect version 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/859,183
FILING DATE: 20-MAY-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/415,999
FILING DATE: 04-APR-1995
APPLICATION NUMBER: PCT/EP92/02179
FILING DATE: 21-SEP-1992
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-859-183-8

Query Match 27.2%; Score 31; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 2.9e+02;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEPGSRGPNP 12
|||:|:|
Db 2 DYEPGPKKCRP 13

RESULT 27

US-08-374-652C-12
Sequence 12, Application US/08374652C
Patent No. 5834286
GENERAL INFORMATION:
APPLICANT: NEVALAINEN, HELENA K.M.
APPLICANT: PALOHAIMO, MARJA T.
APPLICANT: PAGERSTROM, RICHARD B.
APPLICANT: MIETTINEN-OINONEN, ARJA S.
APPLICANT: TURUNEN, MARJA K.
APPLICANT: RAMBOSER, JOHN A.
APPLICANT: PIDDINGTON, CHRISTOPHER S.
APPLICANT: HOUSTON, CHRISTOPHER S.
APPLICANT: CANTRELL, MICHAEL A.
TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
TITLE OF INVENTION: ENZYMES IN DESIRED RATIOS
NUMBER OF SEQUENCES: 94
CORRESPONDENCE ADDRESS:

ADDRESSEE: STERN, KESSLER, GOLDSTEIN & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/374,652C
FILING DATE: 24-MAY-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07058
FILING DATE: 27-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/925,401
FILING DATE: 31-JUL-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: REED, GRANT E.
REGISTRATION NUMBER: 41,264
REFERENCE/DOCKET NUMBER: 1050.071001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: not relevant
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-Site
LOCATION: 4
OTHER INFORMATION: /NOTE= "Can be His or Leu"
US-08-374-652C-12

Query Match 27.2%; Score 31; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRGPNKAP 15
|||:|:|
Db 1 YPGXGAGNPLCP 12

RESULT 28

US-09-012-097A-19
Sequence 19, Application US/09012097A
Patent No. 6187757
GENERAL INFORMATION:
APPLICANT: Clackson, Timothy
APPLICANT: Gilman, Michael
APPLICANT: Holt, Dennis
APPLICANT: Keenan, Terence
APPLICANT: Rozamus, Leonard
APPLICANT: Yang, Wu
TITLE OF INVENTION: Regulation of Biological Events Using
TITLE OF INVENTION: No. 6187757el Compounds
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARIAD Pharmaceuticals, Inc.
STREET: 26 Landsdowne Street
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02139

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/012,097A
FILING DATE: 22-JAN-1998
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Berstein Esq., David L.
REGISTRATION NUMBER: 31,235
REFERENCE/DOCKET NUMBER: 31,235 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-494-0400
TELEFAX: 617-494-0208
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
US-09-012-097A-19

Query Match 27.2%; Score 31; DB 2; Length 15;
Best Local Similarity 54.5%; Pred. No. 3.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGNPKAPLYR 19
DB 4 LGGSSSPKKR 14

RESULT 29
US-08-602-999A-189
Sequence 189, Application US/08602999A
GENERAL INFORMATION:
PATENT No. 6184205
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999A
FILING DATE: 16-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-602-999A-189

Query Match 27.2%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPKAPLYK 18
DB 4 LGRPERPLRK 13

RESULT 30
US-09-500-124-189
Sequence 189, Application US/09500124
PATENT No. 6432920
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLKES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/500,124
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELFX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-09-500-124-189

Query Match 27.2%; Score 31; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LGNPKAPLYK 18
|||:||||
Db 4 LGRPEIRPLRK 13

RESULT 31

US-09-017-205-29
Sequence 29, Application US/09017205

Patent No. 5965357
GENERAL INFORMATION:
APPLICANT: Mardden, Howard S
TITLE OF INVENTION: PEPTIDE STRUCTURES AND THEIR USE IN
NUMBER OF INVENTIONS: DIAGNOSIS OF HERPES SIMPLEX VIRUS TYPE 2
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhuy PC
STREET: 8th Floor, 1100 No. 5965357th Giebe Road
CITY: Arlington
STATE: Virginia
COUNTRY: USA

ZIP: 22201-4714
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/017,205
FILING DATE: 02-FEB-1998
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mitchell, Leonard C
REGISTRATION NUMBER: 29,009
REFERENCE/DOCKET NUMBER: 604-436
TELEPHONE: (703) 816-4000
TELEFAX: (703) 816-4100
INFORMATION FOR SEQ ID NO: 29:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear

MOLECULE TYPE: peptide from HSV-2 glycoprotein G
FRAGMENT TYPE: internal

US-09-017-205-29

Query Match 27.2%; Score 31; DB 1; Length 18;
Best Local Similarity 43.8%; Pred. No. 3.8e+02;
Matches 7; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

Qy 5 PGRRLGNPKAPLYKRP 20
|||:|||||
Db 2 PGLADGDPYAPPPRP 17

RESULT 32

US-08-469-005A-3
Sequence 3, Application US/08469005A

Patent No. 5665874
GENERAL INFORMATION:
APPLICANT: KUHAJDA, FRANCIS P.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: BAKER & BOTS, L.L.P.
STREET: 1299 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20004-2400
COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 1.5

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,005A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/188,426
FILING DATE: 24-JAN-1994
APPLICATION NUMBER: 08/096,908
FILING DATE: 26-JUL-1993
APPLICATION NUMBER: 07/917,716
FILING DATE: 24-JUL-1992

ATTORNEY/AGENT INFORMATION:
NAME: Pogoreke, Laurence H
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 062482-0113
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-639-7700
TELEFAX: 202-639-7890
TELEX:

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO

ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
US-08-469-005A-3

Query Match 27.2%; Score 31; DB 1; Length 19;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 4 YPSRLGNPKAPLY 17
|||:|||||
Db 1 HPESPPTNPRPLP 14

RESULT 33

US-08-188-426-3
Sequence 3, Application US/08188426

Patent No. 5759791
GENERAL INFORMATION:
APPLICANT: KUHAJDA, Francis P.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W. -- 11th Floor
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/188,426
FILING DATE: 24-JAN-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Pogoreke, Laurence H.
REGISTRATION NUMBER: 34,698

REFERENCE/DOCKET NUMBER: 1107.45253
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-188-426-3

Query Match 27.2%; Score 31; DB 1; Length 19;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
DB 1 HPESPTNPTEPLF 14

RESULT 34
US-08-469-009-3
Sequence 3, Application US/08469009
Patent No. 5864011
GENERAL INFORMATION:
APPLICANT: Kuhajda, Francis P.
APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W. -- 11th Floor
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,009
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,426
FILING DATE: 24-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poborske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.45253
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-469-009-3

Query Match 27.2%; Score 31; DB 1; Length 19;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
DB 1 HPESPTNPTEPLF 14

RESULT 35
US-08-469-007-3
Sequence 3, Application US/08469007
Patent No. 5872217
GENERAL INFORMATION:
APPLICANT: Kuhajda, Francis P.
APPLICANT: Pasternack, Gary R.
TITLE OF INVENTION: CANCER RELATED ANTIGEN
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W. -- 11th Floor
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,007
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/188,426
FILING DATE: 24-JAN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Poborske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107.45253
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 508-9100
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
US-08-469-007-3

Query Match 27.2%; Score 31; DB 1; Length 19;
Best Local Similarity 42.9%; Pred. No. 4e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPGSRIGNPKAPLY 17
DB 1 HPESPTNPTEPLF 14

RESULT 36
US-08-938-830-21
Sequence 21, Application US/08938830
Patent No. 6040437
GENERAL INFORMATION:
APPLICANT: Laskey, Laurence A.
APPLICANT: Dowbenko, Donald J.
TITLE OF INVENTION: Tyrosine Phosphorylated Cleavage
NUMBER OF SEQUENCES: 73
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,830
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066P1
TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-938-830-21

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 6 GSRLGNPKAP 15
|:|:|:|:
DB 3 GNRFSKPKGP 12

RESULT 37
US-09-020-222-21
Sequence 21, Application US/09020222
Patent No. 611073
GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine phosphorylated Cleavage
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/020,222
FILING DATE: 06-FEB-1998
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/798419
FILING DATE: 02/07/1997
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P1066P1
TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-3216
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-020-222-21

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 6 GSRLGNPKAP 15
|:|:|:|:
DB 3 GNRFSKPKGP 12

RESULT 38
US-08-821-278A-22
Sequence 22, Application US/08821278A
Patent No. 6238902
GENERAL INFORMATION:
APPLICANT: Cheng, Jili
TITLE OF INVENTION: Protein Tyrosine Phosphatases
FILE REFERENCE: P1010R1
CURRENT APPLICATION NUMBER: US/08/821,278A
CURRENT FILING DATE: 1997-03-20
NUMBER OF SEQ ID NOS: 23
SEQ ID NO 22
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic oligonucleotide probe
US-08-821-278A-22

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 6 GSRLGNPKAP 15
|:|:|:|:
DB 3 GNRFSKPKGP 12

RESULT 39
US-09-068-377-21
Sequence 21, Application US/09068377
Patent No. 6887705
GENERAL INFORMATION:
APPLICANT: Laeky, Laurence A.
TITLE OF INVENTION: Tyrosine phosphorylated Cleavage Furrow-Associated
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Minipatn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/068,377
FILING DATE: 1999-05-08
EARLIER APPLICATION NUMBER: US 08/938,300
EARLIER FILING DATE: 1997-09-29
EARLIER APPLICATION NUMBER: US 08/798,419
EARLIER FILING DATE: 1997-02-07
NUMBER OF SEQ ID NOS: 73
SEQ ID NO 21
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
NAME/KEY: Artificial Sequence
LOCATION: 1-19
OTHER INFORMATION: Synthetic oligopeptide
US-09-068-377-21

Query Match 27.2%; Score 31; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRIGNPKAP 15
| | | | |
Db 3 GNRFSKPKP 12

RESULT 40

US-08-461-005-6
; Sequence 6, Application US/08461005
; Patent No. 5734035
; GENERAL INFORMATION:
; APPLICANT: Sharp, Phillip J
; APPLICANT: Magland, Barry M
; TITLE OF INVENTION: Nematode Vaccine
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Foley and Lardner
; STREET: Suite 500, 1800 Diagonal Road
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: United States of America
; ZIP: 22313-0299
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/461,005
; FILING DATE: 05-JUN-1995
; CLASSIFICATION: 536
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/930,685
; FILING DATE: 06-OCT-1992
; CLASSIFICATION: 536
; APPLICATION NUMBER: AT PK4487
; FILING DATE: 06-FEB-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/AU92/00041
; FILING DATE: 06-FEB-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Bent, Stephen A
; REGISTRATION NUMBER: 29,768
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-9300
; TELEFAX: (703) 683-4109
; TELEX: 899149
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ORIGINAL SOURCE: Haemonchus contortus
; ORGANISM: Haemonchus contortus
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 9
; OTHER INFORMATION: /note= "May be Gln or Tyr"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 14
; OTHER INFORMATION: /note= "May be Gly or Ser"
US-08-461-005-6

Query Match 26.3%; Score 30; DB 1; Length 14;
Best Local Similarity 75.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16
| | | | |
Db 6 LGNQAPL 13

RESULT 41

US-08-374-652C-13
; Sequence 13, Application US/08374652C
; Patent No. 5634286
; GENERAL INFORMATION:
; APPLICANT: NEVALAINEN, HELENA K.M.
; APPLICANT: PALOHIMO, MARJA T.
; APPLICANT: FAGERSTROM, RICHARD B.
; APPLICANT: MIETTINEN-OINONEN, ARJA S.
; APPLICANT: TURUNEN, MARJA K.
; APPLICANT: RAMBOSEK, JOHN A.
; APPLICANT: PIDDINGTON, CHRISTOPHER S.
; APPLICANT: HOUSTON, CHRISTINE S.
; TITLE OF INVENTION: RECOMBINANT CELLS, DNA CONSTRUCTS,
; TITLE OF INVENTION: VECTORS AND METHODS FOR EXPRESSING PHYTATE DEGRADING
; ENZYMES IN DESIRED RATIOS
; NUMBER OF SEQUENCES: 94
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX P.L.L.C.
; STREET: 1100 NEW YORK AVENUE, SUITE 600
; CITY: WASHINGTON
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/374,652C
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/925,401
; FILING DATE: 31-JUL-1992
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: REED, GRANT E.
; REGISTRATION NUMBER: 41,264
; REFERENCE/DOCKET NUMBER: 1050.071001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-371-2600
; TELEFAX: 202-371-2540
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: not relevant
; MOLECULE TYPE: peptide
US-08-374-652C-13

Query Match 26.3%; Score 30; DB 1; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 4 YPSRLGNPKAP 15
| | | | |
Db 1 YRGHGNPLGP 12

RESULT 42

US-07-930-685-6
 ; Sequence 6, Application US/07930685
 ; Patent No. 5871738
 ; GENERAL INFORMATION:
 ; APPLICANT: Sharp, Phillip J
 ; APPLICANT: Magland, Barry M
 ; TITLE OF INVENTION: Nemacode Vaccine
 ; NUMBER OF SEQUENCES: 13
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Foley and Lardner
 ; STREET: Suite 500, 1800 Diagonal Road
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: United States of America
 ; ZIP: 22313-0299
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/07/930.685
 ; FILING DATE: 19921006
 ; CLASSIFICATION: 424
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: AU PK4487
 ; FILING DATE: 06-FEB-1991
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/AU92/00041
 ; FILING DATE: 06-FEB-1992
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Bent, Stephen A
 ; REGISTRATION NUMBER: 29,768
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 836-9300
 ; TELEFAX: (703) 683-4109
 ; TELEX: 899149
 ; INFORMATION FOR SEQ ID NO: 6:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 14 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; ORIGINAL SOURCE: Haemonchus contortus
 ; FEATURE:
 ; NAME/KEY: Modified-site
 ; LOCATION: 9
 ; OTHER INFORMATION: /note= "May be Gln or Tyr"
 ; NAME/KEY: Modified-site
 ; LOCATION: 14
 ; OTHER INFORMATION: /note= "May be Gly or Ser"
 ; US-07-930-685-6

Query Match 26.3%; Score 30; DB 1; Length 14;
 Best Local Similarity 75.0%; Pred. No. 4.1e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 LGNKPAPL 16
 |||||
 DB 6 LGNKPAPL 13

RESULT 43
 US-08-505-318-27
 ; Sequence 27, Application US/08505318
 ; Patent No. 6107459
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Richard T
 ; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 ; TITLE OF INVENTION: Diagnostic Imaging
 ; NUMBER OF SEQUENCES: 28

CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
 ; STREET: 300 South Wacker Drive, Seventh Floor
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/505,318
 ; FILING DATE: 07-DEC-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5989519nan, Kevin B
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 90,1104-PF
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-913-0001
 ; TELEFAX: 312-913-0002
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 27:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 15 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-505-318-27

Query Match 26.3%; Score 30; DB 2; Length 15;
 Best Local Similarity 71.4%; Pred. No. 4.4e+02;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19
 :|||||:
 DB 1 QAPLYKR 7

RESULT 44
 US-08-290-853-37
 ; Sequence 37, Application US/08290853
 ; Patent No. 5989519
 ; GENERAL INFORMATION:
 ; APPLICANT: Dean, Richard T
 ; TITLE OF INVENTION: Technetium-99m Labeled Peptides for
 ; TITLE OF INVENTION: Imaging Inflammation
 ; NUMBER OF SEQUENCES: 37
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Banner & Allegretti, Ltd.
 ; STREET: 10 South Wacker Drive, Suite 3000
 ; CITY: Chicago
 ; STATE: Illinois
 ; COUNTRY: USA
 ; ZIP: 60606
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/290,853
 ; FILING DATE: 11-OCT-1994
 ; CLASSIFICATION: 424
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: No. 5989519nan, Kevin B
 ; REGISTRATION NUMBER: 35,303
 ; REFERENCE/DOCKET NUMBER: 92,112-H
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 312-715-1000

TELEFAX: 312-715-1234
TELEX: 910-221-5317
INFORMATION FOR SEQ ID NO: 37:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= Modified-Cys
OTHER INFORMATION: /note= "The thiol group of each cysteine is
OTHER INFORMATION: protected with an acetamidomethyl group."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= acetyl-Cys
OTHER INFORMATION: /note= "The amino terminal residue is
OTHER INFORMATION: linked to an acetyl group."
US-08-290-853-37

Query Match 26.3%; Score 30; DB 1; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19
DB 4 QAPLYKK 10

RESULT 45
US-08-505-318-21

Sequence 21, Application US/08505318
Patent No. 6107459
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Diagnostic Imaging
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,318
FILING DATE: 07-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6107459nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-505-318-21

Query Match 26.3%; Score 30; DB 2; Length 18;

Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19
DB 4 QAPLYKK 10

RESULT 46
US-08-505-318-23

Sequence 23, Application US/08505318
Patent No. 6107459
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Diagnostic Imaging
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,318
FILING DATE: 07-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: NO. 6107459nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..3
OTHER INFORMATION: /label= Tc-99m-chelator
OTHER INFORMATION: /note= "The N-terminal amino group is acetylated,
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys
OTHER INFORMATION: residues are each protected by an acetamidomethyl
OTHER INFORMATION: group"
US-08-505-318-23

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19
DB 4 QAPLYKK 10

RESULT 47
US-08-974-549A-163

Sequence 163, Application US/08974549A
Patent No. 6166178
GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Langner, Joachim

APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-002610US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 163:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-974-549A-163

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Oy 11 NPKAPLYK 18
Db 5 NPKTPICK 12

RESULT 48

US-09-402-181B-163

Sequence 163: Application US/09402181B

Patent No. 6610839

GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

Lingner, Joachim

Nakamura, Toru

Chapman, Karen B.

Morin, Gregg B.

Harley, Calvin B.

Andrews, William H.

TITLE OF INVENTION: Human Telomerase Catalytic Subunit

NUMBER OF SEQUENCES: 633

CORRESPONDENCE ADDRESS:

ADDRESSEE: Townsend and Townsend and Crew LLP

STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco

STATE: California

COUNTRY: USA

ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/402,181B

FILING DATE: 29-Sep-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

APPLICATION NUMBER: US 08/851,843

FILING DATE: 06-MAY-1997

APPLICATION NUMBER: US 08/854,050

FILING DATE: 09-MAY-1997

APPLICATION NUMBER: US 08/911,312

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/912,951

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: US 08/915,503

FILING DATE: 14-AUG-1997

APPLICATION NUMBER: WO PCT/US97/17885

FILING DATE: 01-OCT-1997

ATTORNEY/AGENT INFORMATION:

NAME: Ausenius, Scott L.

REGISTRATION NUMBER: 42,271

REFERENCE/DOCKET NUMBER: 015389-002620US

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 163:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 163:

US-09-402-181B-163

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYK 18
Db 5 NPKTPIKK 12

RESULT 49
US-09-721-456-163
; Sequence 163, Application US/09721456
; Patent No. 6617110
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toshi
; Chapman, Karen B.
; Morin, Gregg B.
; Harley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/721,456
; FILING DATE: 22-No. 6617110-2000
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/974,549A
; FILING DATE: 19-NOV-1997
; APPLICATION NUMBER: US 08/724,643
; FILING DATE: 01-OCT-1996
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-APR-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-APR-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-MAY-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-MAY-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-AUG-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-OCT-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-OCT-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear

MOLECULE TYPE: Peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-09-721-456-163

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 5.3e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYK 18
Db 5 NPKTPIKK 12

RESULT 50
US-09-623-548A-1140
; Sequence 1140, Application US/09623548A
; Patent No. 6849714
; GENERAL INFORMATION:
; APPLICANT: Conjugchem, Inc.
; APPLICANT: Bridon, Dominique
; APPLICANT: Ezrin, Alan
; APPLICANT: Milner, Peter
; APPLICANT: Holmes, Darren
; APPLICANT: Thibodeau, Karen
; TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
; TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
; FILE REFERENCE: 2110
; CURRENT APPLICATION NUMBER: US/09/623,548A
; CURRENT FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/134,406
; PRIOR FILING DATE: 1999-05-17
; PRIOR APPLICATION NUMBER: 60/153,406
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: 60/159,783
; PRIOR FILING DATE: 1999-10-18
; NUMBER OF SEQ ID NOS: 1617
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1140
; LENGTH: 18
; TYPE: PPT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: Peptide
US-09-623-548A-1140

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 42.1%; Pred. No. 5.3e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEPGSRILNPKAPLYKRP 20
Db 1 YEKPGS----PPRRVPRP 15

RESULT 51
US-10-131-346-8
; Sequence 8, Application US/10131346
; Patent No. 6881396
; GENERAL INFORMATION:
; APPLICANT: Cyr, John B.
; TITLE OF INVENTION: STRABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
; FILE REFERENCE: 09744-017001
; CURRENT APPLICATION NUMBER: US/10/131,346
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 09/695,360
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: PCT/US01/50423
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 8
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetic construct
US-10-131-346-8

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KAPLYKR 19
Db 4 QAPLYKK 10

RESULT 52
US-09-657-276-1140
Sequence 1140, Application US/09657276
Patent No. 6887470
GENERAL INFORMATION:
APPLICANT: Conjuchem, Inc.
APPLICANT: Bridon, Dominique
APPLICANT: Ezrin, Alan
APPLICANT: Milner, Peter
APPLICANT: Holmes, Darren
APPLICANT: Thibaudau, Karen
TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
TITLE OF INVENTION: PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
FILE REFERENCE: 2110
CURRENT APPLICATION NUMBER: US/09/657,276
CURRENT FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: 60/134,406
PRIOR FILING DATE: 1999-05-17
PRIOR APPLICATION NUMBER: 60/153,406
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: 60/159,783
PRIOR FILING DATE: 1999-10-18
NUMBER OF SEQ ID NOS: 1617
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1140
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-657-276-1140

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 42.1%; Pred. No. 5.3e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

Qy 2 YETPGRLGNPKAPLYKR 20
Db 1 YERKGS---PPEVVRP 15

RESULT 53
US-10-131-543-8
Sequence 8, Application US/10131543
Patent No. 6902718
GENERAL INFORMATION:
APPLICANT: Cyr, John E.
APPLICANT: Pearson, Daniel A.
TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
FILE REFERENCE: 09744-016001
CURRENT APPLICATION NUMBER: US/10/131,543
CURRENT FILING DATE: 2002-04-24
PRIOR APPLICATION NUMBER: US 09/694,992

PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: PCT/US01/50423
PRIOR FILING DATE: 2001-10-24
NUMBER OF SEQ ID NOS: 29
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Synthetic construct
US-10-131-543-8

Query Match 26.3%; Score 30; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 13 KAPLYKR 19
Db 4 QAPLYKK 10

RESULT 54
US-07-805-437-4
Sequence 4, Application US/07805437
Patent No. 5364757
GENERAL INFORMATION:
APPLICANT: Garry, R.F. et al.
TITLE OF INVENTION: Association Between A Human
TITLE OF INVENTION: Immunodeficiency Virus-Related Retrovirus And Autoimmune
TITLE OF INVENTION: Disease
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/805,437
FILING DATE: 19911211
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5113-034
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9080
TELEFAX: 212 8698864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-07-805-437-4

Query Match 26.3%; Score 30; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 PKAPLYK 18
Db 5 PKPPFYK 11

RESULT 55
US-08-291-349A-1
; Sequence 1, Application US/08291349A
; Patent No. 5545620
; GENERAL INFORMATION:
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; APPLICANT: Furcht, Leo T.
; TITLE OF INVENTION: Synthetic Fibronectin Fragments As
; TITLE OF INVENTION: Inhibitors of Retroviral Infection
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Allegretti & Witcoff
; STREET: 10 S. Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/291,349A
; FILING DATE: 16 AUG 1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/006,121
; FILING DATE: 19 JAN 1993
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: McDonnell, John J.
; REGISTRATION NUMBER: 26,949
; REFERENCE/DOCKET NUMBER: 92,673-B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-715-1000
; TELEFAX: 312-715-1234
; TELETYPE: 910-221-5317
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Peptide
; LOCATION: 1..19
; OTHER INFORMATION: /note="FNI (1906-1924)
; OTHER INFORMATION: fibronectin fragment : FN-C/H-I"
US-08-291-349A-1
Query Match 26.3%; Score 30; DB 1; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
QY 2 YEYPSRLGNPKAPLYKRP 20
DB 1 YEKPGS----PPREVVRP 15
RESULT 56
US-07-990-296-1
; Sequence 1, Application US/07990296
; Patent No. 5591719
; GENERAL INFORMATION:
; APPLICANT: Furcht, Leo T.
; APPLICANT: Allen, Janice B.
; APPLICANT: Wahl, Sharon M.
; APPLICANT: McCarthy, James B.
; TITLE OF INVENTION: Method for Treating Acute and

; TITLE OF INVENTION: Chronic Inflammatory Disorders Using Polypeptides
; TITLE OF INVENTION: with Fibronectin Activity
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merchant & Gould
; STREET: 3100 No. 5591719west Center
; CITY: Minneapolis
; STATE: MN
; COUNTRY: USA
; ZIP: 55402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: WordPerfect 5.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/990,296
; FILING DATE: 19921210
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Kowalchuk, Alan W.
; REGISTRATION NUMBER: 31,535
; REFERENCE/DOCKET NUMBER: 600,252-US-01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 612-332-5300
; TELEFAX: 612-332-9081
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acid residues
; TYPE: AMINO ACID
; TOPOLOGY: linear
; MOLECULE TYPE: Peptide
; FRAGMENT TYPE: Internal Fragment
; ORIGINAL SOURCE: Synthetically Derived
; FEATURE:
; NAME/KEY: Fragment of the 33 KD carboxy
; NAME/KEY: terminal heparin-binding fragment of the A
; NAME/KEY: chain of fibronectin
; LOCATION: Represents isolated fibronectin
; LOCATION: residues 1906-1924 from all plasma isoforms
; LOCATION: of fibronectin
US-07-990-296-1
Query Match 26.3%; Score 30; DB 1; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
QY 2 YEYPSRLGNPKAPLYKRP 20
DB 1 YEKPGS----PPREVVRP 15
RESULT 57
US-08-462-784-1
; Sequence 1, Application US/08462784
; Patent No. 5714313
; GENERAL INFORMATION:
; APPLICANT: Dean, Richard T.
; APPLICANT: Moyer, Brian
; TITLE OF INVENTION: Technetium-99m labeled Peptides for
; TITLE OF INVENTION: Imaging Inflammation
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
; STREET: 300 South Wacker Drive Seventh Floor
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60606
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/462,784
FILING DATE: 05-JUN-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 571433man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 913 0001
TELEFAX: 312 913 0002
TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label= MODIFIED-CYS
OTHER INFORMATION: /note= "The thiol group of each cysteine is
OTHER INFORMATION: protected by an acetamidomethyl group; the amino
OTHER INFORMATION: terminal amine is acetylated."
US-08-462-784-1

Query Match 26.3%; Score 30; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYRK 19
Db 5 QAPLYRK 11

RESULT 58
US-08-202-989-2
Sequence 2, Application US/08202989
Patent No. 5795860
GENERAL INFORMATION:
APPLICANT: MITT, DAVID P.
APPLICANT: HERLIHY, WALTER C.
TITLE OF INVENTION: ANALOGS FOR SPECIFIC OLIGOSACCHARIDE
TITLE OF INVENTION: -PROTEIN INTERACTIONS AND USES THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESSEE: THIBEAULT
STREET: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/202,989
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,558
FILING DATE: 01-MAR-1993
ATTORNEY/AGENT INFORMATION:
NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: GLY-003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000

TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..19
OTHER INFORMATION: /label= PR4
OTHER INFORMATION: /note= "OPENHEIM ET AL. (1991) ANN. REV. IMMUNOL.
OTHER INFORMATION: 9:617-648"
US-08-202-989-2

Query Match 26.3%; Score 30; DB 1; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYRK 19
Db 5 QAPLYRK 11

RESULT 59
US-08-480-133A-1
Sequence 1, Application US/08480133A
Patent No. 5840691
GENERAL INFORMATION:
APPLICANT: Furcht, Leo T.
APPLICANT: McCarthy, James B.
APPLICANT: Wahl, Sharon M.
APPLICANT: Allen, Janice B.
APPLICANT: Billups, Kevin L.
APPLICANT: Everett, Jeffrey E.
TITLE OF INVENTION: Method for Treating Inflammatory
TITLE OF INVENTION: Diseases Using Polypeptides with Fibronectin Activity
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Merchant & Gould
STREET: 90 South 7th Street, 3100 No. 5840691west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,133A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600-308US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-480-133A-1

Query Match 26.3%; Score 30; DB 1; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
DB 1 YEYPSG---PPREVVRP 15

RESULT 60

US-08-394-748A-9
Sequence 9, Application US/08394748A

PATENT No. 6013628
GENERAL INFORMATION:
APPLICANT: Skubitz, Amy P.N.
APPLICANT: Furcht Leo T.
APPLICANT: Balles, Mark
APPLICANT: Geregerson, Dale S.
APPLICANT: Agarwal, Anita
APPLICANT: Wright, Martha M.
APPLICANT: Murali, Shobana
TITLE OF INVENTION: Method for Treating Conditions of the Eye
TITLE OF INVENTION: Using Polypeptides
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merchant & Gould
STREET: 3100 No. 6013628west Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,748A
FILING DATE: 27-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Carter, Charles G.
REGISTRATION NUMBER: 35,093
REFERENCE/DOCKET NUMBER: 600.307US01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081

INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: FN-C/H-1
US-08-394-748A-9

Query Match 26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
DB 1 YEYPSG---PPREVVRP 15

RESULT 61

US-08-564-315-1
Sequence 1, Application US/08564315

PATENT No. 601958
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Moyer, Brian
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,315
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,784
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 601958man, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 913 0001
TELEFAX: 312 913 0002

TELEX:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..4

OTHER INFORMATION: /label= MODIFIED-CYS
OTHER INFORMATION: /notes="The thiol group of each cysteine is
OTHER INFORMATION: protected by an acetamidomethyl group; the amino
OTHER INFORMATION: terminal amine is acetylated."
US-08-564-315-1

Query Match 26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYK 19
DB 5 QAPLYK 11

RESULT 62

US-08-505-318-12
Sequence 12, Application US/08505318

PATENT No. 6107459
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Diagnostic Imaging
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor

CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,318
FILING DATE: 07-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 6107459nan, Kevin E
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label=Tc-99m-chelator
OTHER INFORMATION: /note="The N-terminal amino group is acetylated,
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys
OTHER INFORMATION: residues are each protected by an acetamidomethyl
US-08-505-318-12

Query Match 26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19
:|||||:
Db 5 QAPLYKK 11

RESULT 63
US-08-505-318-22
Sequence 22, Application US/08505318
Patent No. 6107459
GENERAL INFORMATION:
APPLICANT: Dean, Richard T
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Diagnostic Imaging
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESS:
ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,318
FILING DATE: 07-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 6107459nan, Kevin E

REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-FP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001
TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..4
OTHER INFORMATION: /label=Tc-99m-chelator
OTHER INFORMATION: /note="The N-terminal amino group is acetylated,
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys
OTHER INFORMATION: residues are each protected by an acetamidomethyl
US-08-505-318-22

Query Match 26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYKR 19
:|||||:
Db 5 QAPLYKK 11

RESULT 64
US-09-675-922-13
Sequence 13, Application US/09675922
Patent No. 6468731
GENERAL INFORMATION:
APPLICANT: Hubbell A., Jeffrey
APPLICANT: Schense C., Jason
APPLICANT: Sakiyama E., Shelley
TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin for Tissue
TITLE OF INVENTION: Engineering: Incorporation of Proteins
FILE REFERENCE: ETH 107 DIV
CURRENT APPLICATION NUMBER: US/09/675,922
CURRENT FILING DATE: 2000-09-29
NUMBER OF SEQ ID NOS: 28
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:
US-09-675-922-13

Query Match 26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKR 20
:|||||:
Db 1 YEKPSG---PPREVPRP 15

RESULT 65
US-09-600-502A-15
Sequence 15, Application US/09600502A
Patent No. 6855329
GENERAL INFORMATION:
APPLICANT: Shakesheff, Kevin
APPLICANT: Nikin, Patal
APPLICANT: Camizazaro, Scott M
APPLICANT: Langer, Robert S.

```

; TITLE OF INVENTION: Surface Coating in Spatially Controlled Patterns
; FILE REFERENCE: MIT 7896 UK
; CURRENT APPLICATION NUMBER: US/09/600,502A
; CURRENT FILING DATE: 2000-10-17
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 15
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: proteoglycan
US-09-600-502A-15

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 66
US-09-563-760A-13
; Sequence 13, Application US/09563760A
; Patent No. 6894022
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A
; APPLICANT: Schense, Jason C
; APPLICANT: Sakiyama-Bibert, Shelly B
; TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
; FILE REFERENCE: ETH 107 CIP
; CURRENT APPLICATION NUMBER: US/09/563,760A
; CURRENT FILING DATE: 2000-05-01
; PRIOR APPLICATION NUMBER: 09/141,153
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:
; OTHER INFORMATION: Heparin-binding sequence
US-09-563-760A-13

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 67
US-09-586-937-52
; Sequence 52, Application US/09586937
; Patent No. 6958212
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Bibert, Donald
; APPLICANT: Schoenmakers, Ronald
; TITLE OF INVENTION: CONTROLLED ADDITION REACTIONS FOR THE
; FILE REFERENCE: 50154/003001
; CURRENT APPLICATION NUMBER: US/09/586,937
; CURRENT FILING DATE: 2000-06-02
; PRIOR APPLICATION NUMBER: US 09/496,231
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; PRIOR FILING DATE: 2000-02-01
; PRIOR APPLICATION NUMBER: US 60/118,093
; PRIOR FILING DATE: 1999-02-01
; NUMBER OF SEQ ID NOS: 75
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 52
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Based on Homo sapiens
US-09-586-937-52

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 68
US-09-798-338B-4
; Sequence 4, Application US/09798338B
; Patent No. 6960452
; GENERAL INFORMATION:
; APPLICANT: Hubbell, Jeffrey A.
; APPLICANT: Schense, Jason C.
; APPLICANT: Sakiyama, Shelly B.
; TITLE OF INVENTION: Enzyme-mediated modifications of fibrin for tissue engineering:
; FILE REFERENCE: ETH 107 CON
; CURRENT APPLICATION NUMBER: US/09/798,338B
; CURRENT FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 09/141,153
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patent In version 3.1
; SEQ ID NO 4
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-798-338B-4

Query Match          26.3%; Score 30; DB 2; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
   ||||| | : |||
Db 1 YEKPGS-----PPREVVRP 15

RESULT 69
PCT-US93-11781-1
; Sequence 1, Application PC/TUS9311781
; GENERAL INFORMATION:
; APPLICANT: Regents of the University of Minnesota
; APPLICANT: Morrill Hall
; APPLICANT: 100 Church Street, S.E.
; APPLICANT: Minneapolis, Minnesota 55455
; APPLICANT: U.S.A.
; APPLICANT: Represented By The Secretary of Health
; APPLICANT: and Human Services
; APPLICANT: 200 Independence Avenue S.W.
; APPLICANT: Washington, D.C. 20201
; APPLICANT: United States of America
; TITLE OF INVENTION: Polypeptides Useful for Treating
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Merchant & Gould
```

STREET: 3100 Norwest Center
CITY: Minneapolis
STATE: MN
COUNTRY: USA
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11781
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/139,903
FILING DATE: 21-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/990,296
FILING DATE: 10-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Kowalchuk, Alan W.
REGISTRATION NUMBER: 31,535
REFERENCE/DOCKET NUMBER: 600.283-US-01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-332-5300
TELEFAX: 612-332-9081
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US93-11781-1

Query Match 26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYGSRLGNPKAPLYKRP 20
DB 1 YEKFGS----PPREVVRP 15

RESULT 70
PCT-US94-02051-2
Sequence 2, Application PC/TUS9402051
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: ANALOGS FOR SPECIFIC OLIGOSACCHARIDE-
NUMBER OF INVENTION: PROTEIN INTERACTIONS AND USES THEREFOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: PATENT ADMINISTRATOR, TESTA, HURWITZ &
ADDRESS: 53 STATE STREET
CITY: BOSTON
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02051
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,558
FILING DATE: 01-MAR-1993
ATTORNEY/AGENT INFORMATION:

NAME: KELLEY, ROBIN D.
REGISTRATION NUMBER: 34,637
REFERENCE/DOCKET NUMBER: GLY-003PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-248-7000
TELEFAX: 617-248-7100
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
FEATURE:
NAME/KEY: Protein
LOCATION: 1..19
OTHER INFORMATION: /label= PP4
OTHER INFORMATION: /note="OPPENHEIM ET AL. (1991) ANN. REV. IMMUNOL.
PCT-US94-02051-2

Query Match 26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 71.4%; Pred. No. 5.6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYK 19
DB 5 QAPLYK 11

RESULT 71
PCT-US95-02478-9
Sequence 9, Application PC/TUS9502478
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Method for Treating Conditions
OF THE EYE USING POLYPEPTIDES
NUMBER OF SEQUENCES: 16
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02478
FILING DATE:
CLASSIFICATION:
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: US 08/203,458
FILING DATE: 28-FEB-1994
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE:
STRAIN: FN-C/H-1
PCT-US95-02478-9

Query Match 26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 5.6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYGSRLGNPKAPLYKRP 20
DB 1 YEKFGS----PPREVVRP 15

RESULT 72
US-08-462-784-2
Sequence 2, Application US/08462784
Patent No. 5714313

```

1 GENERAL INFORMATION:
2 APPLICANT: Dean, Richard T.
3 APPLICANT: Moyer, Brian
4 TITLE OF INVENTION: Technetium-99m Labeled Peptides for
5 TITLE OF INVENTION: Imaging Inflammation
6 NUMBER OF SEQUENCES: 10
7 CORRESPONDENCE ADDRESS:
8 ADDRESSEE: McDonnell Boehnen Hulbert & Berghoff
9 STREET: 300 South Wacker Drive Seventh Floor
10 CITY: Chicago
11 STATE: Illinois
12 COUNTRY: USA
13 ZIP: 60606
14
15 COMPUTER READABLE FORM:
16 MEDIUM TYPE: Floppy disk
17 COMPUTER: IBM PC compatible
18 OPERATING SYSTEM: PC-DOS/MS-DOS
19 SOFTWARE: Patent Release #1.0, Version #1.25
20 CURRENT APPLICATION DATA:
21 APPLICATION NUMBER: US/08/462,784
22 FILING DATE: 05-JUN-1995
23 CLASSIFICATION: 530
24 ATTORNEY/AGENT INFORMATION:
25 NAME: No. 571433nan, Kevin E
26 REGISTRATION NUMBER: 35,303
27 REFERENCE/DOCKET NUMBER: 90,1104-X
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: 312 913 0001
30 TELEFAX: 312 913 0002
31 TELEX:
32
33 INFORMATION FOR SEQ ID NO. 2:
34 SEQUENCE CHARACTERISTICS:
35 LENGTH: 20 amino acids
36 TYPE: amino acid
37 TOPOLOGY: linear
38 MOLECULE TYPE: peptide
39 FEATURE:
40 NAME/KEY: Modified-site
41 LOCATION: 1..5
42 OTHER INFORMATION: /label= MODIFIED-CYS
43 OTHER INFORMATION: /notes="The thiol group of each cysteine is
44 OTHER INFORMATION: protected by an acetamidomethyl group; the amino
45 OTHER INFORMATION: terminal amine is acetylated."
46
47 US-08-462-784-2
48
49 Query Match 26.3% Score 30; DB 1; Length 20;
50 Best Local Similarity 71.4% Pred. No.6e+02;
51 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
52
53 QY 13 KAPLYKR 19
54 :||||:
55 Db 6 QAPLYKK 12
56
57 RESULT 73
58 US-07-923-724-43
59 ; Sequence 43, Application US/07923724
60 ; Patent No. 5780292
61 ; GENERAL INFORMATION:
62 APPLICANT: Nevalainen, Helena K.M.
63 APPLICANT: Paloneimo, Marja T.
64 APPLICANT: Miettinen-Oinonen, Arja S.K.
65 APPLICANT: Torkkeli, Tuula K.
66 APPLICANT: Cantrell, Michael
67 APPLICANT: Piddington, Christopher S.
68 APPLICANT: Rambosek, John A.
69 APPLICANT: Turunen, Marja K.
70 APPLICANT: Fagerstr m, Richard B.
71 TITLE OF INVENTION: Production of Phytase Degrading Enzymes
72 TITLE OF INVENTION: in Trichoderma
73 NUMBER OF SEQUENCES: 66
74 CORRESPONDENCE ADDRESS:
75 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
76

```

```

1 STREET: 1100 New York Avenue, Suite 600
2 CITY: Washington
3 STATE: D.C.
4 COUNTRY: U.S.A.
5 ZIP: 20005
6 COMPUTER READABLE FORM:
7 MEDIUM TYPE: Floppy disk
8 COMPUTER: IBM PC compatible
9 OPERATING SYSTEM: PC-DOS/MS-DOS
10 SOFTWARE: Patentln Release #1.0, Version #1.25
11 CURRENT APPLICATION DATA:
12 APPLICATION NUMBER: US/07/923,724
13 FILING DATE: 31-JUL-1992
14 CLASSIFICATION: 435
15 PRIOR APPLICATION DATA:
16 APPLICATION NUMBER: US 07/496,155
17 FILING DATE: 19-MAR-1990
18 PRIOR APPLICATION DATA:
19 APPLICATION NUMBER: US 07/044,077
20 FILING DATE: 29-APR-1987
21 PRIOR APPLICATION DATA:
22 APPLICATION NUMBER: UK 8610600
23 FILING DATE: 30-APR-1986
24 ATTORNEY/AGENT INFORMATION:
25 NAME: Cimbala, Michele A.
26 REGISTRATION NUMBER: 33,851
27 REFERENCE/DOCKET NUMBER: 1050, 0240004
28 TELECOMMUNICATION INFORMATION:
29 TELEPHONE: (202) 371-2600
30 TELEFAX: (202) 371-2540
31 INFORMATION FOR SEQ ID NO: 43:
32 SEQUENCE CHARACTERISTICS:
33 LENGTH: 20 amino acids
34 TYPE: amino acid
35 TOPOLOGY: both
36 FEATURE:
37 NAME/KEY: Peptide
38 LOCATION: 17
39 OTHER INFORMATION: /label= Peptide
40 OTHER INFORMATION: /note= "The amino acid at position 17 may also be
41 OTHER INFORMATION: Tyrosine."
42 US-07-923-724-43
43
44 Query Match 26.3%; Score 30; DB 1; Length 20;
45 Best Local Similarity 50.0%; Pred. No. 6e+02;
46 Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
47
48 QY 4 YPGSRIGNPKAP 15
49 | | | | |
50 Db 1 YYGHGAGNPLGP 12
51
52 RESULT 74
53 US-08-609-426A-43
54 ; Sequence 43, Application US/08609426A
55 ; Patent No. 5830733
56 ; GENERAL INFORMATION:
57 APPLICANT: Nevalainen, Helena K.M.
58 APPLICANT: Palohelmo, Marja T.
59 APPLICANT: Miettinen-Oinonen, Arja S.K.
60 APPLICANT: Torkkeli, Tuula K.
61 APPLICANT: Cantrell, Michael
62 APPLICANT: Piddington, Christopher S.
63 APPLICANT: Rambosek, John A.
64 APPLICANT: Turunen, Marja K.
65 APPLICANT: Ragerstr m, Richard B.
66 APPLICANT: Houston, Christine S.
67 TITLE OF INVENTION: Production of Phytase Degrading Enzymes
68 TITLE OF INVENTION: In Trichoderma
69 NUMBER OF SEQUENCES: 69
70 CORRESPONDENCE ADDRESS:
71 ADDRESSEE: Sterne, Kessler, Goldstein & Fox
72 STREET: 1100 New York Avenue, Suite 600

```

CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/609,426A
FILING DATE: 01-MAR-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/923,724
FILING DATE: 31-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/496,155
FILING DATE: 19-MAR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/044,077
FILING DATE: 29-APR-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: UK 8610600
FILING DATE: 30-APR-1986
ATTORNEY/AGENT INFORMATION:
NAME: Reed, Grant E.
REGISTRATION NUMBER: P-41,264
REFERENCE/DOCKET NUMBER: 1050,0080001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: both
FEATURE:
NAME/KEY: Peptide
LOCATION: 17
OTHER INFORMATION: /label= Peptide
OTHER INFORMATION: /note= "The amino acid at position 17 may also be
OTHER INFORMATION: Tyrosine."
US-08-609-426A-43
Query Match 26.3%; Score 30; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 6e+02;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
QY 4 YPSRLGNPKAP 15
DB 1 YYGHGAGNPLGP 12
RESULT 75
US-08-564-315-2
Sequence 2, Application US/08564315
Patent No. 6019958
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
APPLICANT: Moyer, Brian
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Imaging Inflammation
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/564,315
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/462,784
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: No. 6019958nan, Kevin B
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-X
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312 913 0001
TELEFAX: 312 913 0002
TELEX:
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..5
OTHER INFORMATION: /label= MODIFIED-CYS
OTHER INFORMATION: /note= "The thiol group of each cysteine is
OTHER INFORMATION: protected by an acetamidomethyl group; the amino
OTHER INFORMATION: terminal amine is acetylated."
US-08-564-315-2

Query Match 26.3%; Score 30; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYR 19
DB 6 QAPLYRK 12

RESULT 76
US-08-505-318-14
Sequence 14, Application US/08505318
Patent No. 6107459
GENERAL INFORMATION:
APPLICANT: Dean, Richard T.
TITLE OF INVENTION: Technetium-99m Labeled Peptides for
TITLE OF INVENTION: Diagnostic Imaging
NUMBER OF SEQUENCES: 28
CORRESPONDENCE ADDRESSES:
ADDRESSER: McDonnell Boehnen Hulbert & Berghoff
STREET: 300 South Wacker Drive, Seventh Floor
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/505,318
FILING DATE: 07-DEC-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: No. 6107459nan, Kevin B
REGISTRATION NUMBER: 35,303
REFERENCE/DOCKET NUMBER: 90,1104-FF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312-913-0001

TELEFAX: 312-913-0002
TELEX:
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1..5
OTHER INFORMATION: /label= Tc-99m-chelator
OTHER INFORMATION: /note= "The N-terminal amino group is acetylated,
OTHER INFORMATION: and the sidechain sulfur atoms of both Cys
OTHER INFORMATION: residues are each protected by an acetamidomethyl
OTHER INFORMATION: group"
US-08-505-318-14

Query Match 26.3%; Score 30; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 6e+02;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPLYRK 19
DB 6 QAPLYRK 12

RESULT 77
US-09-600-432-42
Sequence 42, Application US/09600432
Patent No. 6849712
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota
TITLE OF INVENTION: PEPTIDES WITH R1 INTEGRIN SUBUNIT DEPENDENT CELL
FILE REFERENCE: 110.01130101
CURRENT APPLICATION NUMBER: US/09/600,432
PRIOR FILING DATE: 2000-10-02
PRIOR APPLICATION NUMBER: PCT/US99/01236
PRIOR FILING DATE: 1999-01-21
PRIOR APPLICATION NUMBER: 60/072,119
PRIOR FILING DATE: 1998-01-22
PRIOR APPLICATION NUMBER: 60/096,211
PRIOR FILING DATE: 1998-08-12
PRIOR APPLICATION NUMBER: 60/096,212
PRIOR FILING DATE: 1998-08-12
NUMBER OF SEQ ID NOS: 46
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 42
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-600-432-42

Query Match 26.3%; Score 30; DB 2; Length 20;
Best Local Similarity 42.1%; Pred. No. 6e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
DB 1 YEKPSG---PPREYVPRP 15

RESULT 78
US-07-972-032-17
Sequence 17, Application US/07972032
Patent No. 5496712
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
APPLICANT: Ferrari, Franco A.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
TITLE OF INVENTION: PROTEIN POLYMERS
NUMBER OF SEQUENCES: 85

CORRESPONDENCE ADDRESS:
ADDRESSEE: Bertam I. Rowland
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: CA 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,032
FILING DATE: 19921105
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/791,960
FILING DATE: 12-NOV-1991
ATTORNEY/AGENT INFORMATION:
NAME: Rowland, Bertam I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-972-032-17

Query Match 25.9%; Score 29.5; DB 1; Length 18;
Best Local Similarity 63.6%; Pred. No. 6.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 5 PGSRLGNPKAP 15
DB 9 PGSR-GDPEPP 18

RESULT 79
US-07-972-032-83
Sequence 83, Application US/07972032
Patent No. 5496712
GENERAL INFORMATION:
APPLICANT: Cappello, Joseph
APPLICANT: Ferrari, Franco A.
TITLE OF INVENTION: HIGH MOLECULAR WEIGHT COLLAGEN-LIKE
TITLE OF INVENTION: PROTEIN POLYMERS
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bertam I. Rowland
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: CA 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/972,032
FILING DATE: 19921105
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/791,960
FILING DATE: 12-NOV-1991
ATTORNEY/AGENT INFORMATION:

NAME: Rowland, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A-55556-1/BIR;PROP-08-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
INFORMATION FOR SEQ ID NO: 83:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-972-032-83

Query Match 25.9%; Score 29.5; DB 1; Length 18;
Best Local Similarity 63.6%; Pred. No. 6.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 5 PGSRLGNPKAP 15
DB 9 PGSR-GDPGP 18

RESULT 80
US-08-642-255-134
Sequence 134, Application US/08642255
Patent No. 5773249
GENERAL INFORMATION:
APPLICANT: CAPPELO, Joseph
APPLICANT: FERRARI, Franco A.
TITLE OF INVENTION: High Molecular Weight Collagen-Like
NUMBER OF SEQUENCES: 135
CORRESPONDENCE ADDRESSES:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/642,255
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROWLAND, Bertram I.
REGISTRATION NUMBER: 20,015
REFERENCE/DOCKET NUMBER: A55556-3/BIR
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 494-8700
TELEFAX: (415) 494-8771
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 134:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-642-255-134

Query Match 25.9%; Score 29.5; DB 1; Length 18;
Best Local Similarity 63.6%; Pred. No. 6.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
QY 5 PGSRLGNPKAP 15
DB 9 PGSR-GDPGP 18

DB 9 PGSR-GDPGP 18

RESULT 81
US-08-147-592A-36
Sequence 36, Application US/08147592A
Patent No. 6096513
GENERAL INFORMATION:
APPLICANT: Bell, Graeme I
APPLICANT: Reisine, Terry
APPLICANT: Yasuda, Kazuki
TITLE OF INVENTION: Opioid Receptor Genes,
TITLE OF INVENTION: Compositions and Methods
NUMBER OF SEQUENCES: 43
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: United States of America
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,592A
FILING DATE: 05-NOV-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/100,694
FILING DATE: 30-JUL-1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/066,296
FILING DATE: 20-MAY-1993
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Wilson, Mark B.
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:105
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (512) 474-7577
TELEX: N/A
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-147-592A-36

Query Match 25.4%; Score 29; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPGS 7
DB 1 EYPGS 5

RESULT 82
US-08-292-694A-36
Sequence 36, Application US/08292694A
Patent No. 6319686
GENERAL INFORMATION:
APPLICANT: BEIL, GRAEME
APPLICANT: REISINE, TERRY
APPLICANT: YASUDA, KAZUKI
TITLE OF INVENTION: OPIOID RECEPTORS: COMPOSITIONS AND METHODS
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESSES:

ADDRESSER: Arnold, White & Durkee
STREET: P. O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/292,694A
FILING DATE: August 19, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/066,296
FILING DATE: 20 May 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/100,694
FILING DATE: 30 July, 1993
CLASSIFICATION: 435
APPLICATION NUMBER: 08/147,592
FILING DATE: 5 No. 631968ember 1993
CLASSIFICATION: 435
APPLICATION NUMBER: PCT/US94/05747
FILING DATE: 20 May 1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MARK B. WILSON
REGISTRATION NUMBER: 37,259
REFERENCE/DOCKET NUMBER: ARCD:140/WIM
TELECOMMUNICATION INFORMATION:
TELEPHONE: (512) 418-3000
TELEFAX: (713) 789-2679
TELEX: 79-0924
INFORMATION FOR SEQ ID NO: 36:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-292-694A-36

Query Match 25.4%; Score 29; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGS 7
|||||
Db 1 EYFGS 5

RESULT 83
US-09-177-249-108
Sequence 108, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramlin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01

NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 108
LENGTH: 12
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-108

Query Match 25.4%; Score 29; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYRK 19
|||||
Db 1 NPKVTIFPK 9

RESULT 84
US-09-812-283-108
Sequence 108, Application US/09812283
Patent No. 6828477
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramlin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/812,283
CURRENT FILING DATE: 2001-03-19
PRIOR APPLICATION NUMBER: 09/177,249
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: US 09/071,838
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO: 108
LENGTH: 12
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-812-283-108

Query Match 25.4%; Score 29; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYRK 19
|||||
Db 1 NPKVTIFPK 9

RESULT 85
US-08-519-196-4
Sequence 4, Application US/08519196
Patent No. 5854206
GENERAL INFORMATION:
APPLICANT: Twardzik, Daniel R.
APPLICANT: Reed, Steven G.
APPLICANT: Vedvick, Thomas S.
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
TITLE OF INVENTION: DIAGNOSIS OF PROSTATE CANCER
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: SEED and BERRY
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA

```

; ZIP: 98104-7092
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/519,196
; FILING DATE: 25-AUG-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Makl, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.412
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-08-519-196-4

Query Match      25.4%; Score 29; DB 1; Length 13;
Best Local Similarity 71.4%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      10 GNPAPL 16
Db      4 GEPKGPL 10

RESULT 86
; US-10-210-428-21
; Sequence 21, Application US/10210428
; Patent No. 6814969
; GENERAL INFORMATION:
; APPLICANT: David M. Koelle
; APPLICANT: Nancy A. Hoeken
; TITLE OF INVENTION: IMMUNOLOGICALLY SIGNIFICANT HERPES
; TITLE OF INVENTION: SIMPLEX VIRUS ANTIGENS AND METHODS FOR USING SAME
; FILE REFERENCE: 30967.8-US-01
; CURRENT APPLICATION NUMBER: US/10/210,428
; PRIOR FILING DATE: 2002-07-31
; PRIOR APPLICATION NUMBER: 60/308,923
; PRIOR FILING DATE: 2001-07-31
; PRIOR APPLICATION NUMBER: 60/309,428
; PRIOR FILING DATE: 2001-08-01
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Herpes simplex virus-1 (HSV-1)
; US-10-210-428-21

Query Match      25.4%; Score 29; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 6.6e+02;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      2 YEPGRLGNPKAP 15
Db      3 YTPSSGMASPDSP 16

RESULT 87
; US-08-436-420-24
; Sequence 24, Application US/08436420
; Patent No. 5840524
; GENERAL INFORMATION:
; APPLICANT: VAN DAMME, Jo; and

```

```

; APPLICANT: PROOST, Paul
; TITLE OF INVENTION: GRANULOCYTE CHEMOTACTIC PROTEIN
; NUMBER OF SEQUENCES: 45
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HALE AND DOR LLP
; STREET: 1455 PENNSYLVANIA AVENUE, N.W.
; CITY: WASHINGTON
; STATE: DISTRICT OF COLUMBIA
; COUNTRY: USA
; ZIP: 20004
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/436,420
; FILING DATE: 24-MAY-1995
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP93/03330
; FILING DATE: 26-NOV-1993
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/982,539
; FILING DATE: 27-NOV-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: BAKER, Hollie L.
; REGISTRATION NUMBER: 31,321
; REFERENCE/DOCKET NUMBER: 102378.215
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 942-8400
; TELEFAX: (202) 942-8484
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FRAGMENT TYPE: C-terminal
; US-08-436-420-24

Query Match      25.4%; Score 29; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
Db      1 PEAPLTK 8

RESULT 88
; US-08-129-722A-8
; Sequence 8, Application US/08129722A
; Patent No. 630365
; GENERAL INFORMATION:
; APPLICANT: Spana, Carl
; APPLICANT: Fargnoli, Joseph
; APPLICANT: Bolen, Joseph B.
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Burton Rodney
; STREET: P.O. Box 4000
; CITY: Princeton
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 08543-4000
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25

```

;/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/129,722A
/ FILING DATE:
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gaul, Timothy J.
/ REGISTRATION NUMBER: 33,111
/ REFERENCE/DOCKET NUMBER: DC25
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (609) 252-5901
/ TELEFAX: 609) 252-4526
/ INFORMATION FOR SEQ ID NO: 8:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-129-722A-8

Query Match 25.4%; Score 29; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPXAPLYR 17
| : | | |
DB 5 GSPGIRPLY 12

RESULT 89
US-09-674-674D-42
/ Sequence 42, Application US/09674674D
/ Patent No. 6706859
/ GENERAL INFORMATION:
/ APPLICANT: Bitger Sorensen
/ TITLE OF INVENTION: HIV Peptides, antigens, vaccine compositions, immunoassay kit and
/ TITLE OF INVENTION: method of detecting antibodies induced by HIV.
/ FILE REFERENCE: 2833.400100
/ CURRENT APPLICATION NUMBER: US/09/674,674D
/ CURRENT FILING DATE: 2000-11-03
/ PRIOR APPLICATION NUMBER: PCT/NO00/00075
/ PRIOR FILING DATE: 2000-03-02
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 42
/ TYPE: PRT
/ LENGTH: 19
/ ORGANISM: Homo sapiens
US-09-674-674D-42

Query Match 25.4%; Score 29; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 10 GNPXAPLYR 19
| : | | |
DB 4 GTPVGRIYXR 13

RESULT 90
US-08-505-250-21
/ Sequence 21, Application US/08505250
/ Patent No. 6183983
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Haruya
/ APPLICANT: Yamamoto, Keiji
/ APPLICANT: Suzuki, Kokiichi
/ APPLICANT: Ikeda, Masahiro
/ APPLICANT: Sakagami, Masahiro
/ APPLICANT: Taniguchi, Makoto
/ TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
/ FILE REFERENCE: 110-511
/ CURRENT APPLICATION NUMBER: US/08/505,250
/ CURRENT FILING DATE: 1995-11-29

;/ EARLIER APPLICATION NUMBER: PCT/JP95/00298
/ EARLIER FILING DATE: 1995-02-27
/ EARLIER APPLICATION NUMBER: JP 198187/94
/ EARLIER FILING DATE: 1994-08-23
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-21

Query Match 25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13
| : | | |
DB 5 ELPEQVGQPK 15

RESULT 91
US-08-505-250-21
/ Sequence 21, Application US/08505250
/ Patent No. 6322996
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Haruya
/ APPLICANT: Yamamoto, Keiji
/ APPLICANT: Suzuki, Kokiichi
/ APPLICANT: Ikeda, Masahiro
/ APPLICANT: Sakagami, Masahiro
/ APPLICANT: Taniguchi, Makoto
/ TITLE OF INVENTION: PROTEIN MODIFICATION METHOD
/ FILE REFERENCE: 110-511
/ CURRENT APPLICATION NUMBER: US/08/505,250
/ CURRENT FILING DATE: 1995-11-29
/ PRIOR APPLICATION NUMBER: PCT/JP95/00298
/ PRIOR FILING DATE: 1995-02-27
/ PRIOR APPLICATION NUMBER: JP 198187/94
/ PRIOR FILING DATE: 1994-08-23
/ NUMBER OF SEQ ID NOS: 53
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 21
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-08-505-250-21

Query Match 25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 8.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13
| : | | |
DB 5 ELPEQVGQPK 15

RESULT 92
US-09-736-457-1844
/ Sequence 1844, Application US/09736457
/ Patent No. 6509448
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Lodes, Michael A.
/ APPLICANT: Panger, Gary
/ APPLICANT: Vedvick, Tom

```

; APPLICANT: Carter, Darlick
; APPLICANT: Recter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 1844
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-736-457-1844

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```

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 8.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

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QY      6 GSRGNPKAPLYKRP 20
DB      4 GKXKDPNAP--KRP 16

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RESULT 93
US-09-991-433-34
; Sequence 34, Application US/09991433
; Patent No. 6818612
; GENERAL INFORMATION:
; APPLICANT: Broiden, Kristina
; TITLE OF INVENTION: USE OF PARVOVIRUS CAPSID PARTICLES IN
; FILE OF INVENTION: THE INHIBITION OF CELL PROLIFERATION AND MIGRATION
; FILE REFERENCE: TRIPR.019CPI
; CURRENT APPLICATION NUMBER: US/09/991,433
; CURRENT FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: US 09/447,693
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: SE 9804022-3
; PRIOR FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 34
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Peptide fragments derived from parvovirus capsid
US-09-991-433-34

```

```

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 85.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      6 GSRGNPK 12
DB      8 GSRNGVP 14

```

```

RESULT 94
US-10-017-754-1844
; Sequence 1844, Application US/10017754
; Patent No. 6858204
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Wang, Tonglong
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Johnson, Jeffrey C.
; APPLICANT: Recter, Marc W.
; APPLICANT: Marnerakis, Margarita

```

```

; APPLICANT: Carter, Darlick
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: McNabb, Andria
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C18
; CURRENT APPLICATION NUMBER: US/10/017,754
; CURRENT FILING DATE: 2001-10-29
; NUMBER OF SEQ ID NOS: 2004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1844
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-017-754-1844

```

```

Query Match      25.4%; Score 29; DB 2; Length 20;
Best Local Similarity 46.7%; Pred. No. 8.4e+02;
Matches 7; Conservative 2; Mismatches 4; Indels 2; Gaps 1;

```

```

QY      6 GSRGNPKAPLYKRP 20
DB      4 GKXKDPNAP--KRP 16

```

```

RESULT 95
PCT-US92-08094-68
; Sequence 68, Application PC/TUS9208094
; GENERAL INFORMATION:
; APPLICANT: GENENTECH, INC.
; APPLICANT: Amanto, Edward P.
; TITLE OF INVENTION: DIAGNOSING AND TREATING AUTOIMMUNE
; FILE OF INVENTION: DISORDERS
; NUMBER OF SEQUENCES: 80
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080-4990
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/08094
; FILING DATE: 19920923
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/765222
; FILING DATE: 23-SEP-1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/779445
; FILING DATE: 18-OCT-1991
; APPLICATION NUMBER: 07/853362
; FILING DATE: 18-MAR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Hensley, Max D.
; REGISTRATION NUMBER: 27,043
; REFERENCE/DOCKET NUMBER: 734P3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 68:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: AMINO ACID

```

```

; TOPOLOGY: linear
PCT-US92-08094-68

Query Match          25.0%; Score 28.5; DB 4; Length 18;
Best Local Similarity 58.3%; Pred. No. 8.9e+02;
Matches 7; Conservative 1; Mismatches 1; Indels 3; Gaps 1;

QY      1 DYEY---PGSRL 9
      ||| |||
      4 DYEYRGPGTRL 15

Db

RESULT 96
US-08-331-394-43
; Sequence 43, Application US/08331394
; Patent No. 5670319
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor
; TITLE OF INVENTION: Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/331,394
; FILING DATE:
; CLASSIFICATION: 436
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897P1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-331-394-43

Query Match          24.6%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 PGSRLGN 11
      ||| |||
      1 PGSRLGS 7

Db

RESULT 97
US-08-250-858-43
; Sequence 43, Application US/08250858
; Patent No. 5708142
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
```

```

; NUMBER OF SEQUENCES: 62
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/250,858
; FILING DATE: 27-May-1994
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Ginger R.
; REGISTRATION NUMBER: 33,055
; REFERENCE/DOCKET NUMBER: 897.1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-3216
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 43:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 7 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-250-858-43

Query Match          24.6%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      5 PGSRLGN 11
      ||| |||
      1 PGSRLGS 7

Db

RESULT 98
US-08-446-915-43
; Sequence 43, Application US/08446915
; Patent No. 5741667
; GENERAL INFORMATION:
; APPLICANT: Goeddel, David V.
; APPLICANT: Roche, Mike
; TITLE OF INVENTION: Tumor Necrosis Factor Receptor-Associated Factors
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESSES:
; ADDRESSER: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,915
; FILING DATE:
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/250858
; FILING DATE: 27-MAY-1994
; PRIORITY APPLICATION DATA:
```

APPLICATION NUMBER: 08/31394
FILING DATE: 28-OCT-1994
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: 897P2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-446-915-43

Query Match 24.6%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGN 11
DB 1 PGSNLS 7

RESULT 99
US-08-744-139-43
Sequence 43, Application US/08744139
Patent No. 5869612
GENERAL INFORMATION:
APPLICANT: Goeddel, David V
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-744-139-43

Query Match 24.6%; Score 28; DB 1; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGN 11
DB 1 PGSNLS 7

RESULT 100
US-08-779-599-43
Sequence 43, Application US/08779599
Patent No. 6500922
GENERAL INFORMATION:
APPLICANT: Goeddel, David V.
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Ginger R.
REGISTRATION NUMBER: 33,055
REFERENCE/DOCKET NUMBER: P0897C2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-3216
TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 7 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-08-779-599-43

Query Match 24.6%; Score 28; DB 2; Length 7;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRLGN 11
DB 1 PGSNLS 7

Search completed: January 20, 2006, 19:14:11
Job time : 21.9615 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 Search time 72.1154 Seconds

(without alignments)
115.878 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114

Sequence: 1 DYVEPGSRRLGNPKAPLYKRP 20

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Litering first 100 summaries

Database : Published Applications AA Main:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	114	100.0	20	4 US-10-218-743-2	Sequence 2, App1
2	33	28.9	16	5 US-10-476-364-135	Sequence 135, App
3	33	28.9	19	4 US-10-394-980-17	Sequence 17, App1
4	33	28.9	19	5 US-10-801-990-103	Sequence 103, App
5	33	28.9	19	5 US-10-952-557-17	Sequence 17, App1
6	33	28.1	14	4 US-10-362-527-93	Sequence 93, App1
7	32	28.1	16	4 US-10-224-999A-1541	Sequence 1541, App
8	32	28.1	17	2 US-08-424-550B-251	Sequence 251, App
9	32	28.1	17	3 US-09-879-857-226	Sequence 226, App
10	32	28.1	17	4 US-10-224-999A-1554	Sequence 1554, App
11	32	28.1	17	4 US-10-224-999A-1555	Sequence 1555, App
12	32	28.1	17	4 US-10-807-856-226	Sequence 226, App
13	32	28.1	17	4 US-10-723-606-19	Sequence 19, App1
14	32	28.1	18	4 US-10-224-999A-1568	Sequence 1568, App
15	32	28.1	18	4 US-10-224-999A-1569	Sequence 1569, App
16	32	28.1	18	4 US-10-224-999A-1570	Sequence 1570, App
17	32	28.1	19	4 US-10-224-999A-1583	Sequence 1583, App
18	32	28.1	19	4 US-10-224-999A-1584	Sequence 1584, App
19	32	28.1	19	4 US-10-224-999A-1585	Sequence 1585, App
20	32	28.1	19	4 US-10-224-999A-1586	Sequence 1586, App
21	32	28.1	20	4 US-10-224-999A-1589	Sequence 1589, App
22	32	28.1	20	4 US-10-224-999A-1600	Sequence 1600, App
23	32	28.1	20	4 US-10-224-999A-1601	Sequence 1601, App
24	32	28.1	20	4 US-10-224-999A-1602	Sequence 1602, App
25	32	28.1	20	4 US-10-224-999A-1603	Sequence 1603, App
26	31	27.2	9	3 US-09-876-904A-119	Sequence 119, App
27	31	27.2	9	3 US-09-876-904A-125	Sequence 125, App

28	31	27.2	9	3 US-09-876-904A-128	Sequence 128, App
29	31	27.2	12	5 US-10-926-542-122	Sequence 122, App
30	31	27.2	13	5 US-10-948-707-803	Sequence 803, App
31	31	27.2	14	3 US-09-880-748-2501	Sequence 2501, App
32	31	27.2	14	4 US-10-293-418-2501	Sequence 2501, App
33	31	27.2	15	4 US-10-224-999A-1528	Sequence 1528, App
34	31	27.2	15	4 US-10-203-815A-58	Sequence 58, App1
35	31	27.2	15	5 US-10-866-773-147	Sequence 147, App
36	31	27.2	15	5 US-10-862-195-182	Sequence 182, App
37	31	27.2	16	4 US-10-224-999A-1540	Sequence 1540, App
38	31	27.2	17	4 US-10-161-791-189	Sequence 189, App
39	31	27.2	17	4 US-10-211-088-254	Sequence 244, App
40	31	27.2	17	4 US-10-224-999A-1553	Sequence 1553, App
41	31	27.2	17	4 US-10-350-405-155	Sequence 155, App
42	31	27.2	17	4 US-10-350-405-158	Sequence 158, App
43	31	27.2	17	5 US-10-482-029-373	Sequence 373, App
44	31	27.2	18	4 US-10-225-567A-2233	Sequence 2233, App
45	31	27.2	18	4 US-10-224-999A-1567	Sequence 1567, App
46	31	27.2	18	4 US-10-350-405-200	Sequence 200, App
47	31	27.2	19	4 US-10-224-999A-1582	Sequence 1582, App
48	31	27.2	19	5 US-10-862-195-1528	Sequence 1528, App
49	31	27.2	19	5 US-10-224-999A-1598	Sequence 1598, App
50	30.5	26.8	13	5 US-10-481-261-459	Sequence 459, App
51	30	26.3	10	3 US-09-572-404B-3190	Sequence 3190, App
52	30	26.3	12	3 US-09-554-285-315	Sequence 315, App
53	30	26.3	12	5 US-10-912-212-315	Sequence 315, App
54	30	26.3	12	5 US-10-235-043-315	Sequence 315, App
55	30	26.3	14	3 US-09-880-748-2378	Sequence 2378, App
56	30	26.3	15	4 US-10-293-418-2378	Sequence 44, App1
57	30	26.3	15	4 US-09-829-549A-44	Sequence 45, App1
58	30	26.3	15	3 US-09-992-665-45	Sequence 1857, App
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64	30	26.3	16	4 US-10-621-401-522	Sequence 522, App
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67	30	26.3	18	4 US-10-131-546-8	Sequence 8, App1
68	30	26.3	18	4 US-10-405-339-6	Sequence 6, App1
69	30	26.3	18	4 US-10-325-810-163	Sequence 163, App
70	30	26.3	18	4 US-10-350-405-181	Sequence 181, App
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72	30	26.3	18	5 US-10-877-124-163	Sequence 163, App
73	30	26.3	18	5 US-10-877-022-163	Sequence 163, App
74	30	26.3	18	5 US-10-877-146-163	Sequence 163, App
75	30	26.3	18	6 US-11-088-596-8	Sequence 8, App1
76	30	26.3	18	6 US-11-086-697-1140	Sequence 1140, App
77	30	26.3	18	6 US-11-086-966-8	Sequence 8, App1
78	30	26.3	19	4 US-10-106-804B-11	Sequence 11, App1
79	30	26.3	19	4 US-10-323-046-13	Sequence 13, App1
80	30	26.3	19	4 US-10-297-229-52	Sequence 52, App1
81	30	26.3	20	4 US-10-225-567A-1614	Sequence 1614, App
82	29.5	25.9	15	4 US-10-327-598-150	Sequence 150, App
83	29.5	25.9	15	4 US-10-327-598-232	Sequence 232, App
84	29	25.4	10	4 US-10-304-443-99	Sequence 99, App1
85	29	25.4	10	4 US-10-415-389-12	Sequence 12, App1
86	29	25.4	11	4 US-10-322-210-4	Sequence 4, App1
87	29	25.4	11	4 US-10-304-443-4	Sequence 4, App1
88	29	25.4	11	4 US-10-362-527-63	Sequence 63, App1
89	29	25.4	11	6 US-11-004-771-4	Sequence 4, App1
90	29	25.4	12	3 US-09-971-838-108	Sequence 108, App
91	29	25.4	12	4 US-10-213-512-108	Sequence 108, App
92	29	25.4	12	4 US-10-304-443-111	Sequence 111, App
93	29	25.4	12	4 US-10-362-527-317	Sequence 317, App
94	29	25.4	12	4 US-10-815-389-24	Sequence 24, App1
95	29	25.4	13	4 US-10-322-210-20	Sequence 20, App1
96	29	25.4	13	4 US-10-304-443-20	Sequence 20, App1
97	29	25.4	13	4 US-10-082-014-272	Sequence 272, App
98	29	25.4	13	4 US-10-372-076-126	Sequence 126, App
99	29	25.4	13	4 US-10-362-527-79	Sequence 79, App1
100	29	25.4	13	4 US-10-732-862A-140	Sequence 140, App

ALIGNMENTS

```
RESULT 1
US-10-218-743-2
; Sequence 2, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Eric R.
; APPLICANT: Weber, Shirley Wu
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; PRIOR FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-2

Query Match          100.0%; Score 114; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e+09;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DYEYPSRLGNPKAPLYKR 20
Db      1 DYEYPSRLGNPKAPLYKR 20

RESULT 2
US-10-476-264-135
; Sequence 135, Application US/10476264
; Publication No. US20050123910A1
; GENERAL INFORMATION:
; APPLICANT: Cookson, William Osmond Charles Michael
; APPLICANT: Moffat, Miriam Fleur
; APPLICANT: Allen, Maxine
; APPLICANT: Lench, Nick
; TITLE OF INVENTION: Enzyme and SNP marker for disease
; FILE REFERENCE: 16721-002U81
; CURRENT APPLICATION NUMBER: US/10/476,264
; CURRENT FILING DATE: 2003-10-24
; PRIOR APPLICATION NUMBER: PCT/GB02/01887
; PRIOR FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: GB0110044.5
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: GB0110046.0
; PRIOR FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: GB0124594.3
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: GB0124575.2
; PRIOR FILING DATE: 2001-10-12
; NUMBER OF SEQ ID NOS: 421
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 135
; LENGTH: 16
; TYPE: PRT
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; ORGANISM: Homo sapiens
US-10-476-264-135

Query Match          28.9%; Score 33; DB 5; Length 16;
Best Local Similarity 54.5%; Pred. No. 8.1e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy      9 LGNPKAPLYKR 19
Db      5 LGQPRSPKSKR 15

RESULT 3
US-10-394-980-17
; Sequence 17, Application US/10394980
; Publication No. US20040005633A1
; GENERAL INFORMATION:
; APPLICANT: Vandekerckhove, Joel
; APPLICANT: Gevaert, Kris
; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
; TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
; FILE REFERENCE: VBV-001
; CURRENT APPLICATION NUMBER: US/10/394,980
; CURRENT FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: PCT/EP02/03368
; PRIOR FILING DATE: 2002-03-22
; PRIOR APPLICATION NUMBER: US60/278,171
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US60/318,749
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: US60/323,999
; PRIOR FILING DATE: 2001-09-20
; NUMBER OF SEQ ID NOS: 473
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 17
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: MISC_FEATURE
; OTHER INFORMATION: part of HBB_HUMAN ((P02023) hemoglobin beta chain)
US-10-394-980-17

Query Match          28.9%; Score 33; DB 4; Length 19;
Best Local Similarity 46.2%; Pred. No. 9.7e+02;
Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy      1 DYEYPSRLGNPK 13
Db      7 DLSTPDVWGNPK 19

RESULT 4
US-10-801-990-103
; Sequence 103, Application US/10801990
; Publication No. US20050048574A1
; GENERAL INFORMATION:
; APPLICANT: Kantor, Aaron B.
; APPLICANT: Schulman, Howard
; APPLICANT: Becker, Christopher
; TITLE OF INVENTION: BIOMARKERS FOR RHEUMATOID ARTHRITIS
; FILE REFERENCE: SURR.121
; CURRENT APPLICATION NUMBER: US/10/801,990
; CURRENT FILING DATE: 2004-03-15
; PRIOR APPLICATION NUMBER: US 60/455,037
; PRIOR FILING DATE: 2003-03-14
; NUMBER OF SEQ ID NOS: 395
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 103
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-801-990-103
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Query Match 28.9%; Score 33; DB 5; Length 19;
 Best Local Similarity 46.2%; Pred. No. 9.7e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPK 13
 | : ||||
 Db 7 DLSTPDVAMGNPK 19

RESULT 5

US-10-952-557-17
 ; Sequence 17, Application US/10952557
 ; Publication No. US20050196823A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Vandekerckhove, Joel
 ; APPLICANT: Gevaert, Ktie
 ; TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
 ; FILE REFERENCE: VAV-001
 ; CURRENT APPLICATION NUMBER: US/10/952,557
 ; CURRENT FILING DATE: 2004-09-28
 ; PRIOR APPLICATION NUMBER: US/10/394,980
 ; PRIOR FILING DATE: 2003-03-21
 ; PRIOR APPLICATION NUMBER: PCT/EP02/03368
 ; PRIOR FILING DATE: 2002-03-22
 ; PRIOR APPLICATION NUMBER: US60/278,171
 ; PRIOR FILING DATE: 2001-03-22
 ; PRIOR APPLICATION NUMBER: US60/318,749
 ; PRIOR FILING DATE: 2001-09-12
 ; PRIOR APPLICATION NUMBER: US60/323,999
 ; PRIOR FILING DATE: 2001-09-20
 ; NUMBER OF SEQ ID NOS: 473
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 17
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: MISC_FEATURE
 ; OTHER INFORMATION: part of HBB_HUMAN ((P02023) hemoglobin beta chain)
 ; US-10-952-557-17

Query Match 28.9%; Score 33; DB 5; Length 19;
 Best Local Similarity 46.2%; Pred. No. 9.7e+02;
 Matches 6; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPK 13
 | : ||||
 Db 7 DLSTPDVAMGNPK 19

RESULT 6

US-10-362-527-93
 ; Sequence 93, Application US/10362527
 ; Publication No. US20040030106A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Friede, Martin
 ; APPLICANT: Mason, Sean
 ; APPLICANT: Turnell, William Gordon
 ; APPLICANT: Vinals y De Basnols, Carlota
 ; TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
 ; TITLE OF INVENTION: and Use thereof in the Treatment of Allergies
 ; FILE REFERENCE: B45236
 ; CURRENT APPLICATION NUMBER: US/10/362,527
 ; CURRENT FILING DATE: 2003-02-21
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09576
 ; PRIOR FILING DATE: 2001-08-17
 ; PRIOR APPLICATION NUMBER: GB 0020717.5
 ; PRIOR FILING DATE: 2000-08-22
 ; NUMBER OF SEQ ID NOS: 328
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 93

LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-362-527-93

Query Match 28.1%; Score 32; DB 4; Length 14;
 Best Local Similarity 75.0%; Pred. No. 1.1e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYEYPSGR 8
 | : ||||
 Db 1 DPEWPGSR 8

RESULT 7

US-10-224-999A-1541
 ; Sequence 1541, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1541
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 ; US-10-224-999A-1541

Query Match 28.1%; Score 32; DB 4; Length 16;
 Best Local Similarity 31.2%; Pred. No. 1.1e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPKAPL 16
 | : ||||
 Db 1 DITPTAPMGTTPSPV 16

RESULT 8

US-08-424-550B-251
 ; Sequence 251, Application US/08424550B
 ; Publication No. US20020119447A1
 ; GENERAL INFORMATION:
 ; APPLICANT: JOHN N. SIMONS
 ; APPLICANT: TAMI J. PILOT-MATIAS
 ; APPLICANT: GEORGE J. DAWSON
 ; APPLICANT: GEORGE G. SCHLAUDER
 ; APPLICANT: THOMAS M. DESAI
 ; APPLICANT: ANTHONY SCOTT MIERHOF
 ; APPLICANT: JAMES C. ERKER
 ; APPLICANT: SHERI L. BUTIK
 ; APPLICANT: ISA K. MUSHAMMAR
 ; TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
 ; TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
 ; NUMBER OF SEQUENCES: 716
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
 ; STREET: 100 ABBOTT PARK ROAD
 ; CITY: ABBOTT PARK
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064-3500
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550B
FILING DATE:
CLASSIFICATION: 435435
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 251:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-424-550B-251

Query Match 28.1%; Score 32; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAPL 16
Db 1 PSERFSSPKLPV 12

RESULT 9

US-09-879-957-226
Sequence 226, Application US/09879957
Patent No. US20020034755A1
GENERAL INFORMATION:

APPLICANT: SPARKS, Andrew B.
HOFFMAN, No. US20020034755A1h
KAY, Brian K.
FOWLES, Dana M.

TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME

NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-Apr-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 226:

SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 226:
US-09-879-957-226

Query Match 28.1%; Score 32; DB 3; Length 17;
Best Local Similarity 63.6%; Pred. No. 1.2e+03;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 6 GSRLGNPKAPL 16
Db 2 GSGLAPPKPPL 12

RESULT 10

US-10-224-999A-1554
Sequence 1554, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton

APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection

FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A

CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20

NUMBER OF SEQ ID NOS: 3484
SOFTWARE: Patentin version 3.1
SEQ ID NO 1554

LENGTH: 17
TYPE: PRT

ORGANISM: Human papillomavirus
US-10-224-999A-1554

Query Match 28.1%; Score 32; DB 4; Length 17;
Best Local Similarity 31.2%; Pred. No. 1.2e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYEYPSRLGNPKAPL 16
Db 2 DTFPTAPMGTFPSV 17

RESULT 11

US-10-224-999A-1555
Sequence 1555, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:

APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton

APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection

FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484

SOFTWARE: Patentin version 3.1
SEQ ID NO 1555

LENGTH: 17
TYPE: PRT

ORGANISM: Human papillomavirus


```

Query Match      28.1%; Score 32; DB 4; Length 18;
Best Local Similarity 31.2%; Pred. No. 1.3e+03;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps

QY      1 DYKPGSRIGNPKAPL 16
      | : | : | : | :
Db      1 DTFPTAPMGTRFSPV 16

RESULT 17
US-10-224-999A-1583
; Sequence 1583, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1583

```

Query Match	28.1%	Score 32;	DB 4;	Length 19;
Best Local Similarity	31.2%;	Pred. No. 1.4e+03;		
Matches	5;	Conservative	5;	Mismatches 6;
			Indels	0;
			Gaps	0

QY 1 DVEYPSRLGNPKAPL 16
 | : | : | : | : | : | :
 Db 2 DITFPTAPMGTPSPV 17

RESULT 20
 US-10-224-999A-1586
 ; Sequence 1586, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1586
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-224-999A-1586

Query Match 28.1%; Score 32; DB 4; Length 19;
 Best Local Similarity 31.2%; Pred. No. 1.4e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPL 16
 | : | : | : | : | : | :
 Db 1 DITFPTAPMGTPSPV 16

RESULT 21
 US-10-224-999A-1599
 ; Sequence 1599, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1599
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-224-999A-1599

Query Match 28.1%; Score 32; DB 4; Length 20;
 Best Local Similarity 31.2%; Pred. No. 1.4e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPL 16
 | : | : | : | : | : | :
 Db 5 DITFPTAPMGTPSPV 20

RESULT 22
 US-10-224-999A-1600
 ; Sequence 1600, Application US/10224999A
 ; Publication No. US20030171318A1

; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1600
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-224-999A-1600

Query Match 28.1%; Score 32; DB 4; Length 20;
 Best Local Similarity 31.2%; Pred. No. 1.4e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPL 16
 | : | : | : | : | : | :
 Db 4 DITFPTAPMGTPSPV 19

RESULT 23
 US-10-224-999A-1601
 ; Sequence 1601, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1601
 ; LENGTH: 20
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-224-999A-1601

Query Match 28.1%; Score 32; DB 4; Length 20;
 Best Local Similarity 31.2%; Pred. No. 1.4e+03;
 Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DVEYPSRLGNPKAPL 16
 | : | : | : | : | : | :
 Db 3 DITFPTAPMGTPSPV 18

RESULT 24
 US-10-224-999A-1602
 ; Sequence 1602, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03

```
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1602
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Human papillomavirus
US-10-224-999A-1602

Query Match
Best Local Similarity 28.1%; Score 32; DB 4; Length 20;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPKAPL 16
DB 2 DTFPTAPMGTPFSPV 17

RESULT 25
US-10-224-999A-1603
/ Sequence 1603, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1603
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Human papillomavirus
US-10-224-999A-1603

Query Match
Best Local Similarity 28.1%; Score 32; DB 4; Length 20;
Matches 5; Conservative 5; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYEYPSRLGNPKAPL 16
DB 1 DTFPTAPMGTPFSPV 16

RESULT 26
US-09-876-904A-119
/ Sequence 119, Application US/09876904A
/ Publication No. US20030072794A1
/ GENERAL INFORMATION:
/ APPLICANT: BOUTLIKAS, TENI
/ TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
/ TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
/ FILE REFERENCE: TB-2002.00
/ CURRENT APPLICATION NUMBER: US/09/876,904A
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 60/210,925
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 629
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 119
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Bos sp.
/ FEATURE:
/ OTHER INFORMATION: Karyophilic peptide
```

```
US-09-876-904A-119

Query Match
Best Local Similarity 27.2%; Score 31; DB 3; Length 9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSRLG 10
DB 2 KHPGRRLG 9

RESULT 27
US-09-876-904A-125
/ Sequence 125, Application US/09876904A
/ Publication No. US20030072794A1
/ GENERAL INFORMATION:
/ APPLICANT: BOUTLIKAS, TENI
/ TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
/ TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
/ FILE REFERENCE: TB-2002.00
/ CURRENT APPLICATION NUMBER: US/09/876,904A
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 60/210,925
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 629
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 125
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Oryctolagus cuniculus
/ FEATURE:
/ OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-125

Query Match
Best Local Similarity 27.2%; Score 31; DB 3; Length 9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSRLG 10
DB 2 KHPGRRLG 9

RESULT 28
US-09-876-904A-128
/ Sequence 128, Application US/09876904A
/ Publication No. US20030072794A1
/ GENERAL INFORMATION:
/ APPLICANT: BOUTLIKAS, TENI
/ TITLE OF INVENTION: ENCAPSULATION OF PLASMID DNA (LIPOGENES TM) AND THERAPEUTIC
/ TITLE OF INVENTION: AGENTS WITH NUCLEAR LOCALIZATION SIGNAL/FUSOGENIC PEPTIDE
/ FILE REFERENCE: TB-2002.00
/ CURRENT APPLICATION NUMBER: US/09/876,904A
/ PRIOR FILING DATE: 2001-06-08
/ PRIOR APPLICATION NUMBER: US 60/210,925
/ PRIOR FILING DATE: 2000-06-09
/ NUMBER OF SEQ ID NOS: 629
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 128
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Rattus sp.
/ FEATURE:
/ OTHER INFORMATION: Karyophilic peptide
US-09-876-904A-128

Query Match
Best Local Similarity 27.2%; Score 31; DB 3; Length 9;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSRLG 10
```


Db 2 KHFGKRLG 9

RESULT 29
US-10-926-542-122
Sequence 122, Application US/10926542
Publication No. US2005005989A1
GENERAL INFORMATION:
APPLICANT: LABAN, ABRAHAM
APPLICANT: SHARON, GIL
TITLE OF INVENTION: LIBRARIES OF RECOMBINANT PROTEINS
FILE REFERENCE: 178.002
CURRENT APPLICATION NUMBER: US/10/926,542
PRIOR FILING DATE: 2004-08-26
PRIOR APPLICATION NUMBER: US 60/497,924
PRIOR FILING DATE: 2003-08-27
NUMBER OF SEQ ID NOS: 127
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 122
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Consensus
US-10-926-542-122

Query Match 27.2%; Score 31; DB 5; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVEYPSGR 8
Db 5 DWEPSGSK 12

RESULT 30
US-10-948-707-803
Sequence 803, Application US/10948707
Publication No. US20050187147A1
GENERAL INFORMATION:
APPLICANT: Ballatore, Carlo
APPLICANT: Castellino, Angelo
APPLICANT: Desharnais, Joel
APPLICANT: Guo, Zijian
APPLICANT: Li, Qing
APPLICANT: Newman, Michael James
APPLICANT: Sun, Chengzao
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
FILE REFERENCE: 17967-003001
CURRENT APPLICATION NUMBER: US/10/948,707
PRIOR FILING DATE: 2004-09-22
PRIOR APPLICATION NUMBER: 60/505,325
PRIOR FILING DATE: 2003-09-22
PRIOR APPLICATION NUMBER: 60/568,340
PRIOR FILING DATE: 2004-05-04
PRIOR APPLICATION NUMBER: 60/581,835
PRIOR FILING DATE: 2004-06-22
NUMBER OF SEQ ID NOS: 1422
SOFTWARE: PasteSeq for Windows Version 4.0
SEQ ID NO 803
LENGTH: 13
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-948-707-803

Query Match 27.2%; Score 31; DB 5; Length 13;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRGNPKAP 15

Db 2 PGSRSRTPSLP 12

RESULT 31
US-09-880-748-2501
Sequence 2501, Application US/09880748
Publication No. US20030059937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523
CURRENT APPLICATION NUMBER: US/09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2501
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-880-748-2501

Query Match 27.2%; Score 31; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKRPLY 17
Db 8 PKRPLY 13

RESULT 32
US-10-293-418-2501
Sequence 2501, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
PRIOR FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2501
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2501

Query Match 27.2%; Score 31; DB 4; Length 14;
 Best Local Similarity 83.3%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 12 PRAPLY 17
 |::|::|
 Db 8 PRAPLY 13

RESULT 33

US-10-224-999A-1528
 ; Sequence 1528, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1528
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Human papillomavirus
 US-10-224-999A-1528

Query Match 27.2%; Score 31; DB 4; Length 15;
 Best Local Similarity 33.3%; Pred. No. 1.5e+03;
 Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DYEYPSRLGNPKAP 15
 |::|::|
 Db 1 DITFPFAPMGTPSP 15

RESULT 34
 US-10-203-915A-58
 ; Sequence 58, Application US/10203915A
 ; Publication No. US20040106159A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Kern, Florian
 ; TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
 ; TITLE OF INVENTION: Lymphocytes with synthetic Peptide Libraries
 ; FILE REFERENCE: 010266wo/JH/ml
 ; CURRENT APPLICATION NUMBER: US/10/203,915A
 ; PRIOR FILING DATE: 2002-08-15
 ; NUMBER OF SEQ ID NOS: 260
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 58
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: HCV IR-1
 US-10-203-915A-58

Query Match 27.2%; Score 31; DB 4; Length 15;
 Best Local Similarity 35.7%; Pred. No. 1.5e+03;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PPSRLGNPKAPLYK 18
 |::|::|
 Db 2 PSSKVPRPPTPVTK 15

RESULT 35

US-10-886-773-147
 ; Sequence 147, Application US/10886773
 ; Publication No. US20050054107A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Chulay, Jeffrey D.
 ; APPLICANT: Dryga, Sergey A.
 ; APPLICANT: Read, Elizabeth A.
 ; APPLICANT: Morris, John S.
 ; APPLICANT: Olmsted, Robert A.
 ; TITLE OF INVENTION: ALPHAVIRUS-BASED CYTOMEGALOVIRUS VACCINES
 ; FILE REFERENCE: 9368-7
 ; CURRENT APPLICATION NUMBER: US/10/886,773
 ; PRIOR FILING DATE: 2004-07-08
 ; PRIOR APPLICATION NUMBER: US 60/486,501
 ; NUMBER OF SEQ ID NOS: 262
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 147
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Human cytomegalovirus
 US-10-886-773-147

Query Match 27.2%; Score 31; DB 5; Length 15;
 Best Local Similarity 35.7%; Pred. No. 1.5e+03;
 Matches 5; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PPSRLGNPKAPLYK 18
 |::|::|
 Db 2 PSSKVPRPPTPVTK 15

RESULT 36
 US-10-862-195-182
 ; Sequence 182, Application US/10862195
 ; Publication No. US20050164324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GYGI, STEVEN P.
 ; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
 ; FILE REFERENCE: 58890(70207)
 ; CURRENT APPLICATION NUMBER: US/10/862,195
 ; PRIOR FILING DATE: 2004-06-04
 ; PRIOR APPLICATION NUMBER: 60/476,010
 ; PRIOR FILING DATE: 2003-06-04
 ; NUMBER OF SEQ ID NOS: 2245
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 182
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: See specification as filed for preferred embodiments
 ; OTHER INFORMATION: and description of phosphorylation sites
 US-10-862-195-182

Query Match 27.2%; Score 31; DB 5; Length 15;
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PPSRLGNPKAP 15
 |::|::|
 Db 3 PPSQVNPBSP 13

RESULT 37
 US-10-224-999A-1540
 ; Sequence 1540, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton

APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1540
LENGTH: 16
TYPE: PRT
ORGANISM: Human papillomavirus
US-10-224-999A-1540

Query Match 27.2%; Score 31; DB 4; Length 16;
Best Local Similarity 33.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYBYGSRIGNPKAP 15
DB 2 DTFPTAWGTPTSP 16

RESULT 38
US-10-161-791-189
Sequence 189, Application US/10161791
Publication No. US2003018686A1
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: KAY, Brian K.
APPLICANT: THORN, Judith M.
APPLICANT: QUILIAM, Lawrence A.
APPLICANT: DER, Channing J.
APPLICANT: FOWLES, Dana M.
APPLICANT: RIDER, James E.
TITLE OF INVENTION: SH3 BINDING PEPTIDES AND METHODS OF
TITLE OF INVENTION: ISOLATING AND USING SAME
NUMBER OF SEQUENCES: 467
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/161,791
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/602,999
FILING DATE: 16-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Mierock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-202
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIR
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-10-161-791-189

Query Match 27.2%; Score 31; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPKAPLYK 18
DB 4 LGRPETPLRK 13

RESULT 39
US-10-211-088-244
Sequence 244, Application US/10211088
Publication No. US20030104479A1
GENERAL INFORMATION:
APPLICANT: Bright, Gary R.
APPLICANT: Premkumar, D. David
APPLICANT: Chen, Yih-Tai
TITLE OF INVENTION: No. US20030104479A1 Fusion Proteins And Assays For Molecular B
FILE REFERENCE: 01-1022-US
CURRENT APPLICATION NUMBER: US/10/211,088
CURRENT FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 60/309,395
PRIOR FILING DATE: 2001-08-01
PRIOR APPLICATION NUMBER: 60/341,589
PRIOR FILING DATE: 2001-12-13
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 244
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Nuclear localization signal
US-10-211-088-244

Query Match 27.2%; Score 31; DB 4; Length 17;
Best Local Similarity 66.7%; Pred. No. 1.7e+03;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPAPLYK 18
DB 7 GNPAPLYK 15

RESULT 40
US-10-224-999A-1553
Sequence 1553, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1553
LENGTH: 17
TYPE: PRT
ORGANISM: Human papillomavirus
US-10-224-999A-1553

Query Match 27.2%; Score 31; DB 4; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.7e+03;
Matches 5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY 1 DYBYGSRIGNPKAP 15


```

1 Publication No. US2003017318A1
2 GENERAL INFORMATION:
3 APPLICANT: Myriad Genetics, Inc.
4 APPLICANT: Morham, Scott
5 APPLICANT: Zavit, Kenton
6 APPLICANT: Hobden, Adrian
7 TITLE OF INVENTION: Composition and Method for Treating Viral Infection
8 FILE REFERENCE: 5004_01
9 CURRENT APPLICATION NUMBER: US/10/224,999A
10 CURRENT FILING DATE: 2003-03-03
11 PRIOR APPLICATION NUMBER: US 60/313,695
12 PRIOR FILING DATE: 2001-08-20
13 NUMBER OF SEQ ID NOS: 3484
14 SOFTWARE: PatentIn version 3.1
15 SEQ ID NO 1567
16 LENGTH: 18
17 TYPE: PRF
18 ORGANISM: Human papillomavirus
19 US-10-224-999A-1567

```

Query Match	27.2%	Score 11; DB 4; Length 18;
Best Local Similarity	33.3%	Pred. NO. 1.8e+03;
Matches	5; Conservative	4; Mismatches 6; Indels 0; Gaps 0.
Qy	1 DRYPSGRLEGNPKAP 15	
	: : : :	
Db	4 DITFPTAEMGTPTFSP 18	

```

RESULT 46
US-10-350-405-200
/ Sequence 200, Application US/10350405
/ Publication No. US20030215894A1
/ GENERAL INFORMATION:
/ APPLICANT: Niman, Henry L.
/ TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors
/ TITLE OF INVENTION: to Protein Ligands
/ FILE REFERENCE: TSRI 35.5 CON 7/LIG
/ CURRENT APPLICATION NUMBER: US/10/350,405
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR APPLICATION NUMBER: 09/427,576
/ PRIOR FILING DATE: 1999-10-26
/ PRIOR APPLICATION NUMBER: 08/461,583
/ PRIOR FILING DATE: 1995-06-02
/ PRIOR APPLICATION NUMBER: 08/294,879
/ PRIOR FILING DATE: 1994-08-23
/ PRIOR APPLICATION NUMBER: 08/054,864
/ PRIOR FILING DATE: 1993-04-28
/ PRIOR APPLICATION NUMBER: 07/900,502
/ PRIOR FILING DATE: 1992-06-16
/ PRIOR APPLICATION NUMBER: 07/780,415
/ PRIOR FILING DATE: 1991-10-22
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 200
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: retrovirus
US-10-350-405-200

```

Query Match	27.2%	Score 31	DB 4	Length 18
Best Local	44.4%	Pred. NO. 1.8e+03		
Matches 4	Conservative 3	Mismatches 2	Indels 0	Gaps 0

Qy	12	PKAPLYKRP	20
		: :	
Db	3	PQVPAFRRP	11

RESULT 47
US-10-224-999A-1582
; Sequence 1582, Application US/10224999A
; Publication No. US20030171318A1

```

? GENERAL INFORMATION:
? APPLICANT: Myriad Genetics, Inc.
? APPLICANT: Morham, Scott
? APPLICANT: Zavitz, Kenton
? APPLICANT: Hobden, Adrian
? TITLE OF INVENTION: Composition and Method for Treating Viral Infection
? FILE REFERENCE: 5004.01
? CURRENT APPLICATION NUMBER: US/10/224,999A
? CURRENT FILING DATE: 2003-03-03
? PRIOR APPLICATION NUMBER: US 60/313,695
? PRIOR FILING DATE: 2001-08-20
? NUMBER OF SEQ ID NOS: 3484
? SOFTWARE: PatentIn version 3.1
? SEQ ID NO 1582
? LENGTH: 19
? TYPE: PRT
? ORGANISM: Human papillomavirus
US-10-224-999A-1582

```

```

Query Match      27.2%; Score 31; DB 4; Length 19;
Best Local      Similarity 33.3%;
Matches         5; Conservative 4; Mismatches 6; Indels 0; Gaps 0;
QY              1 DYEPGSRLENGPKAP 15
                | : : : : :
Db              5 DTFPTNAPMGPPSP 19

```

```

RESULT 48
US-10-862-195-1528
: Sequence 1528, Application US/10862195
: Publication No. US2005016432A1
: GENERAL INFORMATION:
: APPLICANT: GYGI, STEVEN P.
: TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
: FILE REFERENCE: 58890(70207)
: CURRENT APPLICATION NUMBER: US/10/862,195
: CURRENT FILING DATE: 2004-06-04
: PRIOR APPLICATION NUMBER: 60/476,010
: PRIOR FILING DATE: 2003-06-04
: NUMBER OF SEQ ID NOS: 2245
: SOFTWARE: PatentIn version 3.2
: SEQ ID NO 1528
: LENGTH: 19
: TYPE: PRT
: ORGANISM: Homo sapiens
: FEATURE:
: OTHER INFORMATION: See specification as filed for preferred embodiments
: US-10-862-195-1528
: OTHER INFORMATION: and description of phosphorylation sites

```

Query Match	27.2%	Score	31	DB	5	Length	19
Best Local Similarity	50.0%	Pred. No.	1.9e+03				
Matches	5	Conservative	1	Mismatches	4	Indels	0
						Gaps	0

```
Qy 11 NPKAPLYKRP 20
      ||: || |
Db 1 NPQMPOYSSP 10
```

```

RESULT 49
US-10-224-999A-1598
; Sequence 1598, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03

```

```

?      PRIOR APPLICATION NUMBER: US 60/313,699
?      PRIOR FILING DATE: 2001-08-20
?      NUMBER OF SEQ ID NOS: 3484
?      SOFTWARE: PatentIn version 3.1
?      SEQ ID NO 1598
?      LENGTH: 20
?      TYPE: PRT
?      ORGANISM: Human papillomavirus
US-10-224-999A-1598
```

Query Match	27.2%	Score 31;	DB 4;	Length 20;
Best Local Similarity	33.3%	Pred. No. 2e+03;		
Matches	5;	Conservative	4;	Mismatches 6;
				Indels 0;
				Gaps 0

```
QY      1 DYEPGSR LGNPKAP 15
          | : | : | : |
Db      6 DTFPTAPMGTPFSP 20
```

```

US-10-481-261-459
SEQUENCE 459, APPLICATION US/10481261
PUBLICATION NO. US2004026792A1
GENERAL INFORMATION:
APPLICANT: GLASS, Jeffrey S.
APPLICANT: MYERS, Tina M.
TITLE OF INVENTION: AGENTS FOR TREATMENT OF HCV AND METHODS OF USE
FILE REFERENCE: STAN-344
CURRENT APPLICATION NUMBER: US/10/481,261
CURRENT FILING DATE: 2003-12-17
PRIORITY APPLICATION NUMBER: PCT/US 02/13951
PRIORITY FILING DATE: 2002-05-03
PRIORITY APPLICATION NUMBER: US 60/288,687
PRIORITY FILING DATE: 2001-05-03
PRIORITY APPLICATION NUMBER: US 60/316,805
PRIORITY FILING DATE: 2001-08-31
NUMBER OF SEQ ID NOS: 470
SOFTWARE: PatentIn version 3.1
SEQ ID NO 459
LENGTH: 13
TYPE: PRN
ORGANISM: Hepatitis C virus
US-10-481-261-459

```

Query Match	26.8%	Score 30.5	DB 5	Length 13
Best Local Similarity	64.3%	Pred. No. 1.5e+03		
Matches 9; Conservative	1	Mismatches 1	Indels 3	Gaps 2

QY 4 YPGSR LGN--PKAP 15
|||:|||||
Db 1 YP-SKPGNVTPKAP 13

```

RESULT 51
US-09-572-404B-3190
; Sequence 3190, Application US/09572404B
; Publication No. US20030078374A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands from the human genome
FILE REFERENCE: Human patent
CURRENT APPLICATION NUMBER: US/09/572,404B
CURRENT FILING DATE: 2000-05-17
NUMBER OF SEQ ID NOS: 4203
SOFTWARE: ProPatent version 1.0
SEQ ID NO 3190
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
OTHER INFORMATION: sequence located in K12A0411 at 417-426 and may interact with Sec
OTHER INFORMATION: 3189 in this patent.

```

US-09-572-404B-3190

Query Match	26.3%	Score 30;	DB 3;	Length 10;
Best Local Similarity	62.5%	Pred. No. 1.4e+03;		
Matches	5;	Conservative	1;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY 5 PGSRLGNP 12
|||
Db 3 PGALGSP 10

```

RESULT 52
US-09-954-385-315
: Sequence 315, Application US/09954385
: Publication NO. US20030100467A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Hsuehming
APPLICANT: Whetelky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
TITLE OF INVENTION: Complexes
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/09/954,385
CURRENT FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 315
LENGTH: 12
TYPE: PRT
FEATURE: Artificial Sequence
OTHER INFORMATION: binding peptide
US-09-954-385-315

```

Query Match	26.3%	Score 30;	DB 3;	Length 12;
Best Local Similarity	54.5%	Pred. No. 1.6e+03;		
Matches	6;	Conservative	0;	Mismatches 5;
			Indels	0;
			Gaps	0;

QY 5 PGSRLGNPKAP 15
Db 2 PHSMLQNPSCP 12

```

RESULT 53
US-10-912-512-315
; Sequence 315, Application US/10912512
; Publication No. US20050042684A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby L.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
APPLICANT: Wineczky, Deborah S.
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
TITLE OF INVENTION: Complexes
FILE REFERENCE: GC690
CURRENT APPLICATION NUMBER: US/10/912,512
CURRENT FILING DATE: 2004-08-05
PRIOR APPLICATION NUMBER: US/09/954,385
PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 433
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 315
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

```

OTHER INFORMATION: binding peptide
US-10-912-512-315

Query Match 26.3%; Score 30; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
DB 2 PHSMLQNPSCP 12

RESULT 54
US-10-235-043-315
Sequence 315, Application US/10235043
Publication No. US20050058996A1
GENERAL INFORMATION:
APPLICANT: Aehle, Wolfgang
APPLICANT: Baldwin, Toby M.
APPLICANT: Van Gastel, Franciscus J.C.
APPLICANT: Janssen, Giselle G.
APPLICANT: Murray, Christopher J.
APPLICANT: Wang, Huaming
TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-Peptide
TITLE OF INVENTION: Complexes
FILE REFERENCE: GC690-2
CURRENT APPLICATION NUMBER: US/10/235,043
CURRENT FILING DATE: 2002-09-03
NUMBER OF SEQ ID NOS: 446
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 315
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: binding peptide
US-10-235-043-315

Query Match 26.3%; Score 30; DB 5; Length 12;
Best Local Similarity 54.5%; Pred. No. 1.6e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
DB 2 PHSMLQNPSCP 12

RESULT 55
US-09-880-748-2378
Sequence 2378, Application US/09880748
Publication No. US2003005937A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523
CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2378
LENGTH: 14
TYPE: PRT

ORGANISM: Homo sapiens
US-09-880-748-2378

Query Match 26.3%; Score 30; DB 3; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17
DB 8 PQAPLY 13

RESULT 56
US-10-293-418-2378
Sequence 2378, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: P5523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2378
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-293-418-2378

Query Match 26.3%; Score 30; DB 4; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17
DB 8 PQAPLY 13

RESULT 57
US-09-829-549A-44
Sequence 44, Application US/09829549A
Patent No. US20020052484A1
GENERAL INFORMATION:
APPLICANT: The Curators of the University of Missouri
TITLE OF INVENTION: PHAGE DISPLAY SELECTION OF ANTI FUNGAL PEPTIDES
FILE REFERENCE: UMO 1521.1
CURRENT APPLICATION NUMBER: US/09/829,549A
CURRENT FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 60/195,785
PRIOR FILING DATE: 2000-04-10
NUMBER OF SEQ ID NOS: 48
SOFTWARE: PatentIn version 3.0
SEQ ID NO 44
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

```
/ NAME/KEY: DOMAIN
/ LOCATION: (1)...(15)
/ OTHER INFORMATION: Random peptide insert
US-09-829-549A-44
```

```
Query Match          26.3%; Score 30; DB 3; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      15 PLYKRP 20
      |||||
Db      2 PLYKRP 7
```

```
RESULT 58
US-09-992-665-45
/ Sequence 45, Application US/09992665
/ Publication No. US20030092009A1
/ GENERAL INFORMATION:
/ APPLICANT: Kala Palm
/ TITLE OF INVENTION: PROFILING TUMOR SPECIFIC MARKERS FOR THE
/ FILE REFERENCE: CEMINES.002A
/ CURRENT APPLICATION NUMBER: US/09/992,665
/ CURRENT FILING DATE: 2001-11-13
/ PRIOR APPLICATION NUMBER: 60/249,508
/ PRIOR FILING DATE: 2000-11-16
/ NUMBER OF SEQ ID NOS: 380
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 45
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Probe
US-09-992-665-45
```

```
Query Match          26.3%; Score 30; DB 3; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 GNPAPLYKR 19
      |||||
Db      5 GSPAPAHSR 14
```

```
RESULT 59
US-10-862-195-1857
/ Sequence 1857, Application US/10862195
/ Publication No. US20050164324A1
/ GENERAL INFORMATION:
/ APPLICANT: GYGI, STEVEN P.
/ TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
/ FILE REFERENCE: 58890(70207)
/ CURRENT APPLICATION NUMBER: US/10/862,195
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: 60/476,010
/ PRIOR FILING DATE: 2003-06-04
/ NUMBER OF SEQ ID NOS: 2245
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1857
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Saccharomyces cerevisiae
US-10-862-195-1857
```

```
Query Match          26.3%; Score 30; DB 5; Length 15;
Best Local Similarity 57.1%; Pred. No. 2.1e+03;
Matches 8; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      6 GSRLLGNPKAPLYKR 19
      |||||
Db      2 GSOLKNLKAALYKR 15
```

```
RESULT 60
US-09-974-879-522
```

```
/ Sequence 522, Application US/09974879
/ Publication No. US20030028003A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 125 Human Secreted Proteins
/ FILE REFERENCE: P2020P2
/ CURRENT APPLICATION NUMBER: US/09/974,879
/ CURRENT FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: US 60/239,893
/ PRIOR FILING DATE: 2000-10-13
/ PRIOR APPLICATION NUMBER: US 09/818,683
/ PRIOR FILING DATE: 2001-03-28
/ PRIOR APPLICATION NUMBER: US 09/305,736
/ PRIOR FILING DATE: 1999-05-05
/ PRIOR APPLICATION NUMBER: PCT/US98/23435
/ PRIOR FILING DATE: 1998-11-04
/ PRIOR APPLICATION NUMBER: US 60/064,911
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,912
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,983
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,900
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,988
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,987
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,908
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,984
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/064,985
/ PRIOR FILING DATE: 1997-11-07
/ PRIOR APPLICATION NUMBER: US 60/066,094
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,100
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,089
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,095
/ PRIOR FILING DATE: 1997-11-17
/ PRIOR APPLICATION NUMBER: US 60/066,090
/ PRIOR FILING DATE: 1997-11-17
/ NUMBER OF SEQ ID NOS: 611
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 522
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-974-879-522
```

```
Query Match          26.3%; Score 30; DB 3; Length 16;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      8 RLGNPKAPLYKRP 20
      |||||
Db      2 RKNPKCRFLFSVP 14
```

```
RESULT 61
US-09-305-736-524
/ Sequence 524, Application US/09305736
/ Publication No. US20030088078A1
/ GENERAL INFORMATION:
/ APPLICANT: Feng et al.
/ TITLE OF INVENTION: 125 Human Secreted Proteins
/ FILE REFERENCE: P2020P1
```


CURRENT APPLICATION NUMBER: US/09/305,736
CURRENT FILING DATE: 1999-05-05
EARLIER APPLICATION NUMBER: PCT/US98/23435
EARLIER FILING DATE: 1998-11-04
EARLIER APPLICATION NUMBER: 60/064,911
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,912
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,983
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,900
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,988
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,987
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,908
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,984
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/064,985
EARLIER FILING DATE: 1997-11-07
EARLIER APPLICATION NUMBER: 60/066,094
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,100
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,089
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60,066,095
EARLIER FILING DATE: 1997-11-17
EARLIER APPLICATION NUMBER: 60/066,090
EARLIER FILING DATE: 1997-11-17
NUMBER OF SEQ ID NOS: 612
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 524
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-305-736-524

Query Match 26.3%; Score 30; DB 3; Length 16;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
DB 2 RFGNPKCRLFSVP 14

RESULT 62
US-09-818-683-524
Sequence 524, Application US/09818683
Publication No. US20030211472A1
GENERAL INFORMATION:
APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P1
CURRENT APPLICATION NUMBER: US/09/818,683
CURRENT FILING DATE: 2001-03-28
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 612
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 524
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-818-683-524

Query Match 26.3%; Score 30; DB 3; Length 16;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20

DB 2 RFGNPKCRLFSVP 14

RESULT 63
US-09-818-683-524
Sequence 524, Application US/09818683
Publication No. US20040185440A9
GENERAL INFORMATION:
APPLICANT: Feng et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P1
CURRENT APPLICATION NUMBER: US/09/818,683
CURRENT FILING DATE: 2001-03-28
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 612
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 524
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-818-683-524

Query Match 26.3%; Score 30; DB 3; Length 16;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKRP 20
DB 2 RFGNPKCRLFSVP 14

RESULT 64
US-10-621-401-522
Sequence 522, Application US/10621401
Publication No. US20040038277A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 125 Human Secreted Proteins
FILE REFERENCE: P2020P2c1
CURRENT APPLICATION NUMBER: US/10/621,401
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: US 09/974,879
PRIOR FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/239,893
PRIOR FILING DATE: 2000-10-13
PRIOR APPLICATION NUMBER: US 09/818,683
PRIOR FILING DATE: 2001-03-28
PRIOR APPLICATION NUMBER: US 09/305,736
PRIOR FILING DATE: 1999-05-05
PRIOR APPLICATION NUMBER: PCT/US98/23435
PRIOR FILING DATE: 1998-11-04
PRIOR APPLICATION NUMBER: US 60/064,911
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,912
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,983
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,900
PRIOR FILING DATE: 1997-11-07
PRIOR APPLICATION NUMBER: US 60/064,988
PRIOR FILING DATE: 1997-11-07
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 611
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 522
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-621-401-522

Query Match 26.3%; Score 30; DB 4; Length 16;
Best Local Similarity 46.2%; Pred. No. 2.2e+03;

Query Match	26.3%	Score 30;	DB 4;	Length 18;
Similarity	71.4%	Pred. No. 2.5e+03;		
Best Local	5;	Conservative	0;	Gaps 0;
Matches	2;	Mismatches	0;	

RESULT 69
US-10-325-810-163

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/ Sequence 163, Application US/10325810
/ Publication No. US20030204069A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/      Ligner, Joachim
/      Nakamura, Toru
/      Chapman, Karen B.
/      Morin, Gregg B.
/      Harley, Calvin B.
/      Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 633
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/325,810
/ FILING DATE: 20-Dec-2002
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/402,181
/ FILING DATE: 29-Sep-1997
/ APPLICATION NUMBER: US 08/724,643
/ FILING DATE: 01-Oct-1996
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-Apr-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-Apr-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-May-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-May-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: WO PCT/US97/17865
/ FILING DATE: 01-Oct-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Aueenhuis, Scott L.
/ REGISTRATION NUMBER: 42,271
/ REFERENCE/DOCKET NUMBER: 015369-002620US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 163:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-10-325-810-163

```

Query Match 26.3%; Score 30; DB 4; Length 18;
 Best local Similarity 62.5%; Pred. No. 2.5e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

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RESULT 70
US-10-350-405-181
/ Sequence 181, Application US/10350405
/ Publication No. US20030215894A1
/ GENERAL INFORMATION:
/ APPLICANT: Niman, Henry L.
/ TITLE OF INVENTION: Polypeptide-Induced Monoclonal Receptors
/ FILE OF INVENTION: to Protein Ligands
/ FILE REFERENCE: TSRI 35.5 CON 7/LIG
/ CURRENT APPLICATION NUMBER: US/10/350,405
/ CURRENT FILING DATE: 2003-01-24
/ PRIOR APPLICATION NUMBER: 09/427,576
/ PRIOR FILING DATE: 1999-10-26
/ PRIOR APPLICATION NUMBER: 08/461,583
/ PRIOR FILING DATE: 1995-06-02
/ PRIOR APPLICATION NUMBER: 08/294,879
/ PRIOR FILING DATE: 1994-08-23
/ PRIOR APPLICATION NUMBER: 08/054,864
/ PRIOR FILING DATE: 1993-04-28
/ PRIOR APPLICATION NUMBER: 07/900,502
/ PRIOR FILING DATE: 1992-06-16
/ PRIOR APPLICATION NUMBER: 07/780,415
/ PRIOR FILING DATE: 1991-10-22
/ NUMBER OF SEQ ID NOS: 227
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 181
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: retrovirus
US-10-350-405-181

```

Query Match 26.3%; Score 30; DB 4; Length 18;
 Best local Similarity 66.7%; Pred. No. 2.5e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

DB 10 PSERLGNLK 18
QY 5 PSERLGNPK 13
US-10-415-024-8
/ Sequence 8, Application US/10415024
/ Publication No. US20040058984A1
/ GENERAL INFORMATION:
/ APPLICANT: Diatide, Inc.
/ TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
/ FILE OF INVENTION: USING HYDROPHILIC THIOETHERS AND HYDROPHILIC 6-HYDROXY
/ FILE REFERENCE: 09744-015WO1
/ CURRENT APPLICATION NUMBER: US/10/415,024
/ CURRENT FILING DATE: 2003-04-24
/ PRIOR APPLICATION NUMBER: US 09/694,992
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 09/695,360
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: US 09/695,494
/ PRIOR FILING DATE: 2000-10-24
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-10-415-024-8

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Query Match 26.3%; Score 30; DB 4; Length 18;
 Best local Similarity 71.4%; Pred. No. 2.5e+03;
 Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 13 KAPLYK 19
:||||:
Db 4 QAPLYK 10

RESULT 72
US-10-877-124-163
; Sequence 163, Application US/10877124
; Publication No. US20040242529A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Hartley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,124
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 163:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-10-877-124-163

Query Match 26.3%; Score 30; DB 5; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

OY 11 NPKAPLYK 18
|||||:
Db 5 NPKTPIK 12

RESULT 73
US-10-877-022-163
; Sequence 163, Application US/10877022
; Publication No. US20040247613A1
; GENERAL INFORMATION:
; APPLICANT: Cech, Thomas R.
; Lingner, Joachim
; Nakamura, Toru
; Chapman, Karen B.
; Morin, Gregg B.
; Hartley, Calvin B.
; Andrews, William H.
; TITLE OF INVENTION: Human Telomerase Catalytic Subunit
; NUMBER OF SEQUENCES: 727
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/877,022
; FILING DATE: 24-Jun-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/432,503
; FILING DATE: 02-Nov-1999
; APPLICATION NUMBER: 08/974,549
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 08/844,419
; FILING DATE: 18-Apr-1997
; APPLICATION NUMBER: US 08/846,017
; FILING DATE: 25-Apr-1997
; APPLICATION NUMBER: US 08/851,843
; FILING DATE: 06-May-1997
; APPLICATION NUMBER: US 08/854,050
; FILING DATE: 09-May-1997
; APPLICATION NUMBER: US 08/911,312
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/912,951
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: US 08/915,503
; FILING DATE: 14-Aug-1997
; APPLICATION NUMBER: WO PCT/US97/17618
; FILING DATE: 01-Oct-1997
; APPLICATION NUMBER: WO PCT/US97/17885
; FILING DATE: 01-Oct-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Apple, Randolph Ted
; REGISTRATION NUMBER: 36,429
; REFERENCE/DOCKET NUMBER: 015389-002610US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 163:

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/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-10-877-022-163

Query Match      26.3%; Score 30; DB 5; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      11 NPKAPLYK 18
Db      5 NPKTPYIK 12

RESULT 74
US-10-877-146-163
/ Sequence 163, Application US/10877146
/ Publication No. US20050013825A1
/ GENERAL INFORMATION:
/ APPLICANT: Cech, Thomas R.
/   Lingner, Joachim
/   Nakamura, Toru
/   Chapman, Karen B.
/   Morin, Gregg B.
/   Harley, Calvin B.
/   Andrews, William H.
/ TITLE OF INVENTION: Human Telomerase Catalytic Subunit
/ NUMBER OF SEQUENCES: 727
/ CORRESPONDING ADDRESS:
/ ADDRESSEE: Townsend and Townsend and Crew LLP
/ STREET: Two Embarcadero Center, Eighth Floor
/ CITY: San Francisco
/ STATE: California
/ COUNTRY: USA
/ ZIP: 94111-3834
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/877,146
/ FILING DATE: 24-Jun-2004
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/09/432,503
/ FILING DATE: 02-Nov-1999
/ APPLICATION NUMBER: 08/974,549
/ FILING DATE: <Unknown>
/ APPLICATION NUMBER: US 08/844,419
/ FILING DATE: 18-Apr-1997
/ APPLICATION NUMBER: US 08/846,017
/ FILING DATE: 25-Apr-1997
/ APPLICATION NUMBER: US 08/851,843
/ FILING DATE: 06-May-1997
/ APPLICATION NUMBER: US 08/854,050
/ FILING DATE: 09-May-1997
/ APPLICATION NUMBER: US 08/911,312
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: US 08/912,951
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: US 08/915,503
/ FILING DATE: 14-Aug-1997
/ APPLICATION NUMBER: WO PCT/US97/17618
/ FILING DATE: 01-Oct-1997
/ APPLICATION NUMBER: WO PCT/US97/17885
/ FILING DATE: 01-Oct-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Apple, Randolph Ted
```

```
/ REGISTRATION NUMBER: 36,429
/ REFERENCE/DOCKET NUMBER: 015389-002610US
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 576-0200
/ TELEFAX: (415) 576-0300
/ INFORMATION FOR SEQ ID NO: 163:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 18 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 163:
US-10-877-146-163

Query Match      26.3%; Score 30; DB 5; Length 18;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      11 NPKAPLYK 18
Db      5 NPKTPYIK 12

RESULT 75
US-11-088-596-8
/ Sequence 8, Application US/11088596
/ Publication No. US20050180918A1
/ GENERAL INFORMATION:
/ APPLICANT: Cyr, John B.
/ APPLICANT: Pearson, Daniel A.
/ TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
/ TITLE OF INVENTION: USING HYDROPHILIC THIOETHERS
/ FILE REFERENCE: 09744-016001
/ CURRENT APPLICATION NUMBER: US/11/088,596
/ CURRENT FILING DATE: 2005-03-24
/ PRIOR APPLICATION NUMBER: US/10/131,543
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 09/694,992
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: PCT/US01/50423
/ PRIOR FILING DATE: 2001-10-24
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Synthetic construct
/ US-11-088-596-8

Query Match      26.3%; Score 30; DB 6; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      13 KAPLYKR 19
Db      4 QAPLYKK 10

RESULT 76
US-11-066-697-1140
/ Sequence 1140, Application US/11066697
/ Publication No. US20050187159A1
/ GENERAL INFORMATION:
/ APPLICANT: Bridon, Dominique P.
/ APPLICANT: Ezrin, Alan M.
/ APPLICANT: Milner, Peter G.
/ APPLICANT: Holmes, Darren L.
/ APPLICANT: Thibodeau, Karen
/ TITLE OF INVENTION: PROTECTION OF ENDOGENOUS THERAPEUTIC PEPTIDES FROM
/ PEPTIDASE ACTIVITY THROUGH CONJUGATION TO BLOOD
```

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/ TITLE OF INVENTION: COMPONENTS
/ FILE REFERENCE: 500862002301
/ CURRENT APPLICATION NUMBER: US/11/066,697
/ CURRENT FILING DATE: 2005-02-25
/ PRIOR APPLICATION NUMBER: 09/657,276
/ PRIOR FILING DATE: 2000-09-07
/ PRIOR APPLICATION NUMBER: 60/153,406
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: 60/159,783
/ PRIOR FILING DATE: 1999-10-15
/ NUMBER OF SEQ ID NOS: 1617
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 1140
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-066-697-1140
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Query Match      26.3%; Score 30; DB 6; Length 18;
Best Local Similarity 42.1%; Pred. No. 2.5e+03;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
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```
QY      2 YEYPSRLGNPKAPLYKRP 20
Db      1 YEKPSG---PPREVPRP 15
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```
RESULT 77
US-11-086-966-8
/ Sequence 8, Application US/11086966
/ Publication No. US20050207973A1
/ GENERAL INFORMATION:
/ APPLICANT: CYT, John E.
/ TITLE OF INVENTION: STABILIZATION OF RADIOPHARMACEUTICAL COMPOSITIONS
/ FILE REFERENCE: 09744-017001
/ CURRENT APPLICATION NUMBER: US/11/086,966
/ CURRENT FILING DATE: 2005-03-22
/ PRIOR APPLICATION NUMBER: US/10/131,346
/ PRIOR FILING DATE: 2002-04-24
/ PRIOR APPLICATION NUMBER: US 09/695,360
/ PRIOR FILING DATE: 2000-10-24
/ PRIOR APPLICATION NUMBER: PCT/US01/50423
/ PRIOR FILING DATE: 2001-10-24
/ NUMBER OF SEQ ID NOS: 29
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic construct
US-11-086-966-8
```

```
Query Match      26.3%; Score 30; DB 6; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.5e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 KAPLYRK 19
Db      4 QAPLYRK 10
```

```
RESULT 78
US-10-106-804B-11
/ Sequence 11, Application US/10106804B
/ Publication No. US2003019186A1
/ GENERAL INFORMATION:
/ APPLICANT: Hubbell, Jeffrey A.
/ APPLICANT: Schense, Jason C.
```

```
/ APPLICANT: Sakiyama-Bibert, Shelly E.
/ TITLE OF INVENTION: Enzyme-Mediated Modification of Fibrin For Tissue Engineering: F
/ FILE REFERENCE: ETH 106 CON
/ CURRENT APPLICATION NUMBER: US/10/106,804B
/ CURRENT FILING DATE: 2003-03-04
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 11
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: artificial sequence
/ FEATURE:
/ OTHER INFORMATION: heparin binding sequence
US-10-106-804B-11
```

```
Query Match      26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.6e+03;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
```

```
QY      2 YEYPSRLGNPKAPLYKRP 20
Db      1 YEKPSG---PPREVPRP 15
```

```
RESULT 79
US-10-323-046-13
/ Sequence 13, Application US/10323046
/ Publication No. US20030187232A1
/ GENERAL INFORMATION:
/ APPLICANT: Hubbell, Jeffrey A
/ APPLICANT: Schense, Jason C
/ APPLICANT: Sakiyama-Bibert, Shelly E
/ TITLE OF INVENTION: Growth Factor Modified Protein Matrices for Tissue
/ FILE REFERENCE: ETH 107 CIP (2)
/ CURRENT APPLICATION NUMBER: US/10/323,046
/ CURRENT FILING DATE: 2002-12-17
/ PRIOR APPLICATION NUMBER: 09/141,153
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 43
/ SOFTWARE: PatentIn Ver. 3.1
/ SEQ ID NO 13
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:
US-10-323-046-13
```

```
Query Match      26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.6e+03;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;
```

```
QY      2 YEYPSRLGNPKAPLYKRP 20
Db      1 YEKPSG---PPREVPRP 15
```

```
RESULT 80
US-10-297-229-52
/ Sequence 52, Application US/10297229
/ Publication No. US20030220245A1
/ GENERAL INFORMATION:
/ APPLICANT: HUBBELL, Jeffrey A.
/ APPLICANT: ELBERT, Donald
/ APPLICANT: SCHOENMAKERS, Ronald
/ TITLE OF INVENTION: CONJUGATE ADDITION REACTIONS FOR THE
/ FILE REFERENCE: 50154/003002
/ CURRENT APPLICATION NUMBER: US/10/297,229
/ CURRENT FILING DATE: 2002-10-02
```

;; PRIOR APPLICATION NUMBER: PCT/US01/18101
;; PRIOR FILING DATE: 2001-06-04
;; PRIOR APPLICATION NUMBER: US 09/586,937
;; PRIOR FILING DATE: 2000-06-02
;; NUMBER OF SEQ ID NOS: 77
;; SOFTWARE: FaastSeq for Windows Version 4.0
;; SEQ ID NO 52
;; LENGTH: 19
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Based on Homo sapiens
US-10-297-229-52

Query Match 26.3%; Score 30; DB 4; Length 19;
Best Local Similarity 42.1%; Pred. No. 2.6e+03;
Matches 8; Conservative 1; Mismatches 6; Indels 4; Gaps 1;

QY 2 YEYGSRLGNPKAPLYRKP 20
|||:|:|
Db 1 YEKRG-----PPREVVRP 15

RESULT 81
US-10-225-567A-1614
;; Sequence 1614, Application US/10225567A
;; Publication No. US20030113798A1
;; GENERAL INFORMATION:
;; APPLICANT: Lifespan Biosciences
;; APPLICANT: Brown, Joseph P.
;; APPLICANT: Burmer, Glenna C.
;; APPLICANT: Roush, Christine L.
;; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
;; FILE REFERENCE: 1920-4-4
;; CURRENT APPLICATION NUMBER: US/10/225,567A
;; CURRENT FILING DATE: 2001-12-19
;; PRIOR APPLICATION NUMBER: 60/257,144
;; PRIOR FILING DATE: 2000-12-19
;; NUMBER OF SEQ ID NOS: 2292
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 1614
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-10-225-567A-1614

Query Match 26.3%; Score 30; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 2.8e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGRRLGNP 12
||:|:|
Db 12 PGTTPGSP 19

RESULT 82
US-10-327-598-150
;; Sequence 150, Application US/10327598
;; Publication No. US20040181039A1
;; GENERAL INFORMATION:
;; APPLICANT: Krah, Eugene
;; APPLICANT: Guo, Hongliang
;; APPLICANT: Aliyappa, Ashok
;; APPLICANT: Lawton, Robert
;; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, and
;; FILE REFERENCE: 01-799-A
;; CURRENT APPLICATION NUMBER: US/10/327,598
;; CURRENT FILING DATE: 2002-12-20
;; PRIOR APPLICATION NUMBER: US 60/344,874
;; PRIOR FILING DATE: 2001-12-21
;; NUMBER OF SEQ ID NOS: 1139
;; SOFTWARE: PatentIn version 3.0

;; SEQ ID NO 150
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: canis familiaris;
US-10-327-598-150

Query Match 25.9%; Score 29.5; DB 4; Length 15;
Best Local Similarity 40.0%; Pred. No. 2.4e+03;
Matches 6; Conservative 3; Mismatches 3; Indels 3; Gaps 1;

QY 3 EYPSRLGNPKAPLY 17
:|:|:|:|
Db 4 QYPTG---GPXTLY 15

RESULT 83
US-10-327-598-232
;; Sequence 232, Application US/10327598
;; Publication No. US20040181039A1
;; GENERAL INFORMATION:
;; APPLICANT: Krah, Eugene
;; APPLICANT: Guo, Hongliang
;; APPLICANT: Aliyappa, Ashok
;; APPLICANT: Lawton, Robert
;; TITLE OF INVENTION: Canine Immunoglobulin Variable Domains, Caninized Antibodies, an
;; FILE REFERENCE: 01-799-A
;; CURRENT APPLICATION NUMBER: US/10/327,598
;; CURRENT FILING DATE: 2002-12-20
;; PRIOR APPLICATION NUMBER: US 60/344,874
;; PRIOR FILING DATE: 2001-12-21
;; NUMBER OF SEQ ID NOS: 1139
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 232
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: canis familiaris;
US-10-327-598-232

Query Match 25.9%; Score 29.5; DB 4; Length 15;
Best Local Similarity 53.8%; Pred. No. 2.4e+03;
Matches 7; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 5 PGR---LGNPKA 14
||:|:|
Db 3 PGTQLTVLGQPKA 15

RESULT 84
US-10-304-443-99
;; Sequence 99, Application US/10304443
;; Publication No. US20030170229A1
;; GENERAL INFORMATION:
;; APPLICANT: SmithKline Beecham Biologicals s.a.
;; APPLICANT: Peptide Therapeutics Ltd.
;; TITLE OF INVENTION: Vaccine
;; FILE REFERENCE: B45173CIP
;; CURRENT APPLICATION NUMBER: US/10/304,443
;; CURRENT FILING DATE: 2002-11-26
;; PRIOR APPLICATION NUMBER: US/09/698,906A
;; PRIOR FILING DATE: 2001-02-20
;; NUMBER OF SEQ ID NOS: 121
;; SOFTWARE: FaastSeq for Windows Version 3.0
;; SEQ ID NO 99
;; LENGTH: 10
;; TYPE: PRT
;; ORGANISM: Human peptide sequence
US-10-304-443-99

Query Match 25.4%; Score 29; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 EYPSGR 8
|:||||
Db 2 EWPGR 7

RESULT 85
US-10-415-389-12

/ Sequence 12, Application US/10415389
/ Publication No. US20040115220A1

/ GENERAL INFORMATION:

/ APPLICANT: De Basois, Carlota Vinals Y

/ TITLE OF INVENTION: Vaccine

/ FILE REFERENCE: B45251

/ CURRENT APPLICATION NUMBER: US/10/415,389

/ PRIOR FILING DATE: 2003-04-25

/ PRIOR APPLICATION NUMBER: PCT/EP01/12932

/ PRIOR FILING DATE: 2001-10-24

/ PRIOR APPLICATION NUMBER: GB 0026334.3

/ PRIOR FILING DATE: 2000-10-27

/ NUMBER OF SEQ ID NOS: 34

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 12

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Human IGE peptide mimotope

US-10-415-389-12

Query Match 25.4%; Score 29; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 EYPSGR 8
|:||||
Db 2 EWPGR 7

RESULT 86
US-10-322-210-4

/ Sequence 4, Application US/10322210

/ Publication No. US20030147906A1

/ GENERAL INFORMATION:

/ APPLICANT: Friede, Martin

/ APPLICANT: Mason, Sean

/ APPLICANT: Turnell, William Gordon

/ APPLICANT: Van Mechelen, Marcelle Paulette

/ APPLICANT: Vinals Y de Basois, Carlota

/ TITLE OF INVENTION: Epitopes or Mimotopes Derived from the

/ TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IGE, Antagonists

/ TITLE OF INVENTION: Thereof, and Their Therapeutic Uses

/ FILE REFERENCE: B45173

/ CURRENT APPLICATION NUMBER: US/10/322,210

/ PRIOR FILING DATE: 2002-12-18

/ PRIOR APPLICATION NUMBER: US/09/914,089

/ PRIOR FILING DATE: 2001-08-22

/ PRIOR APPLICATION NUMBER: GB 9904408.3

/ PRIOR FILING DATE: 1999-02-25

/ PRIOR APPLICATION NUMBER: GB 9917144.9

/ PRIOR FILING DATE: 1999-07-21

/ PRIOR APPLICATION NUMBER: GB 9918598.5

/ PRIOR FILING DATE: 1999-08-07

/ PRIOR APPLICATION NUMBER: GB 9918599.3

/ PRIOR FILING DATE: 1999-08-07

/ PRIOR APPLICATION NUMBER: GB 9918601.7

/ PRIOR FILING DATE: 1999-08-07

/ PRIOR APPLICATION NUMBER: GB 9918604.1

/ PRIOR FILING DATE: 1999-08-07

/ PRIOR APPLICATION NUMBER: GB 9918606.6

/ PRIOR FILING DATE: 1999-08-07

/ PRIOR APPLICATION NUMBER: GB 9925618.2

/ PRIOR FILING DATE: 1999-10-29

/ NUMBER OF SEQ ID NOS: 86

/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Chimeric
US-10-322-210-4

Query Match 25.4%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 EYPSGR 8
|:||||
Db 2 EWPGR 7

RESULT 87

US-10-304-443-4

/ Sequence 4, Application US/10304443

/ Publication No. US20030170229A1

/ GENERAL INFORMATION:

/ APPLICANT: SmithKline Beecham Biologicals s.a.

/ APPLICANT: Peptide Therapeutics Ltd.

/ TITLE OF INVENTION: Vaccine

/ FILE REFERENCE: B45173CIP

/ CURRENT APPLICATION NUMBER: US/10/304,443

/ PRIOR FILING DATE: 2002-11-26

/ PRIOR APPLICATION NUMBER: US/09/698,906A

/ PRIOR FILING DATE: 2001-02-20

/ NUMBER OF SEQ ID NOS: 121

/ SOFTWARE: FastSeq for Windows Version 3.0

/ SEQ ID NO 4

/ LENGTH: 11

/ TYPE: PRT

/ ORGANISM: Human peptide sequence

US-10-304-443-4

Query Match 25.4%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 2.1e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 3 EYPSGR 8
|:||||
Db 2 EWPGR 7

RESULT 88

US-10-362-527-63

/ Sequence 63, Application US/10362527

/ Publication No. US20040030106A1

/ GENERAL INFORMATION:

/ APPLICANT: Friede, Martin

/ APPLICANT: Mason, Sean

/ APPLICANT: Turnell, William Gordon

/ APPLICANT: Vinals Y de Basois, Carlota

/ TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide

/ TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies

/ FILE REFERENCE: B45236

/ CURRENT APPLICATION NUMBER: US/10/362,527

/ PRIOR FILING DATE: 2003-02-21

/ PRIOR APPLICATION NUMBER: PCT/EP01/09576

/ PRIOR FILING DATE: 2001-08-17

/ PRIOR APPLICATION NUMBER: GB 0020717.5

/ NUMBER OF SEQ ID NOS: 328

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 63

/ LENGTH: 11

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-362-527-63

Query Match 25.4%; Score 29; DB 4; Length 11;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8
 | : |||||
 Db 2 EWPGR 7

RESULT 89
 US-11-004-771-4
 / Sequence 4, Application US/11004771
 / Publication No. US20050152892A1
 / GENERAL INFORMATION:
 / APPLICANT: Friede, Martin
 / APPLICANT: Mason, Sean
 / APPLICANT: Turnell, William Gordon
 / APPLICANT: Van Mechelen, Marcelle Paulette
 / APPLICANT: Vinals y de Basols, Carlota
 / TITLE OF INVENTION: Biotopes or Mimotopes Derived from the
 / TITLE OF INVENTION: C-Epsilon-3 or C-Epsilon-4 Domains of IgE, Antagonists
 / FILE REFERENCE: B45173
 / CURRENT APPLICATION NUMBER: US/11/004,771
 / CURRENT FILING DATE: 2004-12-03
 / PRIOR APPLICATION NUMBER: US/10/322,210
 / PRIOR FILING DATE: 2002-12-18
 / PRIOR APPLICATION NUMBER: US/09/914,089
 / PRIOR FILING DATE: 2001-08-22
 / PRIOR APPLICATION NUMBER: GB 9904408.3
 / PRIOR FILING DATE: 1999-02-25
 / PRIOR APPLICATION NUMBER: GB 9917144.9
 / PRIOR FILING DATE: 1999-07-21
 / PRIOR APPLICATION NUMBER: GB 9918598.5
 / PRIOR FILING DATE: 1999-08-07
 / PRIOR APPLICATION NUMBER: GB 9918599.3
 / PRIOR FILING DATE: 1999-08-07
 / PRIOR APPLICATION NUMBER: GB 9918601.7
 / PRIOR FILING DATE: 1999-08-07
 / PRIOR APPLICATION NUMBER: GB 9918604.1
 / PRIOR FILING DATE: 1999-08-07
 / PRIOR APPLICATION NUMBER: GB 9918606.6
 / PRIOR FILING DATE: 1999-08-07
 / PRIOR APPLICATION NUMBER: GB 9925618.2
 / PRIOR FILING DATE: 1999-10-29
 / NUMBER OF SEQ ID NOS: 86
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 4
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Chimeric
 US-11-004-771-4

Query Match 25.4%; Score 29; DB 6; Length 11;
 Best Local Similarity 83.3%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8
 | : |||||
 Db 2 EWPGR 7

RESULT 90
 US-09-071-838-108
 / Sequence 108, Application US/09071838
 / Patent No. US20020152501A1
 / GENERAL INFORMATION:
 / APPLICANT: Fischer, Robert L.
 / APPLICANT: Ohad, Nir
 / APPLICANT: Kiyosue, Tomohiro

APPLICANT: Yadegari, Ramim
 APPLICANT: Margossian, Linda
 APPLICANT: Harada, John
 APPLICANT: Goldberg, Robert B.
 TITLE OF INVENTION: Nucleic Acids That Control Seed and
 TITLE OF INVENTION: Fruit Development in Plants
 NUMBER OF SEQUENCES: 324
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: California
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/071,838
 FILING DATE: 01-MAY-1998
 CLASSIFICATION: 800
 ATTORNEY/AGENT INFORMATION:
 NAME: Baetian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 023070-086100US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 108:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULAR TYPE: peptide
 US-09-071-838-108

Query Match 25.4%; Score 29; DB 3; Length 12;
 Best Local Similarity 44.4%; Pred. No. 2.3e+03;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYR 19
 | : |||||
 Db 1 NPKVTIFPK 9

RESULT 91
 US-10-213-512-108
 / Sequence 108, Application US/10213512
 / Publication No. US20030110536A1
 / GENERAL INFORMATION:
 / APPLICANT: Fischer, Robert L.
 / APPLICANT: Ohad, Nir
 / APPLICANT: Kiyosue, Tomohiro
 / APPLICANT: Yadegari, Ramim
 / APPLICANT: Margossian, Linda
 / APPLICANT: Harada, John
 / APPLICANT: Goldberg, Robert B.
 TITLE OF INVENTION: The Regents of the University of California
 TITLE OF INVENTION: Fruit Development in Plants
 FILE REFERENCE: 023070-086110US
 CURRENT APPLICATION NUMBER: US/10/213,512
 CURRENT FILING DATE: 2002-08-06
 PRIOR APPLICATION NUMBER: US/09/177,206
 PRIOR FILING DATE: 1998-10-22
 PRIOR APPLICATION NUMBER: US 09/071,838
 PRIOR FILING DATE: 1998-05-01
 NUMBER OF SEQ ID NOS: 324
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 108
 LENGTH: 12

TYPE: PRT
ORGANISM: Arabidopsis sp.
US-10-213-512-108

Query Match 25.4%; Score 29; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 2.3e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPLYKR 19
DB 1 NPKVTTFKK 9

RESULT 92
US-10-304-443-111
Sequence 111, Application US/10304443
Publication No. US20030170229A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Biologicals s.a.
APPLICANT: Peptide Therapeutics Ltd.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45173C1P
CURRENT APPLICATION NUMBER: US/10/304,443
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US/09/698,906A
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FaastSeq for Windows Version 3.0
SEQ ID NO 111
LENGTH: 12
TYPE: PRT
ORGANISM: Human peptide sequence
US-10-304-443-111

Query Match 25.4%; Score 29; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8
DB 3 EWPGR 8

RESULT 93
US-10-362-527-317
Sequence 317, Application US/10362527
Publication No. US20040030106A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnell, William Gordon
APPLICANT: Vinals y De Basols, Carlota
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptide
TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
FILE REFERENCE: B45236
CURRENT APPLICATION NUMBER: US/10/362,527
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/EP01/09576
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: GB 0020717.5
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 317
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Artificial variant of Homo sapiens IGE peptide
US-10-362-527-317

Query Match 25.4%; Score 29; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;

Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 EYPSGR 8
DB 3 EWPGR 8

RESULT 94
US-10-415-389-24
Sequence 24, Application US/10415389
Publication No. US20040115220A1
GENERAL INFORMATION:
APPLICANT: De Basols, Carlota Vinals y
APPLICANT: Vaccine
FILE REFERENCE: B45251
CURRENT APPLICATION NUMBER: US/10/415,389
CURRENT FILING DATE: 2003-04-25
PRIOR APPLICATION NUMBER: PCT/EP01/12932
PRIOR FILING DATE: 2001-10-24
PRIOR APPLICATION NUMBER: GB 0026334.3
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 34
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 24
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Human IGE peptide mimotope
US-10-415-389-24

Query Match 25.4%; Score 29; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 2.3e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYPSGR 8
DB 3 EWPGR 8

RESULT 95
US-10-322-210-20
Sequence 20, Application US/10322210
Publication No. US20030147906A1
GENERAL INFORMATION:
APPLICANT: Friede, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnell, William Gordon
APPLICANT: Van Mechelen, Marcelle Paulette
APPLICANT: Vinals y de Basols, Carlota
TITLE OF INVENTION: Epitopes or Mimotopes Derived from the
TITLE OF INVENTION: C-Epitolon-3 or C-Epitolon-4 Domains of IGE, Antagonists
TITLE OF INVENTION: Thereof, and Their Therapeutic Uses
FILE REFERENCE: B45173
CURRENT APPLICATION NUMBER: US/10/322,210
CURRENT FILING DATE: 2002-12-18
PRIOR APPLICATION NUMBER: US/09/914,089
PRIOR FILING DATE: 2001-08-22
PRIOR APPLICATION NUMBER: GB 9904408.3
PRIOR FILING DATE: 1999-02-25
PRIOR APPLICATION NUMBER: GB 9917144.9
PRIOR FILING DATE: 1999-07-21
PRIOR APPLICATION NUMBER: GB 9918598.5
PRIOR FILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: GB 9918599.3
PRIOR FILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: GB 9918601.7
PRIOR FILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: GB 9918604.1
PRIOR FILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: GB 9918606.6
PRIOR FILING DATE: 1999-08-07
PRIOR APPLICATION NUMBER: GB 9925618.2

PRIOR FILING DATE: 1999-10-29
NUMBER OF SEQ ID NOS: 86
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 20
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Chimeric
US-10-322-210-20

Query Match 25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGR 8
|:||||
Db 3 EWPGR 8

RESULT 96
US-10-304-443-20
Sequence 20; Application US/10304443
Publication No. US20030170229A1
GENERAL INFORMATION:
APPLICANT: SmithKline Beecham Biologicals s.a.
TITLE OF INVENTION: Vaccine
FILE REFERENCE: B45173CIP
CURRENT APPLICATION NUMBER: US/10/304,443
CURRENT FILING DATE: 2002-11-26
PRIOR APPLICATION NUMBER: US/09/698,906A
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 121
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 20
LENGTH: 13
TYPE: PRT
ORGANISM: Human peptide sequence
US-10-304-443-20

Query Match 25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGR 8
|:||||
Db 3 EWPGR 8

RESULT 97
US-10-082-014-272
Sequence 272; Application US/10082014
Publication No. US20030185858A1
GENERAL INFORMATION:
APPLICANT: Birkett, Ashley J.
TITLE OF INVENTION: IMMUNOGENIC HBC CHIMER PARTICLES STABILIZED WITH AN N-TERMINAL CY
FILE REFERENCE: ICC-130.0 4564/85124
CURRENT APPLICATION NUMBER: US/10/082,014
CURRENT FILING DATE: 2002-02-22
PRIOR APPLICATION NUMBER: 09/930,915
PRIOR FILING DATE: 2001-08-15
NUMBER OF SEQ ID NOS: 290
SOFTWARE: PatentIn version 3.1
SEQ ID NO 272
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-082-014-272

Query Match 25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGR 8
|:||||
Db 3 EWPGR 8

RESULT 98
US-10-372-076-126
Sequence 126; Application US/10372076
Publication No. US20030198645A1
GENERAL INFORMATION:
APPLICANT: Page, Mark
TITLE OF INVENTION: STABILIZED HBC CHIMER PARTICLES AS THERAPEUTIC VACCINE FOR
FILE REFERENCE: 4564/87179
CURRENT APPLICATION NUMBER: US/10/372,076
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: 10/080,299
PRIOR FILING DATE: 2002-02-21
PRIOR APPLICATION NUMBER: 10/082,014
PRIOR FILING DATE: 2002-02-22
NUMBER OF SEQ ID NOS: 308
SOFTWARE: PatentIn version 3.2
SEQ ID NO 126
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-372-076-126

Query Match 25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGR 8
|:||||
Db 3 EWPGR 8

RESULT 99
US-10-362-527-79
Sequence 79; Application US/10362527
Publication No. US20040030106A1
GENERAL INFORMATION:
APPLICANT: Friele, Martin
APPLICANT: Mason, Sean
APPLICANT: Turnell, William Gordon
APPLICANT: Vinals y De Baesols, Carlota
TITLE OF INVENTION: Vaccine Immunogens Comprising Disulphide Bridged Cyclised Peptid
TITLE OF INVENTION: and Use Thereof in the Treatment of Allergies
FILE REFERENCE: B45236
CURRENT APPLICATION NUMBER: US/10/362,527
CURRENT FILING DATE: 2003-02-21
PRIOR APPLICATION NUMBER: PCT/EP01/09576
PRIOR FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: GB 0020717.5
PRIOR FILING DATE: 2000-08-22
NUMBER OF SEQ ID NOS: 328
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 79
LENGTH: 13
TYPE: PRT
ORGANISM: Homo sapiens
US-10-362-527-79

Query Match 25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 EYFGR 8
|:||||
Db 3 EWPGR 8

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RESULT 100
US-10-732-862A-140
; Sequence 140, Application US/10732862A
; Publication No. US20040146524A1
; GENERAL INFORMATION:
; APPLICANT: ASHLEY, BIRKETT J.
; APPLICANT: Lyons, Katelyne J.
; APPLICANT: Jay, Haron J.
; TITLE OR INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
; FILE REFERENCE: ICC-136.0 (4564-88881)
; CURRENT APPLICATION NUMBER: US/10/732,862A
; PRIOR FILING DATE: 2003-12-10
; PRIOR APPLICATION NUMBER: US 60/432,123
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 10/274,616
; PRIOR FILING DATE: 2002-10-21
; PRIOR APPLICATION NUMBER: US 10/080,299
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: US 10/082,014
; PRIOR FILING DATE: 2002-02-22
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 140
; LENGTH: 13
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-732-862A-140

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Query Match      25.4%; Score 29; DB 4; Length 13;
Best Local Similarity 83.3%; Pred. No. 2.5e+03;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY      3 EYPSGR 8
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Db      3 EWPGR 8

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Search completed: January 20, 2006, 19:45:36
 Job time : 73.1154 secs

GenCore version 5.1.6
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OM protein - protein search, using bw model

Run on: January 20, 2006, 19:12:21 ; Search time 8.07692 Seconds
(without alignments)
25.093 Million cell updates/sec

Title: US-09-662-293-2
Perfect score: 114
Sequence: 1 DYEPGSRILGNPKAPLYKRP 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA, New:
1: /cgn2_6/ptodaca/1/pubppaa/US08_NEW_PUB pep: *
2: /cgn2_6/ptodaca/1/pubppaa/US06_NEW_PUB pep: *
3: /cgn2_6/ptodaca/1/pubppaa/US07_NEW_PUB pep: *
4: /cgn2_6/ptodaca/1/pubppaa/PTCT_NEW_PUB pep: *
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8: /cgn2_6/ptodaca/1/pubppaa/US60_NEW_PUB pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	28.9	18	6	US-10-956-755A-6
2	31	27.2	14	7	US-11-054-515-2501
3	30	26.3	14	7	US-11-054-515-2378
4	30	26.3	20	6	US-10-889-197-30
5	29	25.4	11	7	US-11-033-365-51
6	29	25.4	11	7	US-11-033-365-52
7	29	25.4	11	7	US-11-033-365-54
8	29	25.4	14	7	US-11-054-515-2387
9	28	24.6	9	7	US-11-010-748A-408
10	28	24.6	9	7	US-11-010-748A-409
11	28	24.6	9	7	US-11-010-748A-410
12	28	24.6	9	7	US-11-010-748A-415
13	28	24.6	9	7	US-11-010-748A-416
14	28	24.6	9	7	US-11-010-748A-417
15	28	24.6	11	7	US-11-033-365-45
16	28	24.6	14	7	US-11-054-515-2535
17	28	24.6	14	7	US-11-054-515-2589
18	28	24.6	14	7	US-11-054-515-2592
19	28	24.6	17	7	US-11-010-748A-405
20	28	24.6	17	7	US-11-010-748A-412
21	27	23.7	9	7	US-11-010-748A-617
22	27	23.7	9	7	US-11-010-748A-621
23	27	23.7	9	7	US-11-010-748A-635
24	27	23.7	12	7	US-11-058-735-35
25	27	23.7	13	6	US-10-511-559-465

26	27	23.7	13	7	US-11-041-893-182	Sequence 182, App
27	27	23.7	14	7	US-11-054-515-2148	Sequence 2148, App
28	27	23.7	14	7	US-11-054-515-2382	Sequence 2382, App
29	27	23.7	14	7	US-11-054-515-2466	Sequence 2466, App
30	27	23.7	14	7	US-11-054-515-2486	Sequence 2486, App
31	27	23.7	14	7	US-11-054-515-2534	Sequence 2534, App
32	27	23.7	14	7	US-11-054-515-2544	Sequence 2544, App
33	27	23.7	14	7	US-11-054-515-2697	Sequence 2697, App
34	27	23.7	19	6	US-10-503-575-271	Sequence 271, App
35	26	22.8	9	7	US-11-105-668-20	Sequence 20, App1
36	26	22.8	9	7	US-11-110-374-331	Sequence 331, App
37	26	22.8	11	7	US-11-033-365-48	Sequence 48, App1
38	26	22.8	11	7	US-11-033-365-213	Sequence 213, App
39	26	22.8	11	7	US-11-073-347-150	Sequence 150, App
40	26	22.8	12	7	US-11-073-347-151	Sequence 151, App
41	26	22.8	13	7	US-11-073-347-152	Sequence 152, App
42	26	22.8	14	7	US-11-054-515-2683	Sequence 2683, App
43	26	22.8	14	7	US-11-054-515-2689	Sequence 2689, App
44	26	22.8	14	7	US-11-054-515-2720	Sequence 2720, App
45	26	22.8	14	7	US-11-073-347-153	Sequence 153, App
46	26	22.8	15	7	US-11-073-347-154	Sequence 154, App
47	26	22.8	16	7	US-11-073-347-156	Sequence 156, App
48	26	22.8	16	7	US-11-152-697-55	Sequence 55, App1
49	26	22.8	17	7	US-11-073-347-158	Sequence 158, App
50	26	22.8	18	7	US-11-220-439-4	Sequence 4, App1
51	26	22.8	18	7	US-11-220-439-22	Sequence 22, App1
52	26	22.8	18	7	US-11-220-439-24	Sequence 24, App1
53	26	22.8	19	7	US-11-220-439-10	Sequence 10, App1
54	26	22.8	19	7	US-11-220-439-25	Sequence 25, App1
55	26	22.8	20	7	US-11-133-65A-6	Sequence 6, App1
56	26	22.8	20	7	US-11-220-439-2	Sequence 2, App1
57	26	22.8	20	7	US-11-220-439-6	Sequence 6, App1
58	26	22.8	20	7	US-11-220-439-11	Sequence 11, App1
59	26	22.8	20	7	US-11-220-439-12	Sequence 12, App1
60	26	22.8	20	7	US-11-220-439-13	Sequence 13, App1
61	26	22.8	20	7	US-11-220-439-16	Sequence 16, App1
62	26	22.8	20	7	US-11-220-439-23	Sequence 23, App1
63	26	22.8	20	7	US-11-220-439-26	Sequence 26, App1
64	25.5	22.4	15	7	US-11-022-562-64	Sequence 64, App1
65	25.5	22.4	15	7	US-11-045-024-13027	Sequence 13027, A
66	25.5	22.4	17	7	US-11-045-024-13086	Sequence 13086, A
67	25.5	22.4	20	7	US-11-022-562-304	Sequence 304, App
68	25.5	22.4	20	7	US-11-022-562-305	Sequence 305, App
69	25	21.9	10	6	US-10-859-643-418	Sequence 418, App
70	25	21.9	10	6	US-10-859-643-429	Sequence 429, App
71	25	21.9	10	7	US-11-097-864-418	Sequence 418, App
72	25	21.9	10	7	US-11-097-864-429	Sequence 429, App
73	25	21.9	10	7	US-11-097-912-418	Sequence 418, App
74	25	21.9	10	7	US-11-097-912-429	Sequence 429, App
75	25	21.9	10	7	US-11-156-843-119	Sequence 119, App
76	25	21.9	10	7	US-11-045-024-2015	Sequence 2015, App
77	25	21.9	11	7	US-11-033-365-49	Sequence 49, App1
78	25	21.9	11	7	US-11-156-843-28	Sequence 28, App1
79	25	21.9	11	7	US-11-156-843-35	Sequence 35, App1
80	25	21.9	11	7	US-11-045-024-2247	Sequence 2247, App
81	25	21.9	11	7	US-11-045-024-5360	Sequence 5360, App
82	25	21.9	11	7	US-11-045-024-7847	Sequence 7847, App
83	25	21.9	13	6	US-10-511-559-464	Sequence 464, App
84	25	21.9	13	7	US-11-054-515-2470	Sequence 2470, App
85	25	21.9	13	7	US-11-006-119-35	Sequence 35, App1
86	25	21.9	14	6	US-10-983-174-6	Sequence 6, App1
87	25	21.9	14	6	US-10-719-150-1	Sequence 1, App1
88	25	21.9	14	7	US-11-054-515-2529	Sequence 2529, App
89	25	21.9	14	7	US-11-054-515-2691	Sequence 2691, App
90	25	21.9	15	6	US-10-719-150-4	Sequence 4, App1
91	25	21.9	15	7	US-11-045-024-13167	Sequence 13167, A
92	25	21.9	15	7	US-11-045-024-13259	Sequence 13259, A
93	25	21.9	15	7	US-11-045-024-13283	Sequence 13283, A
94	25	21.9	17	6	US-10-201-525-23	Sequence 23, App1
95	25	21.9	17	7	US-11-006-119-38	Sequence 38, App1
96	25	21.9	19	7	US-11-128-059-11	Sequence 11, App1
97	25	21.9	20	6	US-10-623-155-493	Sequence 493, App
98	24.5	21.5	15	7	US-11-045-024-13091	Sequence 13091, A

99 24 21.1 9 7 US-11-105-708-25 Sequence 25, Appl
100 24 21.1 10 6 US-10-859-643-448 Sequence 448, App

ALIGNMENTS

RESULT 1
US-10-956-755A-6
; Sequence 6, Application US/10956755A
; Publication No. US20050282747A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Prestwich, Glenn
; TITLE OF INVENTION: Methods and Compositions for Wound Healing
; FILE REFERENCE: STONYB-09223
; CURRENT APPLICATION NUMBER: US/10/956,755A
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-755A-6

Query Match 28.9%; Score 33; DB 6; Length 18;
Best Local Similarity 42.1%; Pred. No. 20;
Matches 8; Conservative 2; Mismatches 5; Indels 4; Gaps 1;

QY 2 YEYPSRLGNPKAPLYKRP 20
DB 1 YEKPS-----PREVVPRP 15

RESULT 2
US-11-054-515-2501
; Sequence 2501, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2501
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens

US-11-054-515-2501

Query Match 27.2%; Score 31; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 32;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17
DB 8 PKAPLY 13

RESULT 3
US-11-054-515-2378
; Sequence 2378, Application US/11054515
; Publication No. US2005025532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2378
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2378

Query Match 26.3%; Score 30; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 45;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17
DB 8 PKAPLY 13

RESULT 4
US-10-889-197-30
; Sequence 30, Application US/10889197
; Publication No. US20050271689A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, CHUN-MING
; APPLICANT: ZHANG, JIANFENG
; APPLICANT: TANG, DE-CHU
; TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN
; TITLE OF INVENTION: DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE
; TITLE OF INVENTION: THERAPY AGAINST ANTHRAX
; FILE REFERENCE: 838610-2006.1
; CURRENT APPLICATION NUMBER: US/10/889,197
; CURRENT FILING DATE: 2004-07-12
; PRIOR APPLICATION NUMBER: 60/486,369

/ PRIOR FILING DATE: 2003-07-11
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 30
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Bacillus anthracis
US-10-889-197-30

Query Match 26.3%; Score 30; DB 6; Length 20;
Best Local Similarity 62.3%; Pred. No. 66;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YPGSRIGN 11
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DB 12 HPGSGVGN 19

RESULT 5
US-11-033-365-51
/ Sequence 51, Application US/11033365
/ Publication No. US20050250678A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies Inc.
/ APPLICANT: Defrees, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Wang, ZhiGuang
/ APPLICANT: Clausen, Henrik
/ TITLE OF INVENTION: O-Linked Glycosylation of peptides
/ FILE REFERENCE: 040853-01-5138
/ CURRENT APPLICATION NUMBER: US/11/033,365
/ PRIOR FILING DATE: 2005-01-10
/ PRIOR APPLICATION NUMBER: 60/535,284
/ PRIOR FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: 60/544,411
/ PRIOR FILING DATE: 2004-02-12
/ PRIOR APPLICATION NUMBER: 60/546,631
/ PRIOR FILING DATE: 2004-02-20
/ PRIOR APPLICATION NUMBER: 60/555,813
/ PRIOR FILING DATE: 2004-03-23
/ PRIOR APPLICATION NUMBER: 60/570,891
/ PRIOR FILING DATE: 2004-05-12
/ NUMBER OF SEQ ID NOS: 213
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 51
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-365-51

Query Match 25.4%; Score 29; DB 7; Length 11;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16
|||
DB 1 LGTFWAPL 8

RESULT 6
US-11-033-365-52
/ Sequence 52, Application US/11033365
/ Publication No. US20050250678A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies Inc.
/ APPLICANT: Defrees, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Wang, ZhiGuang
/ APPLICANT: Clausen, Henrik
/ TITLE OF INVENTION: O-Linked Glycosylation of peptides
/ FILE REFERENCE: 040853-01-5138
/ CURRENT APPLICATION NUMBER: US/11/033,365
/ CURRENT FILING DATE: 2005-01-10

/ PRIOR APPLICATION NUMBER: 60/535,284
/ PRIOR FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: 60/544,411
/ PRIOR FILING DATE: 2004-02-12
/ PRIOR APPLICATION NUMBER: 60/546,631
/ PRIOR FILING DATE: 2004-02-20
/ PRIOR APPLICATION NUMBER: 60/555,813
/ PRIOR FILING DATE: 2004-03-23
/ PRIOR APPLICATION NUMBER: 60/570,891
/ PRIOR FILING DATE: 2004-05-12
/ NUMBER OF SEQ ID NOS: 213
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 52
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-365-52

Query Match 25.4%; Score 29; DB 7; Length 11;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16
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DB 1 LGTFWAPL 8

RESULT 7
US-11-033-365-54
/ Sequence 54, Application US/11033365
/ Publication No. US20050250678A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies Inc.
/ APPLICANT: Defrees, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Wang, ZhiGuang
/ APPLICANT: Clausen, Henrik
/ TITLE OF INVENTION: O-Linked Glycosylation of peptides
/ FILE REFERENCE: 040853-01-5138
/ CURRENT APPLICATION NUMBER: US/11/033,365
/ PRIOR FILING DATE: 2005-01-10
/ PRIOR APPLICATION NUMBER: 60/535,284
/ PRIOR FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: 60/544,411
/ PRIOR FILING DATE: 2004-02-12
/ PRIOR APPLICATION NUMBER: 60/546,631
/ PRIOR FILING DATE: 2004-02-20
/ PRIOR APPLICATION NUMBER: 60/555,813
/ PRIOR FILING DATE: 2004-03-23
/ PRIOR APPLICATION NUMBER: 60/570,891
/ PRIOR FILING DATE: 2004-05-12
/ NUMBER OF SEQ ID NOS: 213
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 54
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-365-54

Query Match 25.4%; Score 29; DB 7; Length 11;
Best Local Similarity 75.0%; Pred. No. 50;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 9 LGNPKAPL 16
|||
DB 2 LGAPWAPL 9

RESULT 8
US-11-054-515-2387
/ Sequence 2387, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:

APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PR523P3
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2387
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-11-054-515-2387

Query Match 25.4%; Score 29; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 65;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PRAPLY 17
Db 8 PSHPLY 13

RESULT 9
US-11-010-748A-408
Sequence 408, Application US/11010748A
Publication No. US2005024421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 408
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HLA-binding peptide of Seq. No. 405
US-11-010-748A-408

Query Match 24.6%; Score 28; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEYPG 6
Db 1 YKYPG 5

RESULT 10
US-11-010-748A-409
Sequence 409, Application US/11010748A
Publication No. US2005024421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 409
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HLA-binding peptide of Seq. No. 405
US-11-010-748A-409

Query Match 24.6%; Score 28; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEYPG 6
Db 3 YKYPG 7

RESULT 11
US-11-010-748A-410
Sequence 410, Application US/11010748A
Publication No. US2005024421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 410
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HLA-binding peptide of Seq. No. 405
US-11-010-748A-410

Query Match 24.6%; Score 28; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEYPG 6

Db 1 YKYPG 5

RESULT 12
US-11-010-748A-415
Sequence 415, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 415
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HLA-binding peptide of Seq. No. 412
US-11-010-748A-415

Query Match 24.6%; Score 28; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6
|:|:|
Db 1 YKYPG 5

RESULT 13
US-11-010-748A-416
Sequence 416, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 416
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HLA-binding peptide of Seq. No. 412
US-11-010-748A-416

Query Match 24.6%; Score 28; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6
|:|:|

Db 3 YKYPG 7

RESULT 14
US-11-010-748A-417
Sequence 417, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
CURRENT FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 417
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HLA-binding peptide of Seq. No. 412
US-11-010-748A-417

Query Match 24.6%; Score 28; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6
|:|:|
Db 1 YKYPG 5

RESULT 15
US-11-033-365-45
Sequence 45, Application US/11033365
Publication No. US20050250678A1
GENERAL INFORMATION:
APPLICANT: Neose Technologies Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Wang, ZhiGuang
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: O-linked glycosylation of peptides
FILE REFERENCE: 040853-01-5138
CURRENT APPLICATION NUMBER: US/11/033,365
CURRENT FILING DATE: 2005-01-10
PRIOR APPLICATION NUMBER: 60/535,284
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: 60/544,411
PRIOR FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 60/546,631
PRIOR FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/555,813
PRIOR FILING DATE: 2004-03-23
PRIOR APPLICATION NUMBER: 60/570,891
PRIOR FILING DATE: 2004-05-12
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PatentIn version 3.2
SEQ ID NO 45
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
OTHER INFORMATION: Homo sapiens
US-11-033-365-45

Query Match 24.6%; Score 28; DB 7; Length 11;
Best Local Similarity 75.0%; Pred. No. 71;

```
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy 9 LGNPKAPL 16
Db 1 LGIPTAPL 8

RESULT 16
US-11-054-515-2535
; Sequence 2535, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2535
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2535

Query Match 24.6%; Score 28; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PKAPLY 17
Db 8 PTPAPLY 13

RESULT 17
US-11-054-515-2589
; Sequence 2589, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2592
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2592
```

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; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2589
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2589

Query Match 24.6%; Score 28; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 92;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PKAPLY 17
Db 8 PTPAPLY 13

RESULT 18
US-11-054-515-2592
; Sequence 2592, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2592
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2592
```

RESULT 19

US-11-010-748A-405
; Sequence 405, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 405
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD42b peptide fragment
US-11-010-748A-405

Query Match 24.6%; Score 28; DB 7; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6
|:|:|
Db 3 YKYPG 7

RESULT 20

US-11-010-748A-412
; Sequence 412, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 412
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: CD42b peptide fragment
US-11-010-748A-412

Query Match 24.6%; Score 28; DB 7; Length 17;
Best Local Similarity 80.0%; Pred. No. 1.1e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 YKYPG 6
|:|:|
Db 3 YKYPG 7

RESULT 21

US-11-010-748A-617
; Sequence 617, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 617
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-617

Query Match 23.7%; Score 27; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.5e+04;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
|||:|
Db 1 PGFPLGSP 8

RESULT 22

US-11-010-748A-621
; Sequence 621, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMATTER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 621
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-621

Query Match 23.7%; Score 27; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.5e+04;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
|||:|
Db 2 PGFPLGSP 9

RESULT 23
US-11-010-748A-635
; Sequence 635, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHAM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 635
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-635

Query Match 23.7%; Score 27; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.5e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PGSRLGNP 12
Db 1 PGEPGLGSP 8

RESULT 24
US-11-058-735-35
; Sequence 35, Application US/11058735
; Publication No. US20050261475A1
; GENERAL INFORMATION:
; APPLICANT: TSENG, HUANG-CHUN
; APPLICANT: TSAI, LI-HUEI
; TITLE OF INVENTION: SOLID-PHASE CAPTURE-RELEASE-TAG METHODS FOR
; TITLE OF INVENTION: PHOSPHOPROTEOMIC ANALYSES
; FILE REFERENCE: HMV-094.01
; CURRENT APPLICATION NUMBER: US/11/058,735
; CURRENT FILING DATE: 2005-02-14
; PRIOR APPLICATION NUMBER: 60/544,748
; PRIOR FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 80
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 35
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-058-735-35

Query Match 23.7%; Score 27; DB 7; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 10 GNPKAPLYKR 19
Db 3 GTPGTPTSPYR 12

RESULT 25
US-10-511-559-465
; Sequence 465, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim

; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 465
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-465

Query Match 23.7%; Score 27; DB 6; Length 13;
Best Local Similarity 45.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 7 SRLGNPKAPLY 17
Db 1 SSLGPPSMFVH 11

RESULT 26
US-11-041-893-182
; Sequence 182, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahalirae, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 182
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Babesia bovis
US-11-041-893-182

Query Match 23.7%; Score 27; DB 7; Length 13;
Best Local Similarity 71.4%; Pred. No. 1.2e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 KAPLYKR 19
Db 1 EAPWYKR 7

RESULT 27
US-11-054-515-2148
; Sequence 2148, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10

```
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2148
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2148
```

```
Query Match      23.7% Score 27; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      12 PKAPL 17
Db      8 PKAPL 13
```

```
RESULT 28
US-11-054-515-2382
/ Sequence 2382, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2382
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```

```
US-11-054-515-2382
```

```
Query Match      23.7% Score 27; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 PKAPL 16
Db      8 PKAPL 12
```

```
RESULT 29
US-11-054-515-2466
/ Sequence 2466, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2466
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2466
```

```
Query Match      23.7% Score 27; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      12 PKAPL 17
Db      8 POSPLY 13
```

```
RESULT 30
US-11-054-515-2486
/ Sequence 2486, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
```

```
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2486
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2486

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy      12 PKAPL 17
Db      8 PKAPL 13

RESULT 31
US-11-054-515-2534
/ Sequence 2534, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2534
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2534

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 PKAPL 16
Db      8 PKAPL 12

RESULT 32
US-11-054-515-2544
/ Sequence 2544, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2544
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2544

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      12 PKAPL 16
Db      8 PKAPL 12

RESULT 33
US-11-054-515-2697
/ Sequence 2697, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
```

```
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2697
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2697

Query Match      23.7%; Score 27; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      12 PRAPLY 17
      |||||
Db      8 PYAPLY 13

RESULT 34
US-10-503-575-271
/ Sequence 271, Application US/10503575
/ Publication No. US20050244823A1
/ GENERAL INFORMATION:
/ APPLICANT: Drijfhout, Jan Wouter
/ APPLICANT: van Veele, Petrus Antonius
/ TITLE OF INVENTION: NOVEL EPITOPES FOR CELLAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
/ TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
/ FILE REFERENCE: 2799/72843-PC-US
/ CURRENT APPLICATION NUMBER: US/10/503,575
/ CURRENT FILING DATE: 2004-08-04
/ PRIOR APPLICATION NUMBER: PCT/NL03/00077
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: EP 02075456.0
/ PRIOR FILING DATE: 2002-02-04
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO 271
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-503-575-271

Query Match      23.7%; Score 27; DB 6; Length 19;
Best Local Similarity 55.6%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      7 SRLGNPKAP 15
      |||||
Db      4 SLDGSGPGP 12

RESULT 35
US-11-105-268-20
/ Sequence 20, Application US/11105268
/ Publication No. US20050260204A1
/ GENERAL INFORMATION:
/ APPLICANT: Allan, Christian
/ TITLE OF INVENTION: ANTI-IL-9 ANTIBODY FORMULATIONS AND USES THEREOF
/ FILE REFERENCE: 10271-126-999
/ CURRENT APPLICATION NUMBER: US/11/105,268
/ PRIOR FILING DATE: 2005-04-12
/ PRIOR APPLICATION NUMBER: 60/561,845
/ PRIOR FILING DATE: 2004-04-12
```

```
/ NUMBER OF SEQ ID NOS: 60
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 20
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-105-268-20

Query Match      22.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      2 YEYP 5
      |||||
Db      4 YEYP 7

RESULT 36
US-11-110-274-331
/ Sequence 331, Application US/11110274
/ Publication No. US2005026502A1
/ GENERAL INFORMATION:
/ APPLICANT: Merchiers, Pascal G.
/ APPLICANT: Hoffmann, Marcel
/ APPLICANT: Spittaels, Koenraad P. F.
/ TITLE OF INVENTION: Methods, Compositions and Compound Assays for Inhibiting
/ TITLE OF INVENTION: Amyloid-Beta Protein Production
/ FILE REFERENCE: P27,697-A USA
/ CURRENT APPLICATION NUMBER: US/11/110,274
/ CURRENT FILING DATE: 2005-04-20
/ PRIOR APPLICATION NUMBER: US 60/563,661
/ PRIOR FILING DATE: 2004-04-20
/ NUMBER OF SEQ ID NOS: 620
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO 331
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-110-274-331

Query Match      22.8%; Score 26; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DYEP 5
      |||||
Db      4 DYEP 8

RESULT 37
US-11-033-365-48
/ Sequence 48, Application US/11033365
/ Publication No. US20050250678A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies Inc.
/ APPLICANT: DeFeese, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Wang, ZhiGuang
/ APPLICANT: Clausen, Henrik
/ TITLE OF INVENTION: O-linked Glycosylation of peptides
/ FILE REFERENCE: 040853-01-5138
/ CURRENT APPLICATION NUMBER: US/11/033,365
/ CURRENT FILING DATE: 2005-01-10
/ PRIOR APPLICATION NUMBER: 60/535,284
/ PRIOR FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: 60/544,411
/ PRIOR FILING DATE: 2004-02-12
/ PRIOR APPLICATION NUMBER: 60/546,631
/ PRIOR FILING DATE: 2004-02-20
/ PRIOR APPLICATION NUMBER: 60/555,813
/ PRIOR FILING DATE: 2004-03-23
/ PRIOR APPLICATION NUMBER: 60/570,891
/ PRIOR FILING DATE: 2004-05-12
```

/ NUMBER OF SEQ ID NOS: 213
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 48
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-365-48

Query Match 22.8%; Score 26; DB 7; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LGNPKAPL 16
|||
1 LGIPQPL 8

RESULT 38
US-11-033-365-213
/ Sequence 213, Application US/11033365
/ Publication No. US20050250678A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies Inc.
/ APPLICANT: Defrees, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Wang, ZhiGuang
/ APPLICANT: Clausen, Henrik
/ TITLE OF INVENTION: O-linked Glycosylation of peptides
/ FILE REFERENCE: 040853-01-5138
/ CURRENT APPLICATION NUMBER: US/11/033,365
/ PRIOR FILING DATE: 2005-01-10
/ PRIOR APPLICATION NUMBER: 60/535,284
/ PRIOR FILING DATE: 2004-01-08
/ PRIOR APPLICATION NUMBER: 60/544,411
/ PRIOR FILING DATE: 2004-02-12
/ PRIOR APPLICATION NUMBER: 60/546,631
/ PRIOR FILING DATE: 2004-02-20
/ PRIOR APPLICATION NUMBER: 60/555,813
/ PRIOR FILING DATE: 2004-03-23
/ PRIOR APPLICATION NUMBER: 60/570,891
/ PRIOR FILING DATE: 2004-05-12
/ NUMBER OF SEQ ID NOS: 213
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 213
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-365-213

Query Match 22.8%; Score 26; DB 7; Length 11;
Best Local Similarity 75.0%; Pred. No. 1.5e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LGNPKAPL 16
|||
1 LGIPWAPL 8

RESULT 39
US-11-073-347-150
/ Sequence 150, Application US/11073347
/ Publication No. US20050260234A1
/ GENERAL INFORMATION:
/ APPLICANT: SIMARD, John J. L.
/ APPLICANT: DIAMOND, David C.
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
/ FILE REFERENCE: MANNK.015C1
/ CURRENT APPLICATION NUMBER: US/11/073,347
/ PRIOR FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 10/094,699
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: 60/274,063

/ PRIOR FILING DATE: 2001-03-07
/ NUMBER OF SEQ ID NOS: 159
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 150
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-11-073-347-150

Query Match 22.8%; Score 26; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17
|||
3 LGLPDRPFY 11

RESULT 40
US-11-073-347-151
/ Sequence 151, Application US/11073347
/ Publication No. US20050260234A1
/ GENERAL INFORMATION:
/ APPLICANT: SIMARD, John J. L.
/ APPLICANT: DIAMOND, David C.
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
/ FILE REFERENCE: MANNK.015C1
/ CURRENT APPLICATION NUMBER: US/11/073,347
/ PRIOR FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 10/094,699
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: 60/274,063
/ PRIOR FILING DATE: 2001-03-07
/ NUMBER OF SEQ ID NOS: 159
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 151
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapien
US-11-073-347-151

Query Match 22.8%; Score 26; DB 7; Length 12;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17
|||
4 LGLPDRPFY 12

RESULT 41
US-11-073-347-152
/ Sequence 152, Application US/11073347
/ Publication No. US20050260234A1
/ GENERAL INFORMATION:
/ APPLICANT: SIMARD, John J. L.
/ APPLICANT: DIAMOND, David C.
/ TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
/ FILE REFERENCE: MANNK.015C1
/ CURRENT APPLICATION NUMBER: US/11/073,347
/ PRIOR FILING DATE: 2005-03-04
/ PRIOR APPLICATION NUMBER: 10/094,699
/ PRIOR FILING DATE: 2002-03-07
/ PRIOR APPLICATION NUMBER: 60/274,063
/ PRIOR FILING DATE: 2001-03-07
/ NUMBER OF SEQ ID NOS: 159
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 152
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapien

US-11-073-347-152

Query Match 22.8%; Score 26; DB 7; Length 13;

Best Local Similarity 55.6%; Pred. No. 1.7e+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 9 LGNPKAPLY 17
| | | | |
Db 5 LGLPDRPFY 13

RESULT 42

US-11-054-515-2683

; Sequence 2683, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2683

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2683

Query Match 22.8%; Score 26; DB 7; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17
| | | | |
Db 8 PQAPLF 13

RESULT 43

US-11-054-515-2689

; Sequence 2689, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2689

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2689

Query Match 22.8%; Score 26; DB 7; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLY 17
| | | | |
Db 8 PQAPLF 13

RESULT 44

US-11-054-515-2720

; Sequence 2720, Application US/11054515

; Publication No. US20050255532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; PRIOR FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2720

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

US-11-054-515-2720

Query Match 22.8%; Score 26; DB 7; Length 14;

Best Local Similarity 66.7%; Pred. No. 1.9e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 PKAPLY 17
| : |||
Db 8 PSSPLY 13

RESULT 45

US-11-073-347-153
; Sequence 153, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; APPLICANT: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: MANNK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 153
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-153

Query Match 22.8%; Score 26; DB 7; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17
| | | | |
Db 6 LGLPDRPFY 14

RESULT 46

US-11-073-347-154
; Sequence 154, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; APPLICANT: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: MANNK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 154
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-154

Query Match 22.8%; Score 26; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17
| | | | |
Db 7 LGLPDRPFY 15

RESULT 47

US-11-073-347-156
; Sequence 156, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; APPLICANT: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: MANNK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 156
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-156

Query Match 22.8%; Score 26; DB 7; Length 16;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17
| | | | |
Db 8 LGLPDRPFY 16

RESULT 48

US-11-152-697-55
; Sequence 55, Application US/11152697
; Publication No. US2006000367A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL HUMAN KUPFFER CELL RECEPTOR
; TITLE OF INVENTION: PROTEIN, BGS-18
; FILE REFERENCE: D0242 NP
; CURRENT APPLICATION NUMBER: US/11/152,697
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER: 60/580,006
; PRIOR FILING DATE: 2004-06-15
; NUMBER OF SEQ ID NOS: 63
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 55
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-152-697-55

Query Match 22.8%; Score 26; DB 7; Length 16;
Best Local Similarity 45.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 GSRLGNPKAPL 16
| | | | |
Db 2 GDHLGNTNADI 12

RESULT 49

US-11-073-347-158
; Sequence 158, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; APPLICANT: DIAMOND, David C.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; TITLE OF INVENTION: CANCER
; FILE REFERENCE: MANNK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347

```

; CURRENT FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 158
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-158

```

```

Query Match      22.8%; Score 26; DB 7; Length 17;
Best Local Similarity 55.6%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

QY      9 LGNPKAPLY 17
      |||||
Db      9 LGLEDRPFY 17

```

```

RESULT 50
US-11-220-439-4
; Sequence 4, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Oltvos Jr., Labazlo
; TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
; FILE REFERENCE: MST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; PRIOR FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/980,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Asp in position 1 is modified by a
; NAME/KEY: MOD_RES
; LOCATION: (18)
; OTHER INFORMATION: 1-aminocyclo-hexane carboxylic acid
; OTHER INFORMATION: Arg in position 18 is modified by an amino linker
; FEATURE:
; OTHER INFORMATION: molety
; OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-4

```

```

Query Match      22.8%; Score 26; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      12 PKAPLYR 19
      |||||
Db      11 PPRPIYR 18

```

```

RESULT 51
US-11-220-439-22
; Sequence 22, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Oltvos Jr., Labazlo

```

```

; TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
; FILE REFERENCE: MST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; CURRENT FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/980,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Asp in position 1 is modified by a
; NAME/KEY: MOD_RES
; LOCATION: (18)
; OTHER INFORMATION: Arg in position 18 is modified by a
; OTHER INFORMATION: beta-acetyl-2,3-diaminopropionic acid group
; FEATURE:
; OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-22

```

```

Query Match      22.8%; Score 26; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      12 PKAPLYR 19
      |||||
Db      11 PPRPIYR 18

```

```

RESULT 52
US-11-220-439-24
; Sequence 24, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Oltvos Jr., Labazlo
; TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
; FILE REFERENCE: MST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; PRIOR FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: US/09/980,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Asp in position 1 is modified by a
; NAME/KEY: MOD_RES
; LOCATION: (18)
; OTHER INFORMATION: Arg in position 18 is modified by a
; OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group
; FEATURE:
; OTHER INFORMATION: modification of Pyrrhocoriclin

```

US-11-220-439-24

Query Match 22.8%; Score 26; DB 7; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19
DB 11 PPRPIYNR 18

RESULT 53

US-11-220-439-10
; Sequence 10, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Octavo Jr., Laszlo
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
; FILE REFERENCE: MST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; PRIOR FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: 60/140,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 10
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)-
; OTHER INFORMATION: Asp in position 1 is modified by a
; OTHER INFORMATION: 1-aminocyclo-hexane carboxylic acid
; FEATURE:
; OTHER INFORMATION: modification of Pyrrhocoricin
US-11-220-439-10

Query Match 22.8%; Score 26; DB 7; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19
DB 11 PPRPIYNR 18

RESULT 54

US-11-220-439-25
; Sequence 25, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Octavo Jr., Laszlo
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
; FILE REFERENCE: MST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; PRIOR FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: 60/140,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 25
; LENGTH: 19

; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (19)
; OTHER INFORMATION: Arg in position 19 is modified by a
; OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group
; FEATURE:
; OTHER INFORMATION: modification of Pyrrhocoricin
US-11-220-439-25

Query Match 22.8%; Score 26; DB 7; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19
DB 12 PPRPIYNR 19

RESULT 55

US-11-133-465A-6
; Sequence 6, Application US/1133465A
; Publication No. US20050277593A1
; GENERAL INFORMATION:
; APPLICANT: Cross, Anne
; TITLE OF INVENTION: Dieckgraefe, Brian
; FILE REFERENCE: 004255,00029
; CURRENT APPLICATION NUMBER: US/11/133,465A
; PRIOR FILING DATE: 2005-05-20
; PRIOR APPLICATION NUMBER: 60/573,340
; PRIOR FILING DATE: 2004-05-24
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-133-465A-6

Query Match 22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 45.5%; Pred. No. 2.8e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13
DB 6 ELPSARIRCPK 16

RESULT 56

US-11-220-439-2
; Sequence 2, Application US/11220439
; Publication No. US20060003938A1
; GENERAL INFORMATION:
; APPLICANT: Octavo Jr., Laszlo
; TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
; FILE REFERENCE: MST91BUSA
; CURRENT APPLICATION NUMBER: US/11/220,439
; PRIOR FILING DATE: 2005-09-07
; PRIOR APPLICATION NUMBER: 60/140,804
; PRIOR FILING DATE: 2001-12-03
; PRIOR APPLICATION NUMBER: 60/140,606
; PRIOR FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 60/154,135
; PRIOR FILING DATE: 1999-09-15
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Pyrrhocoricin

```
/
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)
/ OTHER INFORMATION: Thr in position 11 is modified with Gal-GalNAc
US-11-220-439-2

Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      12 PPRPIYR 19

Db

RESULT 57
US-11-220-439-6
/ Sequence 6, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 6
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-6

Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      12 PPRPIYR 19

Db

RESULT 58
US-11-220-439-11
/ Sequence 11, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 11
/ LENGTH: 20
/ TYPE: PRT
```

```
/
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: MOD_RES
/ LOCATION: (11)
/ OTHER INFORMATION: Thr in position 11 is modified with Gal-GalNAc
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-11

Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      12 PPRPIYR 19

Db

RESULT 59
US-11-220-439-12
/ Sequence 12, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: Patentln Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: MOD_RES
/ LOCATION: (20)
/ OTHER INFORMATION: Arg in position 20 is modified by an imide group
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoriclin
US-11-220-439-12

Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYR 19
      | | | |
      13 PPRPIYR 20

Db

RESULT 60
US-11-220-439-13
/ Sequence 13, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoriclin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
```

```
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: MOD_RES
/ LOCATION: (20)
/ OTHER INFORMATION: Arg in position 20 is modified by a
/ OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoricin
US-11-220-439-13
```

```
Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKR 19
      | | | |
Db      13 PPPPIYNR 20
```

```
RESULT 61
US-11-220-439-16
/ Sequence 16, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 16
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: Val in position 1 is in the D configuration
/ NAME/KEY: MOD_RES
/ LOCATION: (20)
/ OTHER INFORMATION: Asn in position 20 is in the D configuration
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoricin
US-11-220-439-16
```

```
Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKR 19
      | | | |
Db      12 PPPPIYNR 19
```

```
RESULT 62
US-11-220-439-23
/ Sequence 23, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 23
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)
/ OTHER INFORMATION: ACETYLATION
/ NAME/KEY: MOD_RES
/ LOCATION: (20)
/ OTHER INFORMATION: Arg in position 20 is modified by a
/ OTHER INFORMATION: beta-acetyl-2,3-diamino propionic acid group
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoricin
US-11-220-439-23
```

```
Query Match      22.8%; Score 26; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKR 19
      | | | |
Db      13 PPPPIYNR 20
```

```
RESULT 63
US-11-220-439-26
/ Sequence 26, Application US/11220439
/ Publication No. US20060003938A1
/ GENERAL INFORMATION:
/ APPLICANT: Oltos Jr., Laszlo
/ TITLE OF INVENTION: Novel Pyrrhocoricin-Derived Peptides, and Methods of
/ FILE REFERENCE: MST91BUSA
/ CURRENT APPLICATION NUMBER: US/11/220,439
/ CURRENT FILING DATE: 2005-09-07
/ PRIOR APPLICATION NUMBER: US/09/980,804
/ PRIOR FILING DATE: 2001-12-03
/ PRIOR APPLICATION NUMBER: 60/140,606
/ PRIOR FILING DATE: 1999-06-23
/ PRIOR APPLICATION NUMBER: 60/154,135
/ PRIOR FILING DATE: 1999-09-15
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

```
/ NAME/KEY: PEPTIDE
/ LOCATION: (1) ..(20)
/ OTHER INFORMATION: D configuration
/ FEATURE:
/ OTHER INFORMATION: modification of Pyrrhocoricin
US-11-220-439-26

Query Match          22.4%; Score 25.5; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      12 PKAPLYKR 19
Db      12 PPRPIYKR 19

RESULT 64
US-11-022-562-64
/ Sequence 64, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jlang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
/ FILE REFERENCE: DPN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency Virus
US-11-022-562-64

Query Match          22.4%; Score 25.5; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY      11 NPKAP---LYKR 19
Db      1 NPKPIVGEIYKR 12

RESULT 65
US-11-045-024-13027
/ Sequence 13027, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
```

```
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13027
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13027

Query Match          22.4%; Score 25.5; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY      11 NPKAP---LYKR 19
Db      1 NPKPIVGEIYKR 12

RESULT 66
US-11-045-024-13086
/ Sequence 13086, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: BpImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13086
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13086
```

Query Match 22.4%; Score 25.5; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 11 NPKAP---LYKR 19
DB 1 NPIPIVGDIYKR 12

RESULT 67
US-11-022-562-304
; Sequence 304, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shiesong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 304
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-304

Query Match 22.4%; Score 25.5; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 11 NPKAP---LYKR 19
DB 3 NPIPIVGDIYKR 14

RESULT 68
US-11-022-562-305
; Sequence 305, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shiesong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 305
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-305

Query Match 22.4%; Score 25.5; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 11 NPKAP---LYKR 19
DB 3 NPIPIVGDIYKR 14

RESULT 69
US-10-859-643-418
; Sequence 418, Application US/10859643
; Publication No. US2006000293A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 418
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-418

Query Match 21.9%; Score 25; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYPG 6
DB 3 DYNIDG 8

RESULT 70
US-10-859-643-429
; Sequence 429, Application US/10859643
; Publication No. US2006000293A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FaastSeq for Windows Version 4.0
; SEQ ID NO 429
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-429

Query Match 21.9%; Score 25; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYPG 6
DB 1 DYNIDG 6

RESULT 71

US-11-097-864-418
Sequence 418, Application US/11097864
Publication No. US200502659241
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fairis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 418
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-418

Query Match

21.9%; Score 25; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6
Db 3 DYNVDG 8

RESULT 72

US-11-097-864-429
Sequence 429, Application US/11097864
Publication No. US200502659241
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fairis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 429
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-429

Query Match

21.9%; Score 25; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6
Db 1 DYNVDG 6

RESULT 73

US-11-097-912-418
Sequence 418, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fairis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
FILE REFERENCE: 511582006204
CURRENT APPLICATION NUMBER: US/11/097,912
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 418
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-912-418

Query Match

21.9%; Score 25; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6
Db 3 DYNVDG 8

RESULT 74

US-11-097-912-429
Sequence 429, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fairis, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
FILE REFERENCE: 511582006204
CURRENT APPLICATION NUMBER: US/11/097,912
CURRENT FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 429
LENGTH: 10
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-912-429

Query Match

21.9%; Score 25; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DYEYPG 6
Db 1 DYNVDG 6

Db 1 DYNVDG 6

RESULT 75

US-11-156-843-119
 ; Sequence 119, Application US/11156843
 ; Publication No. US20050267035A1
 ; GENERAL INFORMATION:
 ; APPLICANT: West, Robert R.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Fox, Brian
 ; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
 ; FILE REFERENCE: 00-33
 ; CURRENT APPLICATION NUMBER: US/11/156,843
 ; PRIOR FILING DATE: 2005-06-20
 ; PRIOR APPLICATION NUMBER: US/09/883,727
 ; NUMBER OF SEQ ID NOS: 140
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 119
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: C1s exosite binding moiety
 US-11-156-843-119

Query Match 21.9%; Score 25; DB 7; Length 10;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DYEY 4
 ||||
 Db 6 DYEY 9

RESULT 76

US-11-045-024-2015
 ; Sequence 2015, Application US/11045024
 ; Publication No. US20050271676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Baker, Denise Marie
 ; APPLICANT: Cells, Stefan
 ; APPLICANT: Kubo, Ralph
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Eplimmune Inc.
 ; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 ; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 ; FILE REFERENCE: 2060.0040007
 ; CURRENT APPLICATION NUMBER: US/11/045,024
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: US 09/412,863
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/159,339
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/347,610
 ; PRIOR FILING DATE: 1994-12-01

; NUMBER OF SEQ ID NOS: 14528
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 2015
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-2015

Query Match 21.9%; Score 25; DB 7; Length 10;
 Best Local Similarity 44.4%; Pred. No. 2.1e+02;
 Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 12 PKAPYKRP 20
 ||:|:|
 Db 1 PQTLMQRP 9

RESULT 77

US-11-033-365-49
 ; Sequence 49, Application US/11033365
 ; Publication No. US20050250678A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Neose Technologies Inc.
 ; APPLICANT: Defrees, Shawn
 ; APPLICANT: Zopf, David
 ; APPLICANT: Wang, ZhiGuang
 ; APPLICANT: Clausen, Henrik
 ; TITLE OF INVENTION: O-linked Glycosylation of peptides
 ; FILE REFERENCE: 040853-01-5138
 ; CURRENT APPLICATION NUMBER: US/11/033,365
 ; CURRENT FILING DATE: 2005-01-10
 ; PRIOR APPLICATION NUMBER: 60/535,284
 ; PRIOR FILING DATE: 2004-01-08
 ; PRIOR APPLICATION NUMBER: 60/544,411
 ; PRIOR FILING DATE: 2004-02-12
 ; PRIOR APPLICATION NUMBER: 60/546,631
 ; PRIOR FILING DATE: 2004-02-20
 ; PRIOR APPLICATION NUMBER: 60/555,813
 ; PRIOR FILING DATE: 2004-03-23
 ; PRIOR APPLICATION NUMBER: 60/570,891
 ; PRIOR FILING DATE: 2004-05-12
 ; NUMBER OF SEQ ID NOS: 213
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 49
 ; LENGTH: 11
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-033-365-49

Query Match 21.9%; Score 25; DB 7; Length 11;
 Best Local Similarity 62.5%; Pred. No. 2.1e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 9 LGNPKAPL 16
 |||:|
 Db 1 LGIPKSP 8

RESULT 78
 US-11-156-843-28
 ; Sequence 28, Application US/11156843
 ; Publication No. US20050267035A1
 ; GENERAL INFORMATION:
 ; APPLICANT: West, Robert R.
 ; APPLICANT: Sheppard, Paul O.
 ; APPLICANT: Fox, Brian
 ; TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
 ; FILE REFERENCE: 00-33
 ; CURRENT APPLICATION NUMBER: US/11/156,843
 ; CURRENT FILING DATE: 2005-06-20
 ; PRIOR APPLICATION NUMBER: US/09/883,727
 ; PRIOR FILING DATE: 2001-06-18

```
/ NUMBER OF SEQ ID NOS: 140
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 28
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: C1s exosite binding moiety
/ NAME/KEY: MUTAGEN
/ LOCATION: (5)...(5)
/ OTHER INFORMATION: Xaa = Phe-(p-CH2)SO3H
US-11-156-843-28

Query Match          21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYEV 4
        ||||
Db       7 DYEV 10

RESULT 79
US-11-156-843-35
/ Sequence 35, Application US/11156843
/ Publication NO. US20050267035A1
/ GENERAL INFORMATION:
/ APPLICANT: West, Robert R.
/ APPLICANT: Sheppard, Paul O.
/ APPLICANT: Fox, Brian
/ TITLE OF INVENTION: Peptide and Polypeptide Inhibitors of
/ FILE REFERENCE: 00-33
/ CURRENT APPLICATION NUMBER: US/11/156,843
/ PRIOR FILING DATE: 2005-06-20
/ PRIOR APPLICATION NUMBER: US/09/883,727
/ PRIOR FILING DATE: 2001-06-18
/ NUMBER OF SEQ ID NOS: 140
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 35
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: C1s exosite binding moiety
/ NAME/KEY: MUTAGEN
/ LOCATION: (5)...(5)
/ OTHER INFORMATION: Xaa = sulfated tyrosine
US-11-156-843-35

Query Match          21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 DYEV 4
        ||||
Db       7 DYEV 10

RESULT 80
US-11-045-024-2247
/ Sequence 2247, Application US/11045024
/ Publication NO. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
```

```
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2247
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2247
```

```
Query Match          21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY      12 PRAPLYKRP 20
        |::|||
Db       1 POTTLMQRP 9

RESULT 81
US-11-045-024-5380
/ Sequence 5380, Application US/11045024
/ Publication NO. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
```

```
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/247,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 5380
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5380
```

```
Query Match      21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKRP 20
      |:|:|:|
DB      2 PQTITWQRP 10
```

```
RESULT 82
US-11-045-024-7847
/ Sequence 7847, Application US/11045024
/ Publication No. US2005021676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esben
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Epimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/247,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 7847
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7847
```

```
Query Match      21.9%; Score 25; DB 7; Length 11;
Best Local Similarity 44.4%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      12 PKAPLYKRP 20
      |:|:|:|
DB      1 PQTITWQRP 9
```

```
RESULT 83
US-10-511-559-464
/ Sequence 464, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 464
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-464
```

```
Query Match      21.9%; Score 25; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      7 SRLGNPKAPL 16
      |||||:|
DB      4 SLLGPPSMFV 13
```

```
RESULT 84
US-11-054-515-2470
/ Sequence 2470, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS2393
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO: 2470
/ LENGTH: 13
/ TYPE: PRT
```

ORGANISM: Homo sapiens
US-11-054-515-2470

Query Match 21.9%; Score 25; DB 7; Length 13;
Best Local Similarity 66.7%; Pred. No. 2.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPLY 17
| : |||
DB 8 PHSPLY 13

RESULT 85

US-11-006-119-35
Sequence 35, Application US/11006119
Publication No. US20050260691A1
GENERAL INFORMATION:
APPLICANT: Ndao, Momar
APPLICANT: Ward, Brian
APPLICANT: Caffrey, Rebecca
APPLICANT: Spithill, Terry
APPLICANT: Li, Hongshan
APPLICANT: Poduel, Vladimir
APPLICANT: Perichon, Regis
APPLICANT: CIPHERGEN Biosystems, Inc.
TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
FILE REFERENCE: 016866-012130US
CURRENT APPLICATION NUMBER: US/11/006,119
CURRENT FILING DATE: 2004-12-06
PRIOR APPLICATION NUMBER: US 60/527,153
PRIOR FILING DATE: 2003-12-05
PRIOR APPLICATION NUMBER: US 60/565,093
PRIOR FILING DATE: 2004-04-22
PRIOR APPLICATION NUMBER: US 60/625,519
PRIOR FILING DATE: 2004-11-06
NUMBER OF SEQ ID NOS: 38
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 35
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:C-terminal
OTHER INFORMATION: truncation 24.7 kDa fragment of Apolipoprotein A-I
OTHER INFORMATION: (ApoA-I) Chagas disease biomarker tryptic digest
US-11-006-119-35

Query Match 21.9%; Score 25; DB 7; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 DY--EYPSRLG 10
| : |||
DB 1 DYVSGEGSALG 12

RESULT 86

US-10-983-174-6
Sequence 6, Application US/10983174
Publication No. US20050261307A1
GENERAL INFORMATION:
APPLICANT: CAI, SHAOPEI
APPLICANT: CHOU, JOYCE
APPLICANT: HARWOOD, ERIC
APPLICANT: HEISE, CARLA C.
APPLICANT: MACHAJBSKI, TIMOTHY D.
APPLICANT: RYCKMAN, DAVID
APPLICANT: SHANG, XIAO
APPLICANT: WIESMANN, MARION
APPLICANT: ZHU, SHUGUANG
TITLE OF INVENTION: INHIBITION OF FGFR3 AND TREATMENT OF MULTIPLE MYELOMA
FILE REFERENCE: 072121-0445

CURRENT APPLICATION NUMBER: US/10/983,174
CURRENT FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: 60/546,017
PRIOR FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: 60/526,425
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/526,426
PRIOR FILING DATE: 2003-12-02
PRIOR APPLICATION NUMBER: 60/517,915
PRIOR FILING DATE: 2003-11-07
PRIOR APPLICATION NUMBER: 10/644,055
PRIOR FILING DATE: 2003-08-19
PRIOR APPLICATION NUMBER: 60/405,729
PRIOR FILING DATE: 2002-08-23
PRIOR APPLICATION NUMBER: 60/428,210
PRIOR FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: 60/484,048
PRIOR FILING DATE: 2003-07-01
PRIOR APPLICATION NUMBER: 60/426,282
PRIOR FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: 60/460,493
PRIOR FILING DATE: 2003-04-03
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 6
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-983-174-6

Query Match 21.9%; Score 25; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPKAP 15
| : |||
DB 3 GGEKTP 8

RESULT 87

US-10-719-150-1
Sequence 1, Application US/10719150
Publication No. US20040120953A1
GENERAL INFORMATION:
APPLICANT: Kevin J. Tracey
APPLICANT: Haichao Wang
TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING
TITLE OF INVENTION: INFLAMMATORY CONDITIONS
FILE REFERENCE: 3268.1000-011
CURRENT APPLICATION NUMBER: US/10/719,150
CURRENT FILING DATE: 2003-11-21
PRIOR APPLICATION NUMBER: US/10/300,068
PRIOR FILING DATE: 2002-11-20
PRIOR APPLICATION NUMBER: US 10/210,747
PRIOR FILING DATE: 2002-07-31
PRIOR APPLICATION NUMBER: US 09/503,632
PRIOR FILING DATE: 2000-02-14
PRIOR APPLICATION NUMBER: US 09/248,574
PRIOR FILING DATE: 1999-02-11
NUMBER OF SEQ ID NOS: 6
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-10-719-150-1

Query Match 21.9%; Score 25; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 GNPAP 15

Db 3 GNPAP 8

RESULT 88
US-11-054-515-2529

; Sequence 2529, Application US/11054515
; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2529

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-054-515-2529

Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 14;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPLK 18

Db 8 PHAPLE 14

RESULT 89

US-11-054-515-2691

; Sequence 2691, Application US/11054515

; Publication No. US2005025532A1

; GENERAL INFORMATION:

; APPLICANT: Ruben et al.

; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

; FILE REFERENCE: PF523P3

; CURRENT APPLICATION NUMBER: US/11/054,515

; CURRENT FILING DATE: 2005-02-10

; PRIOR APPLICATION NUMBER: 60/543,296

; PRIOR FILING DATE: 2004-02-11

; PRIOR APPLICATION NUMBER: 60/580,347

; PRIOR FILING DATE: 2004-06-18

; PRIOR APPLICATION NUMBER: 10/293,418

; PRIOR FILING DATE: 2002-11-14

; PRIOR APPLICATION NUMBER: 60/331,469

; PRIOR FILING DATE: 2001-11-16

; PRIOR APPLICATION NUMBER: 60/340,817

; PRIOR FILING DATE: 2001-12-19

; PRIOR APPLICATION NUMBER: 09/880,748

; PRIOR FILING DATE: 2001-06-15

; PRIOR APPLICATION NUMBER: 60/293,499

; PRIOR FILING DATE: 2001-05-25

; PRIOR APPLICATION NUMBER: 60/277,379

; PRIOR FILING DATE: 2001-03-21

; PRIOR APPLICATION NUMBER: 60/276,248

; PRIOR FILING DATE: 2001-03-16

; PRIOR APPLICATION NUMBER: 60/240,816

; PRIOR FILING DATE: 2000-10-17

; Remaining Prior Application data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 3247

; SEQ ID NO 2691

; LENGTH: 14

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-11-054-515-2691

Query Match

Best Local Similarity 21.9%; Score 25; DB 7; Length 14;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 12 PKAPLK 17

Db 8 PQAPLH 13

RESULT 90

US-10-719-150-4

; Sequence 4, Application US/10719150

; Publication No. US20040120953A1

; GENERAL INFORMATION:

; APPLICANT: Kevin J. Tracey

; APPLICANT: Haichao Wang

; TITLE OF INVENTION: ANTAGONISTS OF HMGI FOR TREATING

; FILE REFERENCE: 3268.1000-011

; CURRENT APPLICATION NUMBER: US/10/719,150

; CURRENT FILING DATE: 2003-11-21

; PRIOR APPLICATION NUMBER: US/10/300,068

; PRIOR FILING DATE: 2002-11-20

; PRIOR APPLICATION NUMBER: US 10/210,747

; PRIOR FILING DATE: 2002-07-31

; PRIOR APPLICATION NUMBER: US 09/503,632

; PRIOR FILING DATE: 2000-02-14

; PRIOR APPLICATION NUMBER: US 09/248,574

; PRIOR FILING DATE: 1999-02-11

; NUMBER OF SEQ ID NOS: 6

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 4

; LENGTH: 15

; TYPE: PRT

; ORGANISM: Artificial Sequence

; FEATURE:

; OTHER INFORMATION: antigen

; US-10-719-150-4

Query Match

Best Local Similarity 21.9%; Score 25; DB 6; Length 15;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 10 GNPAP 15

Db 3 GNPAP 8

RESULT 91

US-11-045-024-13167

; Sequence 13167, Application US/11045024

; Publication No. US20050271676A1

; GENERAL INFORMATION:

; APPLICANT: Sette, Alessandro

```
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Estebean
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13167
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13167

Query Match      21.9%; Score 25; DB 7; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

```
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Estebean
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13283
LENGTH: 15
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13283

Query Match      21.9%; Score 25; DB 7; Length 15;
Best Local Similarity 44.4%; Pred. No. 2.9e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
```

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 12 PKAPLYKRP 20
|:|:|
Db 7 PQTLMQRP 15

RESULT 94
US-10-201-525-23
; Sequence 23, Application US/10201525
; Publication No. US20060009631A1
; GENERAL INFORMATION:
; APPLICANT: Board of Regents of the University of Oklahoma
; TITLE OF INVENTION: TYROSYLPROTEIN SULFOTRANSFERASES AND METHODS OF USE THEREOF
; FILE REFERENCE: 5827,005
; CURRENT APPLICATION NUMBER: US/10/201,525
; CURRENT FILING DATE: 2002-07-22
; PRIOR APPLICATION NUMBER: 09/785,343
; PRIOR FILING DATE: 2001-02-16
; PRIOR APPLICATION NUMBER: PCT/US99/16750
; PRIOR FILING DATE: 1999-07-23
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 23
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-201-525-23

Query Match 21.9%; Score 25; DB 6; Length 17;
Best Local Similarity 100.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEX 4
| | | |
Db 8 DYEX 11

RESULT 95
US-11-006-119-38
; Sequence 38, Application US/11006119
; Publication No. US20050260691A1
; GENERAL INFORMATION:
; APPLICANT: Ndao, Momar
; APPLICANT: Ward, Brian
; APPLICANT: Caffrey, Rebecca
; APPLICANT: Spithill, Terry
; APPLICANT: Li, Hongshan
; APPLICANT: Poduet, Vladimir
; APPLICANT: Perichon, Regis
; APPLICANT: CIPHERGEN Biosystems, Inc.
; TITLE OF INVENTION: Serum Biomarkers for Chagas Disease
; FILE REFERENCE: 016866-012130US
; CURRENT APPLICATION NUMBER: US/11/006,119
; CURRENT FILING DATE: 2004-12-06
; PRIOR APPLICATION NUMBER: US 60/527,153
; PRIOR FILING DATE: 2003-12-05
; PRIOR APPLICATION NUMBER: US 60/565,093
; PRIOR FILING DATE: 2004-04-22
; PRIOR APPLICATION NUMBER: US 60/625,519
; PRIOR FILING DATE: 2004-11-06
; NUMBER OF SEQ ID NOS: 38
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 38
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:C-terminal
; OTHER INFORMATION: truncation 24.7 kDa fragment of Apolipoprotein A-1
; OTHER INFORMATION: ApoA-1 Chagas disease biomarker cryptic digest
US-11-006-119-38

Query Match 21.9%; Score 25; DB 7; Length 17;
Best Local Similarity 50.0%; Pred. No. 3.3e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 1 DY--EYPSRLG 10
| | : | | |
Db 5 DYVSQFEGSALG 16

RESULT 96
US-11-128-059-11
; Sequence 11, Application US/11128059
; Publication No. US20050287638A1
; GENERAL INFORMATION:
; APPLICANT: WEIGEL, PAUL H
; APPLICANT: WEIGEL, JANET A
; TITLE OF INVENTION: HYALURONAN RECEPTOR FOR ENDOCYTOSIS, VARIANTS THEREOF, AND
; FILE REFERENCE: 5864,033
; CURRENT APPLICATION NUMBER: US/11/128,059
; CURRENT FILING DATE: 2005-05-12
; PRIOR APPLICATION NUMBER: 60/570,915
; PRIOR FILING DATE: 2004-05-13
; PRIOR APPLICATION NUMBER: 10/133,172
; PRIOR FILING DATE: 2002-04-25
; PRIOR APPLICATION NUMBER: 60/286,468
; PRIOR FILING DATE: 2001-04-25
; PRIOR APPLICATION NUMBER: 09/842,930
; PRIOR FILING DATE: 2001-04-25
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-128-059-11

Query Match 21.9%; Score 25; DB 7; Length 19;
Best Local Similarity 50.0%; Pred. No. 3.7e+02;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 10 GNPAPLYKRP 19
| | | | | |
Db 7 GGPDAFCNNR 16

RESULT 97
US-10-623-155-493
; Sequence 493, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 493
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-493

Query Match 21.9%; Score 25; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
 Db 7 PGNFLONRPEPTAP 14

RESULT 98
 US-11-045-024-13091

/ Sequence 13091, Application US/11045024
 / Publication No. US20050271676A1

/ GENERAL INFORMATION:

/ APPLICANT: Sette, Alessandro

/ APPLICANT: Sidney, John

/ APPLICANT: Southwood, Scott

/ APPLICANT: Livingston, Brian

/ APPLICANT: Chesnut, Robert

/ APPLICANT: Baker, Denise Marie

/ APPLICANT: Celis, Eskeban

/ APPLICANT: Kubo, Ralph

/ APPLICANT: Grey, Howard M.

/ APPLICANT: Epiimmune Inc.

/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 / TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

/ FILE REFERENCE: 2060, 0040007

/ CURRENT APPLICATION NUMBER: US/11/045,024

/ CURRENT FILING DATE: 2005-01-28

/ PRIOR APPLICATION NUMBER: US 09/412,863

/ PRIOR FILING DATE: 1999-10-05

/ PRIOR APPLICATION NUMBER: US 08/027,146

/ PRIOR FILING DATE: 1993-03-05

/ PRIOR APPLICATION NUMBER: US 08/073,205

/ PRIOR FILING DATE: 1993-06-04

/ PRIOR APPLICATION NUMBER: US 08/103,396

/ PRIOR FILING DATE: 1993-08-06

/ PRIOR APPLICATION NUMBER: US 08/159,184

/ PRIOR FILING DATE: 1993-11-29

/ PRIOR APPLICATION NUMBER: US 08/159,339

/ PRIOR FILING DATE: 1993-11-29

/ PRIOR APPLICATION NUMBER: US 08/205,713

/ PRIOR FILING DATE: 1994-03-04

/ PRIOR APPLICATION NUMBER: US 08/347,610

/ PRIOR FILING DATE: 1994-12-01

/ NUMBER OF SEQ ID NOS: 14528

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 13091

/ LENGTH: 15

/ TYPE: PRT

/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS

/ US-11-045-024-13091

Query Match

Best Local Similarity 21.5%; Score 24.5; DB 7; Length 15;

Matches 7; Conservative 1; Mismatches 3; Indels 3; Gaps 1;

QY 5 PGSRLGNP 15

Db 1 PGNFLONRPEPTAP 14

RESULT 99

US-11-105-708-25

/ Sequence 25, Application US/11105708

/ Publication No. US20050281821A1

/ GENERAL INFORMATION:

/ APPLICANT: Pernaas, Flavia

/ APPLICANT: Freimark, Bruce

/ APPLICANT: Van Epps, Dennis

/ APPLICANT: Brooks, Peter C

/ TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition

/ FILE REFERENCE: 30797-704.501

/ CURRENT APPLICATION NUMBER: US/11/105,708

/ CURRENT FILING DATE: 2005-04-13

/ PRIOR APPLICATION NUMBER: 09/478,977

/ PRIOR FILING DATE: 2000-01-06

/ PRIOR APPLICATION NUMBER: 60/152,496
 / PRIOR FILING DATE: 1999-09-02
 / PRIOR APPLICATION NUMBER: 60/143,534
 / PRIOR FILING DATE: 1999-09-02
 / PRIOR APPLICATION NUMBER: 60/114,878
 / PRIOR FILING DATE: 1999-01-06
 / PRIOR APPLICATION NUMBER: 60/114,877
 / PRIOR FILING DATE: 1999-01-06
 / NUMBER OF SEQ ID NOS: 25
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 25
 / LENGTH: 9
 / TYPE: PRT
 / ORGANISM: Artificial
 / FEATURE:
 / OTHER INFORMATION: Synthetic peptide
 / US-11-105-708-25

Query Match
 Best Local Similarity 21.1%; Score 24; DB 7; Length 9;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEXP 5
 Db 3 DHQYP 7

RESULT 100
 US-10-859-643-448

/ Sequence 448, Application US/10859643

/ Publication No. US20060002993A1

/ GENERAL INFORMATION:

/ APPLICANT: Chalilata-Eid, Pia M.

/ APPLICANT: Raitano, Arthur B.

/ APPLICANT: Fails, Mary

/ APPLICANT: Hubert, Rene S.

/ APPLICANT: Morison, Karen Jane Meyrick

/ APPLICANT: Jakobovits, Aya

/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

/ FILE REFERENCE: 511582006203

/ CURRENT APPLICATION NUMBER: US/10/859,643

/ CURRENT FILING DATE: 2004-06-02

/ PRIOR APPLICATION NUMBER: US 10/005,480

/ PRIOR FILING DATE: 2001-11-07

/ NUMBER OF SEQ ID NOS: 765

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 448

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Homo Sapien

/ US-10-859-643-448

Query Match

Best Local Similarity 21.1%; Score 24; DB 6; Length 10;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEXP 9

Db 1 YEXP 8

Search completed: January 20, 2006, 19:46:28
 Job time : 9.07692 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 : Search time 11.3462 Seconds
(without alignment)
169.602 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114

Sequence: 1 DYEPGSRIGNPKAPLYKRP 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR 80:*

2: p1r1:*

3: p1r2:*

4: p1r3:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	33	28.9	18	2	S36120	lectin - Euphorbia
2	29	25.4	16	2	PH0137	T-cell receptor be
3	29	25.4	19	2	S59485	hydroxyproline-rich
4	27	23.7	15	2	A08416	lombicine kinase
5	26	22.8	13	2	IS0173	alpha-2 collagen -
6	26	22.8	20	2	S44465	pyrithocoridin - Py
7	25.5	22.4	16	2	PT0224	Ig heavy chain CDR
8	25.5	22.4	18	2	PQ0072	T-cell receptor be
9	25	21.9	9	2	S70332	endospem protein,
10	25	21.9	11	2	PT0217	T-cell receptor be
11	25	21.9	16	2	PH1302	Ig heavy chain DJ
12	25	21.9	16	2	B28587	T-cell receptor be
13	25	21.9	10	2	S62880	polygalacturonase
14	24	21.1	15	2	D28587	T-cell receptor be
15	24	21.1	15	2	F28587	T-cell receptor be
16	24	21.1	15	2	PH0772	T-cell receptor be
17	24	21.1	16	2	A49255	T-cell receptor be
18	24	21.1	16	2	F53284	T-cell receptor be
19	24	21.1	19	2	A05505	hemoglobin beta-2
20	23	20.2	14	2	S62374	hemoglobin beta-2
21	23	20.2	15	2	S27248	pseudogerm - whe
22	23	20.2	15	2	PN0665	dystrophin-associ
23	23	20.2	15	2	PT0097	glutathione peroxi
24	23	20.2	16	2	PH0749	T-cell receptor be
25	23	20.2	16	2	S10678	aldehyde dehydrog
26	23	20.2	17	2	G85956	hypothetical prote
27	23	20.2	20	2	PQ0046	citrate (si)-synth
28	22.5	19.7	14	2	S23369	T-cell receptor al
29	22	19.3	11	2	S04875	nifs protein - Bra

30	22	19.3	11	4	IS4081	retinoic acid rece
31	22	19.3	15	2	S21238	hydrogenulfite re
32	22	19.3	17	2	S58660	H+-transporting tw
33	22	19.3	18	1	A58589	alpha-conotoxin EI
34	22	19.3	18	2	S56715	hydroxymethylgluta
35	22	19.3	18	2	A29558	pigment-dispersing
36	22	19.3	20	2	G61491	seed protein wa-25
37	22	19.3	20	2	A49142	hyaluronidase (EC
38	22	19.3	20	2	A34859	heliothermine - Mex
39	21.5	18.9	10	1	XASNPC	angiotensin-conver
40	21	18.4	11	2	I33098	173k exoantigen -
41	21	18.4	14	1	BSTD	bombesin - fire-be
42	21	18.4	14	2	PH1322	Ig heavy chain DJ
43	21	18.4	14	2	PN0666	dystrophin-associ
44	21	18.4	15	2	PQ0195	Sfil1-glycoprotein
45	21	18.4	15	2	S29485	GTP-binding protei
46	21	18.4	15	2	S51735	T-cell receptor be
47	21	18.4	15	2	I53284	T-cell receptor be
48	21	18.4	15	2	PT0091	H+-transporting tw
49	21	18.4	16	2	PH1580	Ig H chain V-D-J r
50	21	18.4	16	2	H35141	T-cell receptor de
51	21	18.4	18	1	MTHO8	melanotropin beta
52	21	18.4	18	1	DRUPD	pigment-dispersing
53	21	18.4	18	1	A45590	beta-pigment-dispe
54	21	18.4	19	2	PH1609	Ig H chain V-D-J r
55	21	18.4	20	2	S72501	protein kinase C 1
56	21	18.4	20	2	S19240	histone H2B (clone
57	21	18.4	20	2	B53592	H+-exporting ATPas
58	20.5	18.0	13	2	PH0756	T-cell receptor be
59	20.5	18.0	20	2	B59326	ribosomal protein
60	20	17.5	4	2	PT0240	Ig heavy chain CRD
61	20	17.5	7	2	A38081	amine oxidase (cop
62	20	17.5	8	2	A41117	acetylcholinestera
63	20	17.5	10	1	A61126	gonadolibertin II -
64	20	17.5	10	1	RHAQ2	gonadolibertin II -
65	20	17.5	10	2	S24190	cryptase (EC 3.4.2
66	20	17.5	10	2	S24630	gonadolibertin II -
67	20	17.5	11	2	B41476	probable antigen 5
68	20	17.5	11	2	S07207	3-hydroxy-3-methyl
69	20	17.5	12	2	S74196	dystrophin-associ
70	20	17.5	12	2	PN0663	Ig kappa-1 chain J
71	20	17.5	12	2	C20907	sterol carrier pro
72	20	17.5	12	2	A61503	dissimilatory sulf
73	20	17.5	13	2	S63492	Ig kappa-1 chain J
74	20	17.5	13	2	S33800	chaperone, TCP1-re
75	20	17.5	14	2	S60353	amylopullulanase -
76	20	17.5	14	2	B60683	malate dehydrogena
77	20	17.5	15	2	S24159	leukocyte elastase
78	20	17.5	15	2	S59492	formate dehydrogen
79	20	17.5	15	2	PA0002	phocovsystem II oxy
80	20	17.5	15	2	PL0143	carbon-monoxide de
81	20	17.5	15	2	S36896	ribosomal protein
82	20	17.5	15	2	S04586	NADH2 dehydrogenas
83	20	17.5	16	2	B54877	alpha-conotoxin Pn
84	20	17.5	16	2	T37075	hypothetical prote
85	20	17.5	16	2	G24304	ribosomal protein
86	20	17.5	16	2	PT0237	Ig heavy chain CDR
87	20	17.5	16	2	A42291	tail fiber protein
88	20	17.5	16	2	JT0609	leukocyte chemotac
89	20	17.5	16	2	B61334	lysozin (EC 3.4.21
90	20	17.5	17	2	I49593	cyclic fibrosis tr
91	20	17.5	17	2	I84733	gene CFRP protein
92	20	17.5	17	2	B25348	glycogen(starch) s
93	20	17.5	18	2	S47196	T-cell receptor J-
94	20	17.5	18	2	B44239	amine oxidase (cop
95	20	17.5	19	2	S25715	hypothetical prote
96	20	17.5	19	2	S43045	translation elonga
97	20	17.5	20	2	JP0059	ribosomal protein
98	20	17.5	20	2	B46174	RNA-binding protei
99	20	17.5	20	2	S38292	30K allergen - rye
100	19.5	17.1	16	2		

ALIGNMENTS

```
RESULT 1
S36120
I:lectin - Euphorbia marginata (fragment)
C:Species: Euphorbia marginata
C:Date: 19-Mar-1997 #sequence_revision 06-Jun-1997 #text_change 09-Jul-2004
C:Accession: S36120
R:Stilpe, F.; Licastro, F.; Morini, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Bolog
Blochm. Biophys. Acta 1150, 33-39, 1993
A>Title: Purification and partial characterization of a mitogenic lectin from the latex
A:Reference number: S36120; PMID:93537266; PMID:8353129
A:Accession: S36120
A:Molecule type: protein
A:Residues: 1-18 <SRI>
A:Cross-references: UNIPROT:P33889; UNIPARC:UPI00001256C1
C:Keywords: lectin

Query Match          28.9%; Score 33; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRLGNP 12
    |||||
    :|
Db 2 YPGSHISGP 10

RESULT 2
PH0137
I:cell receptor beta chain V-D-J region M320 - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
C:Accession: PH0137
R:Martin, R.; Howell, M.D.; Jaraquemada, D.; Pierlage, M.; Richert, J.; Brostoff, S.; Lo
J. Exp. Med. 173, 19-24, 1991
A>Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the contex
A:Reference number: PH0135; PMID:91086843; PMID:1702137
A:Accession: PH0137
A:Molecule type: mRNA
A:Residues: 1-16 <MAR>
A:Cross-references: UNIPARC:UPI000017C3AF
C:Keywords: T-cell receptor

Query Match          25.4%; Score 29; DB 2; Length 16;
Best Local Similarity 37.5%; Pred. No. 3.3e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 YEPGSRGNPKAPLY 17
    |||||
    :|
Db 1 YFCASRKDPSPLH 16

RESULT 3
S59485
I:hydroxyproline-rich cell wall glycoprotein (42K and others) - kidney bean (fragment)
C:Species: Phaseolus vulgaris (kidney bean)
C:Date: 27-Apr-1996 #sequence_revision 26-Jul-1996 #text_change 09-Jul-2004
C:Accession: S59485; S59486; S59483
R:Wojtaszek, P.; Trechowar, J.; Bolwell, G.P.
Plant Mol. Biol. 28, 1075-1087, 1995
A>Title: Specificity in the immobilization of cell wall proteins in response to differen
A:Reference number: S59481; PMID:96011753; PMID:7548825
A:Accession: S59485
A:Molecule type: protein
A:Residues: 1-19 <WOJ>
A:Cross-references: UNIPROT:Q7M1M8; UNIPARC:UPI0000177E5D
A>Note: hydroxyproline-rich cell wall glycoprotein, 42K
A:Accession: S59484
A:Molecule type: protein
A:Residues: 1-15 <WOW>
A:Cross-references: UNIPARC:UPI0000177E5E
A>Note: hydroxyproline-rich cell wall glycoprotein, 84K
```

```
A:Accession: S59483
A:Molecule type: protein
A:Residues: 1-14 <WOF>
A:Cross-references: UNIPARC:UPI0000177E5F
A>Note: hydroxyproline-rich cell wall glycoprotein, 136K, minor component
C:Superfamily: proline-rich protein 3
C:Keywords: glycoprotein; hydroxyproline
F:6,11,16/Modified site: hydroxyproline (Pro) #status experimental

Query Match          25.4%; Score 29; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 KAPLYKRP 20
    |||||
    :|
Db 9 KPVYIKRP 16

RESULT 4
A08416
I:lombiricne kinase (EC 2.7.3.5) - earthworm (lumbiricus terrestris) (fragment)
C:Species: Lumbiricus terrestris (common earthworm)
C:Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C:Accession: A08416
R:der Terrosian, B.; Desvages, G.; Pradel, L.A.; Kassab, R.; van Thoai, N.
Eur. J. Biochem. 22, 585-592, 1971
A>Title: Comparative structural studies of the active site of ATP: guanidine phosphotran
A:Reference number: A08416; PMID:72066544; PMID:5128744
A:Accession: A08416
A:Molecule type: protein
A:Residues: 1-15 <DER>
A:Cross-references: UNIPROT:P11918; UNIPARC:UPI000012DEBE
C:Keywords: phosphotransferase

Query Match          23.7%; Score 27; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGRSLG 10
    |||||
    :|
Db 7 PGRSLG 12
```

```
RESULT 5
I50173
I:alpha-2 collagen - chicken (fragment)
C:Species: Gallus gallus (chicken)
C:Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
C:Accession: I50173
R:Avvedimento, E.V.; Vogel, G.; Yamada, Y.; Maisel, J.V.
Cell 21, 689-696, 1980
A>Title: Correlation between splicing sites within an intron and their sequence compleme
A:Reference number: I50172; PMID:81064671; PMID:6159982
A:Accession: I50173
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-13 <AVV>
A:Cross-references: UNIPROT:P02467; UNIPARC:UPI00001712AB; GB:M10540; NID:G211324; PIDN
C:Genetics:
A:introns: 12/3

Query Match          22.8%; Score 26; DB 2; Length 13;
Best Local Similarity 45.5%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGRSLGNPKAP 15
    |||||
    :|
Db 2 PGRSLGNPKAP 12

RESULT 6
S44465
I:pyrithocoridin - Pyrithocoris apterus
```

C/Species: Pyrihocoris apterus
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S44465

R/Cocciandich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holder, F.; Hetru, C.; Hoffmann, J.A.

Biochem. J. 300, 567-575, 1994

A/Title: Novel inducible antibacterial peptides from a hemipteran insect, the sap-sucking

A/Reference number: S44463; PMID:94271176; PMID:8002963

A/Accession: S44465

A/Molecule type: protein

A/Residues: 1-20 <COC>

A/Cross-references: UNIPROT:P37362; UNIPARC:UPI0000132E13

C/Function: antibacterial protein

A/Description: active against Gram-negative bacteria

C/Keywords: antibacterial; hemolymph; immune response

Query Match 22.8%; Score 26; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.2e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKR 19

DB 12 PPRPIYNR 19

RESULT 7

Ig heavy chain CDR3 region (clone 1-91) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0224

R/Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A/Reference number: PT0222; PMID:9108337; PMID:1899102

A/Accession: PT0224

A/Molecule type: DNA

A/Residues: 1-16 <YAM>

A/Cross-references: UNIPARC:UPI000017C1D6

A/Experimental source: B lymphocyte

A/Note: the authors translated the stop codon for residue 9 as X

C/Keywords: heterotetramer; immunoglobulin

Query Match 22.4%; Score 25.5; DB 2; Length 16;

Best Local Similarity 57.1%; Pred. No. 1.2e+03;

Matches 8; Conservative 0; Mismatches 3; Indels 3; Gaps 2;

QY 1 DYEYPSRL--GNP 12

DB 4 DYSY-GXLLGPNP 16

RESULT 8

PO0072

T-cell receptor beta chain (BTB98) - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 20-Feb-1995

C/Accession: PQ0072

R/Tanaka, A.; Ishiguro, N.; Shingawa, M.

submitted to JIPID, May 1990

A/Description: Sequence analysis of bovine T-cell receptor beta chain genes.

A/Reference number: JQ0472

A/Accession: PQ0072

A/Molecule type: mRNA

A/Residues: 1-18 <TAN>

A/Cross-references: UNIPARC:UPI000011D084

A/Experimental source: T cell

C/Genetics:

A/Gene: BTB98

C/Keywords: receptor

Query Match 22.4%; Score 25.5; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 1.3e+03;

Matches 5; Conservative 3; Mismatches 1; Indels 1; Gaps 1;

QY 1 DYEYPSRL 9

DB 6 DYHGPETKL 15

RESULT 9

endosperm protein, 10K - rye (fragment)

C/Species: Secale cereale (rye)

C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998

C/Accession: S70332

R/Rocher, A.; Calero, M.; Soriano, F.; Mendez, E.

Biochim. Biophys. Acta 1295, 13-22, 1996

A/Title: Identification of major rye secalins as coeliac immunoreactive proteins.

A/Reference number: S70327; PMID:96283789; PMID:8679669

A/Accession: S70332

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <ROC>

A/Cross-references: UNIPARC:UPI000017B132

Query Match 21.9%; Score 25; DB 2; Length 9;

Best Local Similarity 66.7%; Pred. No. 2.8e+05;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 YEYPSG 7

DB 4 YEYAGN 9

RESULT 10

T-cell receptor beta chain V-J region (4-1-E-2) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C/Accession: PT0217

R/Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of Iaet beta cell-reactive T cells is not restri

A/Reference number: PT0209; PMID:91217621; PMID:1902501

A/Accession: PT0217

A/Molecule type: mRNA

A/Residues: 1-11 <NAK>

A/Cross-references: UNIPARC:UPI000017C851

C/Keywords: T-cell receptor

Query Match 21.9%; Score 25; DB 2; Length 11;

Best Local Similarity 100.0%; Pred. No. 9.4e+02;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SRLGN 11

DB 3 SRLGN 7

RESULT 11

Ig heavy chain DJ region (clone C76-105) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1302

R/Masserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymphi

A/Reference number: PH1302; PMID:93094761; PMID:1460419

A/Accession: PH1302

A/Molecule type: DNA

A/Residues: 1-16 <WAS>

A/Cross-references: UNIPARC:UPI000017C24C

C/Keywords: heterotetramer; immunoglobulin

Query Match 21.9%; Score 25; DB 2; Length 16;
Best Local Similarity 46.2%; Pred. No. 1.4e+03;
Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 EYPSRLGNPKAP 15
| | | | |
| | | | |
Db 1 EYISQLVRLPG 13

RESULT 12
B28587
T-cell receptor beta-2 chain J-B2.3 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: B28587
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region genes
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: B28587
A/Molecule type: DNA
A/Residues: 1-16 <TOY>
A/Cross-references: UNIPARC:UPI000002FDD6; GB:M14159; NID:G338852; PIDN:AAA60677.1; PID:
C/Keywords: T-cell receptor

Query Match 21.9%; Score 25; DB 2; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.4e+03;
Matches 6; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

QY 1 DYEX--PGSRL 9
| | | | |
| | | | |
Db 3 DYQYFGPGTRL 13

RESULT 13
S62880
polygalacturonase (EC 3.2.1.15) IV - Aspergillus sp. (fragment)
C/Species: Aspergillus sp.
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S62880
R/Stratillova, E.; Dzurova, M.; Markovic, O.; Joernvall, H.
FEBS Lett. 382, 164-166, 1996
A/Title: An essential tyrosine residue of Aspergillus polygalacturonase.
A/Reference number: S62880; MUID:96196586; PMID:8612742
A/Accession: S62880
A/Molecule type: protein
A/Residues: 1-10 <STR>
A/Cross-references: UNIPROT:Q7M500; UNIPARC:UPI000017B3DA
C/Keywords: glycosidase; hydrolase
F/4/Active site: Tyr #status predicted

Query Match 21.1%; Score 24; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEPYG 6
| | | | |
| | | | |
Db 1 DYAYTG 6

RESULT 14
D28587
T-cell receptor beta-2 chain J-B2.5 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: D28587
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region genes
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: D28587
A/Molecule type: DNA
A/Residues: 1-15 <TOY>

A/Cross-references: UNIPARC:UPI0000113C7C; GB:M14159; NID:G338852; PIDN:AAA60679.1; PID:
C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEYPSRL 9
| | | | |
| | | | |
Db 5 YRPGGTRL 12

RESULT 15
F28587
T-cell receptor beta-2 chain J-B2.7 segment - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
C/Accession: F28587
R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
A/Title: Organization and sequences of the diversity, joining, and constant region genes
A/Reference number: A94081; MUID:86094276; PMID:3866244
A/Accession: F28587
A/Molecule type: DNA
A/Residues: 1-15 <TOY>
A/Cross-references: UNIPARC:UPI0000113C7E; GB:M14159; NID:G338852; PIDN:AAA60681.1; PID:
C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEYPSRL 9
| | | | |
| | | | |
Db 5 YRPGGTRL 12

RESULT 16
PH0772
T-cell receptor beta chain (t4) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0772
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-1
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1836010
A/Accession: PH0772
A/Molecule type: mRNA
A/Residues: 1-15 <MS>
A/Cross-references: UNIPARC:UPI0000115PBF; EMBL:X60866; NID:G52749; PIDN:CAA43256.1; PIR:
A/Experimental source: T lymphocyte
C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 15;
Best Local Similarity 45.5%; Pred. No. 1.9e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRLGNPKAPLY 17
| | | | |
| | | | |
Db 4 SRDRDQAPLF 14

RESULT 17
A42255
T-cell receptor beta chain V-D-J-C region (V beta 7, J beta 1.6) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
C/Accession: A42255
R/Rosenberg, W.M.; Moss, P.A.; Bell, J.I.
Eur. J. Immunol. 22, 541-549, 1992
A/Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A/Reference number: A49039; MUID:92164737; PMID:1311263
 A/Accession: A49255
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-16 <ROS>
 A/Cross-references: UNIPARC:UPI000017C3B9
 A/Note: sequence extracted from NCBI backbone (NCBIF:90722)
 C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 16;
 Best Local Similarity 35.7%; Pred. No. 2e+03;
 Matches 5; Conservative 4; Mismatches 1; Indels 4; Gaps 1;

QY 4 YPGSRGNPKAPY 17
 |||:|
 Db 5 YPGTQ---NSPLH 14

RESULT 18

F53284

T-cell receptor beta 2 chain J region, Dbeta2.3 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C/Accession: F53284

R/Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germ-line diversity and

A/Reference number: A53284; MUID:91342695; PMID:1678859

A/Accession: F53284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-16 <HAR>

A/Cross-references: UNIPARC:UPI0000115415; GB:S60737; NID:g233916; PIDN:AA19522.1; PID:

A/Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIF:60744)
 C/Keywords: T-cell receptor

Query Match 21.1%; Score 24; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 2e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 YBYPGSR 9
 |||:|
 Db 6 YBPGTRRL 13

RESULT 19

A05305

hemoglobin beta-2 chain - Indian spiny-tailed lizard (fragment)

C/Species: Uromastyx hardwickii (Indian spiny-tailed lizard)

C/Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C/Accession: A05305

R/Nagy, S.; Zaldi, Z.H.; von Bahr-Lindstrom, H.; Carlquist, M.; Jernvall, H.

FEBS Lett. 162, 290-295, 1983

A/Reference number: A9314; MUID:84029159; PMID:6628672

A/Accession: A05305

A/Molecule type: protein

A/Residues: 1-19 <NMO>

A/Cross-references: UNIPROT:P18992; UNIPARC:UPI000012C204

C/Keywords: erythrocyte; oxygen carrier

Query Match 21.1%; Score 24; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GNP 13
 |||:|
 Db 16 GNP 19

RESULT 20

S62374

alpha-1-antichymotrypsin - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004

C/Accession: S62374

R/Tsuda, M.; Sei, Y.; Ohkubo, T.; Yamamura, M.; Kamiguchi, H.; Akatsuka, A.; Tsuda, T.;

Eur. J. Biochem. 235, 821-827, 1996

A/Title: The defective secretion of a naturally occurring alpha-1-antichymotrypsin vari

A/Reference number: S62374; MUID:96184564; PMID:8654434

A/Accession: S62374

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-14 <TSU>

A/Cross-references: UNIPROT:Q9UNU9; UNIPROT:Q96DW6; UNIPROT:Q8N177; UNIPARC:UPI000017C0

C/Superfamily: serpin

Query Match 20.2%; Score 23; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 2.5e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SRLGNPK 13
 |||:|
 Db 6 SKVTNPK 12

RESULT 21

S27248

pseudogerm - wheat

C/Species: Triticum aestivum (common wheat)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 29-Aug-1997

C/Accession: S27248

R/Lane, B.G.; Cumling, A.C.; Preegeau, J.; Carpita, N.C.; Hurkman, W.J.; Bernier, F.; Dra

Bur. J. Biochem. 209, 961-969, 1992

A/Title: Germ-line isoforms are discrete temporal markers of wheat development. Pseudogerm

ated embryos, it is incorporated into cell walls.

A/Reference number: S27247; MUID:93049354; PMID:1425703

A/Accession: S27248

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 <LAN>

A/Cross-references: UNIPARC:UPI000017B14D

Query Match 20.2%; Score 23; DB 2; Length 15;
 Best Local Similarity 30.8%; Pred. No. 2.7e+03;
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 3 EYPSRLGNPKAP 15
 |||:|
 Db 3 DYXPNPPTXPXP 15

RESULT 22

PN0665

dystrophin-associated glycoprotein A3a-IV - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C/Accession: PN0665

R/Toshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A/Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A/Reference number: PN0662; MUID:94156881; PMID:8113213

A/Accession: PN0665

A/Molecule type: protein

A/Residues: 1-15 <YOS>

A/Cross-references: UNIPARC:UPI000017C5C4

C/Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C/Keywords: glycoprotein; skeletal muscle

Query Match 20.2%; Score 23; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 2.7e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 PRAPLTK 18
 |||:|
 Db 9 PNAAPPYQ 15

RESULT 23

P00097

glutathione peroxidase, non-selenium containing - mouse (fragment)

N/Alternate names: antioxidant protein 2

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 24-Nov-1999

C/Accession: P00097

R./Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPI, July 1998

A/Description: Proteome analysis of mouse brain.

A/Reference number: P00091

A/Accession: P00097

A/Molecule type: protein

A/Residues: 1-15 <KAW>

A/Cross-references: UNIPARC:UPI000017C66B

A/Experimental source: brain, striatum

Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 15;

Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 PGSRLEGNPKAPLYK 18

DB 1 PGGLLGXBPSPF 14

RESULT 24

P00749

T-cell receptor beta chain (883) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999

C/Accession: P00749

R./Casanova, J.L.; Romero, P.; Widmann, C.; Koutlikky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
allelic exclusion and antigen-specific repertoire.

A/Reference number: P00746; MUID:92078846; PMID:1836010

A/Accession: P00749

A/Molecule type: mRNA

A/Residues: 1-16 <CAS>

A/Cross-references: UNIPARC:UPI0000115FA8; EMBL:X60840; NID:G50116; PIDD:CAA43233.1; PIDD

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 16;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPKAPLY 17

DB 9 NNQAPLY 15

RESULT 25

S10678

aldehyde dehydrogenase (EC 1.-.-.-) - rat

C/Species: Rattus norvegicus (Norway rat)

C/Date: 21-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S10678

R./Ibe, T.; Takada, K.; Ohkawa, K.; Matsuda, M.

Biochem. J. 269, 25-29, 1990

A/Title: Purification and characterization of a rat brain aldehyde dehydrogenase able to

A/Reference number: S10678; MUID:90328980; PMID:2375753

A/Accession: S10678

A/Molecule type: protein

A/Residues: 1-16 <ABB>

A/Cross-references: UNIPROT:Q7M053; UNIPARC:UPI000017C8AR

C/Keywords: oxidoreductase

Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 16;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPAPLY 17

DB 3 GZPTAVMY 10

RESULT 26

G85956

hypothetical protein 24331 [imported] - Escherichia coli (strain O157:H7, substrain EDL9

C/Species: Escherichia coli

C/Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 09-Jul-2004

C/Accession: G85956

R./Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaesner, J.D.; Rose, D.J.; Mayhew

iller, L.; Grobeck, B.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,

Nature 409, 529-533, 2001

A/Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.

A/Reference number: A85480; MUID:21074935; PMID:11206551

A/Accession: G85956

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-17 <STO>

A/Cross-references: UNIPROT:Q8X4A4; UNIPARC:UPI00000D081B; GB:AE005174; NID:G12517539; P

A/Experimental source: strain O157:H7, substrain EDL933

C/Genetics:

A/Gene: 24331

Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 17;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 YPSRLG 10

DB 7 PFGKXYG 13

RESULT 27

P00046

citrate (61)-synthase (EC 4.1.3.7) - Streptomyces hygroscopicus (fragment)

N/Alternate names: citrate condensing enzyme; citrogenase; condensing enzyme; oxaloaceta

C/Species: Streptomyces hygroscopicus

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004

C/Accession: P00046

R./Shimotohno, K.W.; Imai, S.; Murakami, T.; Seto, H.

Agric. Biol. Chem. 54, 463-470, 1990

A/Title: Purification and characterization of citrate synthase from Streptomyces hygrosc

A/Reference number: P00106; MUID:90334852; PMID:1366511

A/Accession: P00046

A/Molecule type: protein

A/Residues: 1-20 <SHI>

A/Cross-references: UNIPROT:P20903; UNIPARC:UPI0000127A2B

A/Experimental source: strain SF-1293

C/Comment: This enzyme catalyzes the synthesis of citric acid.

C/Keywords: carbon-carbon lyase; coenzyme A; oxo-acid-lyase; tricarboxylic acid cycle

Query Match

Best Local Similarity 20.2%; Score 23; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYKYP 5

DB 13 EYSYP 17

RESULT 28

S23369

T-cell receptor alpha chain J region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 22-Nov-1993 #sequence_revision 26-May-1995 #text_change 17-Mar-1999

C/Accession: S23369

R./Pluschke, G.; Ricken, G.; Taube, H.; Kroninger, S.; Melchers, I.; Peter, H.H.; Bichmai

Eur. J. Immunol. 21, 2749-2754, 1991

A/Title: Biased T cell receptor V(alpha) region repertoire in the synovial fluid of rhe

A/Reference number: S23364; MUID:92037820; PMID:1657615

A/Accession: S23369
 A/Status: preliminary; translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-14 <PIV>
 A/Cross-references: UNIPARC:UPI000017C390; EMBL:X58163
 C/Keywords: T-cell receptor

Query Match 19.7%; Score 22.5; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 3e+03;
 Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;

OY 3 EYPSRLGN 11
 |||
 Db 4 EYGSQ-GN 11

RESULT 29
 S04875
 nifs protein - Bradyrhizobium japonicum (fragment)
 C/Species: Bradyrhizobium japonicum
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: S04875
 R/Boeing, S.
 submitted to the EMBL Data Library, December 1988
 A/Reference number: S04873
 A/Accession: S04875
 A/Molecule type: DNA
 A/Residues: 1-11 <EBR>
 A/Cross-references: UNIPROT:P37030; UNIPARC:UPI000016E719; EMBL:X13691; NID:G39544; PIDN
 A/Genetics:
 A/Status: nifs
 A/Start codon: GTG

Query Match 19.3%; Score 22; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 2.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 13 KAPLY 17
 |||
 Db 5 KAPLY 9

RESULT 30
 I54081
 retinoic acid receptor alpha, exon 3 (mistranslated) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 09-Jul-2004
 C/Accession: I54081
 R/Dong, S.; Geng, J.P.; Tong, J.H.; Wu, Y.; Cai, J.R.; Sun, G.L.; Chen, S.R.; Wang, Z.Y.
 Genes Chromosomes Cancer 6:133-139, 1993
 A/Title: Breakpoint clusters of the PML gene in acute promyelocytic leukemia: primary st
 A/Reference number: I54081; MUID:93222087; PMID:7682097
 A/Accession: I54081
 A/Status: translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-11 <DON>
 A/Cross-references: UNIPROT:Q1597; UNIPARC:UPI00006E517; GB:S57794; NID:G299073; PIDN:
 A/Note: the translation is from an incorrect reading frame
 C/Genetics:
 A/Genes: GDB:RARA
 A/Cross-references: GDB:I20337; OMIM:180240
 A/Map position: 17q12-17q12

Query Match 19.3%; Score 22; DB 4; Length 11;
 Best Local Similarity 50.0%; Pred. No. 2.8e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 PKAPLYR 19
 |||
 Db 4 PRAAVLR 11

RESULT 31

S21238

hydrogensulfite reductase (EC 1.8.99.3) beta chain - Desulfovibrio vulgaris (fragment)
 N/Alternate names: Bisulfite reductase; desulfotubercidin; desulfotubidin; desulfovibridi
 C/Species: Desulfovibrio vulgaris
 C/Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C/Accession: S21238
 R/Pierik, A.J.; Duyvis, M.G.; van Helvoort, J.M.L.M.; Wolbert, R.B.G.; Hagen, W.R.
 Eur. J. Biochem. 205:111-115, 1992
 A/Title: The third subunit of desulfovibridin-type dissimilatory sulfite reductases.
 A/Reference number: S21197; MUID:92209491; PMID:1555572
 A/Accession: S21238
 A/Molecule type: protein
 A/Residues: 1-15 <PIR>
 A/Cross-references: UNIPARC:UPI000017AB71
 A/Experimental source: strain Hildenborough
 C/Genetics:
 A/Genes: dsyB
 C/Complex: heterohexamer; two alpha, two beta and two gamma chains
 C/Function:
 A/Description: catalyzes the six-electron reduction of sulfite to sulfide
 A/Pathway: the terminal oxidase in the sulfate-reduction pathway
 C/Keywords: heterohexamer; oxidoreductase

Query Match 19.3%; Score 22; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.9e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 11 NPRAPL 16
 |||
 Db 8 NPKEPM 13

RESULT 32
 S58660
 H+-transporting two-sector ATPase (EC 3.6.3.14) chain c - mouse (fragments)
 C/Species: Mus musculus (house mouse)
 C/Date: 15-Feb-1996 #sequence_revision 01-Mar-1996 #text_change 03-Jun-2002
 C/Accession: S58660
 R/Katz, M.L.; Gao, C.L.; Tompkins, J.A.; Bronson, R.T.; Chin, D.T.
 Biochem. J. 310:887-892, 1995
 A/Title: Mitochondrial ATP synthase subunit c stored in hereditary ceroid-lipofusinosi
 A/Reference number: S58658; MUID:96033188; PMID:7575423
 A/Accession: S58660
 A/Molecule type: protein
 A/Residues: 1-10;11-17 <KAT>
 A/Cross-references: UNIPARC:UPI0000172E45; UNIPARC:UPI000017CD8E
 C/Genetics:
 A/Genome: nuclear
 C/Keywords: hydrolase; mitochondrion

Query Match 19.3%; Score 22; DB 2; Length 17;
 Best Local Similarity 33.3%; Pred. No. 4.4e+03;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

OY 1 DYEPGRLGNP 12
 |||
 Db 1 DIDTAKRFGNP 12

RESULT 33
 A58589
 alpha-conotoxin EI - cone shell (Conus ermineus)
 C/Species: Conus ermineus (ermine cone)
 C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C/Accession: A58589
 R/Martinez, J.S.; Olivera, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;
 Biochemistry 34:14519-14526, 1995
 A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with nov
 A/Reference number: A58589; MUID:96062516; PMID:7578057
 A/Accession: A58589
 A/Molecule type: protein
 A/Residues: 1-18 <MAR>
 A/Cross-references: UNIPROT:P50982; UNIPARC:UPI00001287C0

A/Note: sequence confirmed by chemical synthesis
 C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
 C/Superfamily: alpha-conotoxin
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pos
 F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
 F/4-10/5-18/disulfide bonds: #status experimental
 F/18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 19.3%; Score 22; DB 1; Length 18;
 Best Local Similarity 30.0%; Pred. No. 4.7e+03;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 4 YPGSRLGNPK 13
 :|:|:|:
 Db 7 HPRGNMNSPQ 16

RESULT 34

556715
 hydroxymethylglutaryl-CoA reductase (NADPH2) (EC 1.1.1.34) (clone hmg3.2) - potato (frag
 C/Species: Solanum tuberosum (potato)
 C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S56715
 R/Bhattacharya, M.K.; Patya, N.L.; Dixon, R.A.; Korth, K.L.; Sterner, B.A.
 Plant Mol. Biol. 28, 1-15, 1995
 A/Title: Features of the hmg 1 subfamily of genes encoding HMG-CoA reductase in potato.
 A/Reference number: 556710; MUID:95306778; PMID:7787174
 A/Accession: S56715
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-18 <BNA>
 A/Cross-references: UNIPROT:Q41458; UNIPARC:UPI00000428D5; EMBL:L34830; NID:G529524; PID
 C/Keywords: coenzyme A; oxidoreductase

Query Match 19.3%; Score 22; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLY 17
 :|:|:|:
 Db 7 PVKPLY 12

RESULT 35

A29558
 pigment-dispersing hormone - eastern lubber grasshopper
 C/Species: Romalea guttata (eastern lubber grasshopper)
 C/Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 09-Jul-2004
 C/Accession: A29558
 R/Rao, K.R.; Mohr, C.J.; Riehm, J.P.; Zahnow, C.A.; Norton, S.; Johnson, L.; Tarr, C
 J. Biol. Chem. 262, 2672-2675, 1987
 A/Title: Primary structure of an analog of crustacean pigment-dispersing hormone from th
 A/Reference number: A29558; MUID:87137516; PMID:3818616
 A/Accession: A29558
 A/Molecule type: protein
 A/Residues: 1-18 <RAO>
 A/Cross-references: UNIPROT:P09929; UNIPARC:UPI000017BE28

Query Match 19.3%; Score 22; DB 2; Length 18;
 Best Local Similarity 54.5%; Pred. No. 4.7e+03;
 Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYPSRLGNPK 13
 :|:|:|:
 Db 3 EITNSLGLPK 13

RESULT 36

G61491
 seed protein ws-25 - winged bean (fragment)
 C/Species: Psophocarpus tetragonolobus (winged bean)
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: G61491
 R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-dim
 A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: G61491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <HIR>

A/Cross-references: UNIPROT:Q7M1P6; UNIPARC:UPI00001763B6

C/Superfamily: Plant Kunitz-type proteinase inhibitor

C/Keywords: glycoprotein; seed

Query Match 19.3%; Score 22; DB 2; Length 20;
 Best Local Similarity 40.0%; Pred. No. 5.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 2 YEPGSRGN 11
 :|:|:|:
 Db 6 YDADGNKLVN 15

RESULT 37

A49142
 hyaluronidase (EC 3.2.1.-) - stonefish (fragment)
 C/Species: Synanceia horrida (stonefish)
 C/Date: 19-Dec-1993 #sequence_revision 11-Apr-1997 #text_change 20-Jun-2000
 C/Accession: A49142
 R/Poh, C.H.; Yuen, R.; Chung, M.C.; Khoo, H.E.
 Comp. Biochem. Physiol. B 101, 159-163, 1992
 A/Title: Purification and partial characterization of hyaluronidase from stonefish (Syna
 A/Reference number: A49142; MUID:92362165; PMID:1499262
 A/Accession: A49142
 A/Molecule type: protein
 A/Residues: 1-20 <POH>
 A/Cross-references: UNIPARC:UPI000017BF6B
 A/Note: sequence extracted from NCBI Backbone (NCBI:111141)
 C/Comment: This venom protein is produced by venom glands attached to the spines of the
 C/Keywords: glycoprotein; glycosidase; hydrolase; venom

Query Match 19.3%; Score 22; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 5.2e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRGNPKA 14
 :|:|:|:
 Db 2 PSXDEGNKKA 11

RESULT 38

A34859
 heliothermine - Mexican beaded lizard (fragment)
 C/Species: Heloderma horridum (Mexican beaded lizard)
 C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
 C/Accession: A34859
 R/Mochca-Morales, J.; Martin, B.M.; Possant, L.D.
 Toxicon 28, 299-309, 1990
 A/Title: Isolation and characterization of heliothermine, a novel toxin from Heloderma h
 A/Reference number: A34859; MUID:90260878; PMID:1695019
 A/Accession: A34859
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <MOC>
 A/Cross-references: UNIPROT:Q91055; UNIPARC:UPI000017BF68

Query Match 19.3%; Score 22; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 5.2e+03;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRGNPK 12
 :|:|:|:
 Db 7 PSLMTSNP 14

RESULT 39

XASNPC

angiotensin-converting enzyme inhibitor - aspic viper

C/Species: Vipera aspis (aspic viper)

C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004

C/Accession: A60377

R/Komori, Y.; Sugihara, H.

Int. J. Biochem. 22, 767-771, 1990

A/Title: Characterization of a new inhibitor for angiotensin converting enzyme from the

A/Reference number: A60377; MUID:90382616; PMID:2169439

A/Accession: A60377

A/Molecule type: protein

A/Cross-references: UNIPROT:P13351; UNIPARC:UPI0000126497

C/Superfamily: bradykinin-potentiating peptide

C/Keyword: angiotensin-converting enzyme inhibitor; pyroglutamic acid

P/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match

Best Local Similarity 18.4%; Score 21.5; DB 1; Length 10;

Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 4 YPSRLGNPKAP 15

Db 3 WPG-----PKVP 9

RESULT 40

I33098

173K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C/Species: Plasmodium falciparum

C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000

C/Accession: I33098

R/Michols, J.H.; Hager, L.P.

Submitted to the Protein Sequence Database, May 1990

A/Reference number: A33098

A/Accession: I33098

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-11 <NIC>

A/Cross-references: UNIPARC:UPI0000178581

Query Match

Best Local Similarity 18.4%; Score 21; DB 2; Length 11;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPLY 17

Db 4 PRLPLP 9

RESULT 41

B87D

bombesin - fire-bellied toad

C/Species: Bombina bombina (fire-bellied toad)

C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 31-Dec-2004

C/Accession: A01564

R/Anaetani, A.; Bräpamer, V.; Buccì, M.

Arch. Biochem. Biophys. 148, 443-446, 1972

A/Title: Isolation and amino acid sequences of alysesin and bombesin, two analogous acti

A/Reference number: A01564; MUID:72163516; PMID:4557042

A/Accession: A01564

A/Molecule type: protein

A/Residues: 1-14 <ANA>

A/Cross-references: UNIPROT:P01296; UNIPARC:UPI0000173523

C/Keywords: amidated carboxyl end; cutaneous gland; hormone; neuropeptide; pyroglutamic

P/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

P/14/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 18.4%; Score 21; DB 1; Length 14;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RLGN 11

Db 3 RLGN 6

RESULT 42

PH1322

Ig heavy chain DJ region (clone C344-99) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1322

R/Wasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lym

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1322

A/Molecule type: DNA

A/Residues: 1-14 <MAS>

A/Cross-references: UNIPARC:UPI000017C23C

C/Keywords: heterotrimer; immunoglobulin

Query Match

Best Local Similarity 18.4%; Score 21; DB 2; Length 14;

Matches 5; Conservative 2; Mismatches 2; Indels 2; Gaps 1;

QY 2 YRPSRLGNP 12

Db 6 WDYWGQ--GNP 14

RESULT 43

PN0666

dystrophin-associated glycoprotein A3a-V - rabbit (fragment)

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C/Accession: PN0666

R/Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A/Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A/Reference number: PN0662; MUID:94156881; PMID:8113213

A/Accession: PN0666

A/Molecule type: protein

A/Residues: 1-14 <YOS>

A/Cross-references: UNIPARC:UPI000017C5C5

C/Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

C/Keywords: glycoprotein; skeletal muscle

Query Match

Best Local Similarity 18.4%; Score 21; DB 2; Length 14;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLY 17

Db 9 PKAPPY 14

RESULT 44

PQ0195

Sf11-glycoprotein - Persian tobacco (fragment)

N/Alternate names: Sf1-glycoprotein

C/Species: Nicotiana glauca (Persian tobacco)

C/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 31-Dec-2004

C/Accession: PQ0195; PQ0173

R/Mau, S.L.; Williams, E.G.; Atkinson, A.; Anderson, M.A.; Cornish, E.C.; Grego, B.; Shi

Planta 169, 184-191, 1986

A/Title: Style proteins of a wild tomato (Lycopersicon peruvianum) associated with expr

A/Reference number: PQ0192

A/Accession: PQ0195

A/Molecule type: protein

A/Residues: 1-15 <MAU>

A/Cross-references: UNIPROT:Q9S8X0; UNIPARC:UPI000009FDA3

A/Experimental source: style

R./Jahnen, W.; Batterham, M.P.; Clarke, A.E.; Moritz, R.L.; Simpson, R.

Plant Cell 1, 493-499, 1989

A:Title: Identification, isolation, and N-terminal sequencing of style glycoproteins and
A:Reference number: P00173; PMID:92404717; PMID:2535548

A:Accession: P00173

A:Molecule type: protein

A:Residues: 1-15 <JAH>

A:Cross-references: UNIPARC:UPI00009PDA3

A:Experimental source: style

C:Comment: This protein is involved in self-incompatibility of flowering plants.

C:Superfamily: RNases

C:Keywords: glycoprotein

Query Match 18.4%; Score 21; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 5.5e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEX 4

DB 1 DPEY 4

RESULT 45

S29485

GTP-binding protein o-ral - Pacific electric ray (fragment)

C:Species: Torpedo californica (Pacific electric ray)

C:Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997

C:Accession: S29485

R./Volkmant, W.; Eiferink, L.A.; Scheller, R.H.

FEBS Lett. 317, 53-56, 1993

A:Title: Association of three small GTP-binding proteins with cholinergic synaptic vesic

A:Reference number: S29485; PMID:93154521; PMID:8428634

A:Accession: S29485

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-15 <VOL>

A:Cross-references: UNIPARC:UPI000017BP33

Query Match 18.4%; Score 21; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 5.5e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEPGS 7

DB 8 DYEPGA 14

RESULT 46

S51735

T-cell receptor beta-chain joining region - human (fragment)

C:Species: Homo sapiens (man)

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 05-Nov-1999

C:Accession: S51735

R./Burinovic-Bello, I.; Steinle, A.; Ziegler, A.G.; Schendel, D.J.

submitted to the EMBL Data Library, November 1993

A:Reference number: S51732

A:Accession: S51735

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-15 <DOR>

A:Cross-references: UNIPARC:UPI00001165DF; EMBL:Z28344; NID:G607122; PIDN:CAA82198.1; PI

C:Keywords: T-cell receptor

Query Match 18.4%; Score 21; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 5.5e+03;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RLGN 11

DB 7 RLGN 10

RESULT 47

I53284

T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C:Accession: I53284

R./Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A:Title: Evolutionarily conserved organization and sequences of germline diversity and J

A:Reference number: A53284; PMID:91342695; PMID:1678859

A:Accession: I53284

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-15 <HAR>

A:Cross-references: UNIPARC:UPI0000115418; GB:S60737; NID:9233916; PIDN:AA319525.1; PID

A:Note: sequence extracted from NCBI backbone (NCBIN:60737, NCBIIP:60747)

C:Keywords: T-cell receptor

Query Match 18.4%; Score 21; DB 2; Length 15;

Best Local Similarity 50.0%; Pred. No. 5.5e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEPGSR 9

DB 5 YEPGRKL 12

RESULT 48

PT0091

H+-transporting two-sector ATPase (EC 3.6.3.14) alpha chain - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 03-Jun-2002

C:Accession: PT0091

R./Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, July 1998

A:Description: Proteome analysis of mouse brain.

A:Reference number: PT0091

A:Accession: PT0091

A:Molecule type: protein

A:Residues: 1-15 <KAW>

A:Cross-references: UNIPARC:UPI000017CD8D

A:Experimental source: brain, striatum

C:Keywords: hydrolase

Query Match 18.4%; Score 21; DB 2; Length 15;

Best Local Similarity 75.0%; Pred. No. 5.5e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPGS 7

DB 9 YPGN 12

RESULT 49

PH1580

Ig H chain V-D-J region (wild-type clone 3) - mouse (fragment)

C:Species: Mus musculus (house mouse)

C:Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C:Accession: PH1580

R./Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A:Title: Molecular characterization of transgene-induced immunodeficiency in B-1ess m/cr

A:Reference number: PH1580; PMID:93301609; PMID:8315387

A:Accession: PH1580

A:Molecule type: DNA

A:Residues: 1-16 <LEV>

A:Cross-references: UNIPARC:UPI000017CGB8

A:Experimental source: bone marrow pre-B lymphocyte

C:Keywords: immunoglobulin

Query Match 18.4%; Score 21; DB 2; Length 16;

Best Local Similarity 45.5%; Pred. No. 5.9e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 SRLGNPKAPLV 17
: ||| : |||
Db 2 ARLGADARAFY 12

RESULT 50

T-cell receptor delta chain V region (105.23) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997
C/Accession: H35141
R/Sim, G.R.; Augustin, A.
Cell 61, 397-405, 1990
A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell recep
A/Reference number: A35141; MUID:90242386; PMID:2110506
A/Accession: H35141
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-16 <SIM>
A/Cross-references: UNIPARC:UPI000017C859
C/Keywords: T-cell receptor

Query Match 18.4%; Score 21; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 5.9e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15
: ||| : |||
Db 4 GYLGGIRAP 13

RESULT 51

MELANO
melanotropin beta - horse
C/Species: Equus caballus (domestic horse)
C/Date: 13-Jul-1981 #sequence_revision 13-Jul-1981 #text_change 09-Jul-2004
C/Accession: A01467
R/Dixon, J.S.; Li, C.H.
Gen. Comp. Endocrinol. 1, 161-169, 1961
A/Title: The isolation and structure of beta-melanocyte-stimulating hormone from horse
A/Reference number: A01467
A/Accession: A01467
A/Molecule type: protein
A/Residues: 1-18 <DIK>
A/Cross-references: UNIPROT:P01202; UNIPARC:UPI000012P1C0
C/Keywords: corticotropin-11pocropin

Query Match 18.4%; Score 21; DB 1; Length 18;
Best Local Similarity 33.3%; Pred. No. 6.7e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 YEPYGSRLGNPK 13
: ||| : |||
Db 5 YKMEHFRWGSPPR 16

RESULT 52

DRUPD
pigment-dispersing hormone - Atlantic sand fiddler crab
N/Alternate names: PDH
C/Species: Uca pugnator (Atlantic sand fiddler crab)
C/Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C/Accession: A25144
R/Nao, K.R.; Riehm, J.P.; Zahnow, C.A.; Kleinholz, L.H.; Tarr, G.E.; Johnson, L.; Norton
Proc. Natl. Acad. Sci. U.S.A. 82, 5319-5322, 1985
A/Title: Characterization of a pigment-dispersing hormone in eyestalks of the fiddler cr
A/Reference number: A25144
A/Accession: A25144
A/Molecule type: protein
A/Residues: 1-18 <RAO>
A/Cross-references: UNIPROT:P08871; UNIPARC:UPI000012989A
C/Superfamily: pigment-dispersing hormone

C/Keywords: amidated carboxyl end; neuropeptide
F18/Modified site: amidated carboxyl end (ala) #status experimental

Query Match 18.4%; Score 21; DB 1; Length 18;
Best Local Similarity 54.5%; Pred. No. 6.7e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYPGSRGNPK 13
: ||| : |||
Db 3 ELINSLGLPK 13

RESULT 53

A45590
beta-pigment-dispersing hormone analog - red swamp crayfish
C/Species: Procambarus clarkii (red swamp crayfish)
C/Date: 22-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: A45590
R/McCallum, M.L.; Rao, K.R.; Riehm, J.P.; Mohrheer, C.J.; Morgan, W.T.
Pigment Cell Res. 4, 201-208, 1991
A/Title: Primary structure and relative potency of an analog of beta-PDH (pigment-dispe
A/Reference number: A45590; MUID:92390305; PMID:1823925
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: nucleic acid
A/Residues: 1-18 <MC>
A/Cross-references: UNIPROT:Q9TWM7; UNIPARC:UPI000007D639
A/Experimental source: eyestalk
A/Note: sequence extracted from NCBI backbone (NCBIP:112439)

Query Match 18.4%; Score 21; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 6.7e+03;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 3 EYPGSRGNPK 13
: ||| : |||
Db 3 ELINSLGLPK 13

RESULT 54

PH1609
Ig H chain V-D-J region (wild-type clone 336) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1609
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mic
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1609
A/Molecule type: DNA
A/Residues: 1-19 <LEV>
A/Cross-references: UNIPARC:UPI000017C6C3
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 18.4%; Score 21; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 7.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEPYGS 7
: ||| : |||
Db 6 YYDGGS 11

RESULT 55

S72501
protein kinase C inhibitor - human (fragment)
N/Alternate names: histidine triad nucleotide-binding protein
C/Species: Homo sapiens (man)
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C/Accession: S72501; S62623
R/Maines, M.D.; Trakshel, G.M.

Arch. Biochem. Biophys. 300, 320-326, 1993
A>Title: Purification and characterization of human hlliverdin reductase.
A'Reference number: S29736; MUID:93143333; PMID:8424666
A'Accession: S72501
A:Molecule type: protein
A:Residues: 1-20 <MAI>
A'Cross-references: UNIPARC:UPI00001756B0
A'Note: this protein was identified as hlliverdin reductase; the identification is quest
R'Maines, M.D.; Poliovoda, B.V.; Huang, T.J.; McCoubrey Jr., W.K.
Eur. J. Biochem. 235, 372-381, 1996
A>Title: Human hlliverdin IX-alpha reductase is a zinc-metalloprotein. Characterization
A'Reference number: S62622; MUID:96202961; PMID:8631357
A'Accession: S62623
A:Molecule type: protein
A:Residues: 1-20 <MAW>
A'Cross-references: UNIPARC:UPI00001756B0
C'Superfamily: histidine triad hydrolase; histidine triad homology
C'Keywords: homodimer; protein kinase inhibitor; zinc

Query Match 18.4%; Score 21; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.5e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPKAPLY 17
:|:|:|:
DB 8 SPQAPTH 14

RESULT 56
S19240
histone H2B (clone pCH1.0BR) - chicken (fragment)
C'Species: Gallus gallus (chicken)
C'Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
C'Accession: I50648; S19240
R'Sturm, R.A.; Dalton, S.; Wells, J.R.
Nucleic Acids Res. 16, 8571-8586, 1988
A>Title: Conservation of histone H2A/H2B intergene regions: a role for the H2B specific
A'Reference number: I50647; MUID:88355608; PMID:3267232
A'Accession: I50648
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-20 <ST2>
A'Cross-references: UNIPROT:Q90859; UNIPARC:UPI00000FD2CA; EMBL:X07765; NID:963429; PIDN
C'Superfamily: histone H2B
C'Keywords: chromosomal protein; nucleosome core

Query Match 18.4%; Score 21; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 7.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNPKA 14
|:|:|:|:
DB 9 PAKKGSKKA 18

RESULT 57
B53592
H+-exporting ATPase (EC 3.6.3.6) 38k chain - Thermus aquaticus (fragment)
C'Species: Thermus aquaticus
C'Date: 01-Dec-1995 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C'Accession: B53592
R.Yokoyama, K.; Akabane, Y.; Ishii, N.; Yoshida, M.
J. Biol. Chem. 269, 12248-12253, 1994
A>Title: Isolation of prokaryotic V-0V-1-ATPase from a thermophilic eubacterium Thermus
A'Reference number: A53592; MUID:94216345; PMID:8163530
A'Accession: B53592
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <YOK>
A'Cross-references: UNIPROT:Q7M195; UNIPARC:UPI000017CD81
C'Keywords: hydrolase

Query Match 18.4%; Score 21; DB 2; Length 20;

Best Local Similarity 27.8%; Pred. No. 7.5e+03;
Matches 5; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 DYEPGSRGNPKAPLYK 18
|:|:|:|:
DB 3 DFAYLNARVRVRGTLTK 20

RESULT 58
PH0756
T-cell receptor beta chain (17) - mouse (fragment)
C'Species: Mus musculus (house mouse)
C'Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C'Accession: PH0756
R.Casanova, J.L.; Romero, P.; Widmann, C.; Kourilesky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A>Title: T cell receptor genes in a series of class I major histocompatibility complex-r
allelic exclusion and antigen-specific repertoire.
A'Reference number: PH0746; MUID:92078846; PMID:1836010
A'Accession: PH0756
A:Molecule type: mRNA
A:Residues: 1-13 <CAS>
A'Cross-references: UNIPARC:UPI0000115FB0; EMBL:X60850; NID:951482; PIDN:CAA43241.1; PID
A'Experimental source: T lymphocyte
C'Keywords: T-cell receptor

Query Match 18.0%; Score 20.5; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 5.7e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 10 GNPKAPLYKRP 20
|:|:|:|:
DB 6 GN-QAPLF 12

RESULT 59
B59326
ribosomal protein S8, mitochondrial [imported] - bovine (fragment)
C'Species: Bos primigenius taurus (cattle)
C'Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 31-Dec-2001
C'Accession: B59326
R.O'Brien, T.
submitted to the Protein Sequence Database, July 2000
A'Description: Mammalian mitochondrial ribosomal proteins (3): Identification of novel p
A'Reference number: A59326
A'Accession: B59326
A>Status: preliminary
A:Molecule type: protein
A:Residues: 1-20 <OBR>
A'Cross-references: UNIPARC:UPI000017CBBF
A'Note: amino terminal of the mature form
C'Keywords: mitochondrion; protein biosynthesis; ribosome

Query Match 18.0%; Score 20.5; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 9e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 3; Gaps 1;

QY 10 GNPKAPLYKRP 20
|:|:|:|:
DB 7 GSPK--IKKP 14

RESULT 60
PT0240
Ig heavy chain CRD3 region (clone 2-100B) - human (fragment)
C'Species: Homo sapiens (man)
C'Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C'Accession: PT0240
R.Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A>Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A'Reference number: PT0222; MUID:91108337; PMID:1899102
A'Accession: PT0240

A/Molecule type: DNA
A/Residues: 1-4 <YAM>
A/Cross-references: UNIPARC:UPI000017C1E2
A/Experimental source: B lymphocyte
C/Keywords: heterotrimer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 4;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6
|||
DB 1 YPG 3

RESULT 61
A38081
amine oxidase (copper-containing) (EC 1.4.3.6) - yeast (*Pichia angusta*) (fragment)
C/Species: *Pichia angusta*
C/Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 20-Apr-2000
C/Accession: A38081
R/Mu, D.; Jones, S.M.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Kliman, J.P.
J. Biol. Chem. 267, 7979-7982, 1992
A/Title: Tyrosine codon corresponds to topa quinone at the active site of copper amine
A/Reference number: A38081; MUID:92235001; PMID:1569055
A/Accession: A38081
A/Molecule type: protein
A/Residues: 1-7 <MDA>
A/Cross-references: UNIPARC:UPI000017CA48
C/Species: copper; oxidoreductase; quinoprotein; topaquinone
C/Keywords: copper; oxidoreductase; quinoprotein; topaquinone
P/1/Modified site: topaquinone (Tyr) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 7;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DYEX 4
|||
DB 3 NYEX 6

RESULT 62
A41117
acetylcholinesterase (EC 3.1.1.7), venom - Asian cobra (fragment)
C/Species: *Naja naja oxiana* (Asian cobra, Oxus cobra)
C/Date: 27-Mar-1992 #sequence_revision 27-Mar-1992 #text_change 09-Jul-2004
C/Accession: A41117
R/Kreienkamp, H.J.; Weise, C.; Rada, R.; Aavikaar, A.; Hucho, F.
Proc. Natl. Acad. Sci. U.S.A. 88, 6117-6121, 1991
A/Title: Antonic subites of the catalytic center of acetylcholinesterase from Torpedo
A/Reference number: A41117; MUID:91296772; PMID:2068091
A/Accession: A41117
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-8 <KRR>
A/Cross-references: UNIPROT:Q7LZ27; UNIPARC:UPI000017BFC2
C/Keywords: carboxylic ester hydrolase

Query Match 17.5%; Score 20; DB 2; Length 8;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRKMP 12
|||
DB 1 GSRMNP 7

RESULT 63
A61126
gonadoliberin - spotted ratfish
N/Alternate names: gonadotropin-releasing hormone
C/Species: *Hydrolagus colliei* (spotted ratfish)
C/Date: 26-May-1994 #sequence_revision 26-May-1994 #text_change 09-Jul-2004

C/Accession: A61126
R/Lovejoy, D.A.; Sherwood, N.M.; Fischer, W.H.; Jackson, B.C.; Rivier, J.E.; Lee, T.
Gen. Comp. Endocrinol. 82, 152-161, 1991
A/Title: Primary structure of gonadotropin-releasing hormone from the brain of a holocoe
A/Reference number: A61126; MUID:91340067; PMID:1678723
A/Accession: A61126

A/Molecule type: protein
A/Residues: 1-10 <LOV>
A/Cross-references: UNIPROT:P37043; UNIPARC:UPI000012B8F8
A/Experimental source: brain
C/Superfamily: gonadoliberin
C/Keywords: amidated carboxyl end; brain; hormone; pyroglutamic acid
P/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
P/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 17.5%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6
|||
DB 8 YPG 10

RESULT 64
BHA02
gonadoliberin II - American alligator
N/Alternate names: gonadotropin-releasing hormone II
C/Species: Alligator mississippiensis (American alligator)
C/Date: 31-Mar-1993 #sequence_revision 31-Mar-1993 #text_change 09-Jul-2004
C/Accession: B60066
R/Lovejoy, D.A.; Fischer, W.H.; Parker, D.B.; McRory, J.E.; Park, M.; Lance, V.; Swanson
Regul. Pept. 33, 105-116, 1991
A/Title: Primary structure of two forms of gonadotropin-releasing hormone from brains o
A/Reference number: A60066; MUID:91352338; PMID:1882082
A/Accession: B60066
A/Molecule type: protein
A/Residues: 1-10 <LOV>
A/Cross-references: UNIPROT:P37043; UNIPARC:UPI000012B8F8
C/Superfamily: gonadoliberin
C/Keywords: amidated carboxyl end; hormone; hypothalamus; pyroglutamic acid
P/1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental
P/10/Modified site: amidated carboxyl end (Gly) #status experimental

Query Match 17.5%; Score 20; DB 1; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6
|||
DB 8 YPG 10

RESULT 65
S24190
trypsin (EC 3.4.21.59) - bovine (fragment)
C/Species: *Bos primigenius taurus* (cattle)
C/Date: 19-Mar-1997 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
C/Accession: S24190
R/Piorucci, L.; Brba, F.; Ascoli, F.
Biol. Chem. Hoppe-Seyler 373, 483-490, 1992
A/Title: Bovine trypsin: purification and characterization.
A/Reference number: S24190; MUID:92384956; PMID:1515079
A/Accession: S24190
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <PRO>
A/Cross-references: UNIPROT:Q8HYJ2; UNIPARC:UPI0000175C26
C/Superfamily: trypsin; trypsin homology
C/Keywords: hydrolase; serine proteinase; zymogen

Query Match 17.5%; Score 20; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 5.1e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYRGS 7
|||
Db 6 EAPGS 10

RESULT 66
B46030

gonadoliberin II - spiny dogfish

NAlternate names: gonadotropin-releasing hormone

C:Species: Squalus acanthias (spiny dogfish)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C:Accession: B46030

R:Lovejoy, D.A.; Fischer, W.H.; Ngamwongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter, R.

Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A:Title: Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain pro

A:Reference number: A46030; MUID:92335300; PMID:1631133

A:Accession: B46030

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-10 <LOV>

A:Cross-references: UNIPROT:P37043; UNIPARC:UPI000012B8F8

C:Superfamily: gonadoliberin

C:Keywords: hormone; pyroglutamic acid

F:1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6
|||
Db 8 YPG 10

RESULT 67
E41476

probable antigen 5 - Mycobacterium leprae (fragment)

C:Species: Mycobacterium leprae

C:Date: 10-Apr-1992 #sequence_revision 10-Apr-1992 #text_change 18-Jun-1993

C:Accession: E41476

R:Hartsekerl, R.A.; van Rens, R.M.; Stabel, L.F.B.M.; de Wit, M.Y.L.; Klatter, P.R.

Infect. Immun. 58, 2821-2827, 1990

A:Title: Selection and characterization of recombinant clones that produce Mycobacterium

A:Reference number: A41476; MUID:90354041; PMID:1696331

A:Accession: E41476

A:Status: preliminary; not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-11 <HAR>

A:Cross-references: UNIPARC:UPI000017AD58

Query Match 17.5%; Score 20; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 5.7e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 6 GSRLGNPKAP 15
|||
Db 1 GSOLPRVGAP 10

RESULT 68
S07207

Crinia-angiotensin, skin - frog (Crinia georgiana)

C:Species: Crinia georgiana

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 16-Aug-2004

C:Accession: S07207

R:Brigamer, V.; Melchiorri, P.; Nakajima, T.; Yasuhara, T.; Endean, R.

Experientia 35, 1133-1133, 1979

A:Title: Amino acid composition and sequence of crinia-angiotensin, an angiotensin II-1

A:Reference number: S07207; MUID:80024575; PMID:488254

A:Accession: S07207

A:Molecule type: protein

A:Residues: 1-11 <ERS>
A:Cross-references: UNIPROT:P09037; UNIPARC:UPI000003525C

Query Match 17.5%; Score 20; DB 2; Length 11;
Best Local Similarity 60.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRL 9
|||
Db 2 PGDRI 6

RESULT 69
S74196

3-hydroxy-3-methylglutaryl CoA synthase homolog - bovine (fragment)

C:Species: Bos priagenius taurus (cattle)

C:Date: 14-Apr-1998 #sequence_revision 24-Apr-1998 #text_change 01-May-1998

C:Accession: S74196

R:Takeuchi, S.; Yoshinaga, T.; Furukawa, T.; Kohno, H.; Tokunaga, R.; Mishimura, K.; Ino

Eur. J. Biochem. 230, 760-765, 1995

A:Title: Induction of terminal enzymes for heme biosynthesis during differentiation of m

A:Reference number: S65629; MUID:9533315; PMID:7607249

A:Accession: S74196

A:Molecule type: protein

A:Residues: 1-12 <YAK>

A:Cross-references: UNIPARC:UPI000017C48E

A:Experimental source: liver

Query Match 17.5%; Score 20; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.2e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYK 18
|||
Db 4 PAVPLAK 10

RESULT 70
PNO663

dystrophin-associated glycoprotein A3a-II - rabbit (fragment)

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 07-May-1999

C:Accession: PNO663

R:Yoshida, M.; Mizuno, Y.; Nonaka, I.; Ozawa, E.

J. Biochem. 114, 634-639, 1993

A:Title: A dystrophin-associated glycoprotein, A3a (one of 43DAG doublets), is retained

A:Reference number: PNO662; MUID:94156881; PMID:8113213

A:Accession: PNO663

A:Molecule type: protein

A:Residues: 1-12 <YOS>

A:Cross-references: UNIPARC:UPI000017C5C2

C:Comment: This protein is retained in Duchenne type muscular dystrophy muscle.

Query Match 17.5%; Score 20; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 6.2e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 KAPL 16
|||
Db 1 KAPL 4

RESULT 71
C20907

Ig kappa-1 chain v3 region - rabbit

C:Species: Oryctolagus cuniculus (domestic rabbit)

C:Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 16-Aug-1996

C:Accession: C20907

R:Morine, L.; Max, E.B.

Nucleic Acids Res. 11, 8877-8890, 1983

A:Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multip

A:Reference number: A20907; MUID:84169523; PMID:6324107

A/Accession: C20907
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-12 <EMO>
 A/Cross-references: UNIPARC:UPI000017C5CP
 C/Keywords: heterotrimer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGSRL 9
 DB 5 PGTKL 9

RESULT 72

A61503
 sterol carrier protein-2-like protein - chicken (fragment)
 C/Species: Gallus gallus (chicken)
 C/Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004
 C/Accession: A61503
 R/Reinart, M.P.; Avarit, S.J.; Foglia, T.
 Comp. Biochem. Physiol. B 100, 243-248, 1991
 A/Title: Purification, characterization and comparison with mammalian SCP-2 of a chicken
 A/Reference number: A61503; PMID:92191564; PMID:1799965
 A/Accession: A61503
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <RSI>
 A/Cross-references: UNIPROT:Q7LZ19; UNIPARC:UPI000017C037

Query Match 17.5%; Score 20; DB 2; Length 12;
 Best Local Similarity 42.9%; Pred. No. 6.2e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 KAPLYR 19
 DB 1 ZTPLYPK 7

RESULT 73

863492
 disulfoglucosyl sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm
 C/Species: Desulfovibrio desulfuricans
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C/Accession: 863492
 R/Staubert, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.
 Eur. J. Biochem. 233, 873-879, 1995
 A/Title: Molecular properties of the disulfoglucosyl sulfite reductase from Desulfovibrio
 A/Reference number: 863489; PMID:96085152; PMID:8521853
 A/Accession: 863492
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <STR>
 A/Cross-references: UNIPARC:UPI000017AB66

Query Match 17.5%; Score 20; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 NPKAPL 16
 DB 8 NPKXPM 13

RESULT 74

C53275
 Ig kappa-1 chain J3 segment b55 allotype - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-1996
 C/Accession: C53275
 R/Ayad, H.; Marche, P.N.; Cazenave, P.A.

Immunogenetics 34, 201-207, 1991
 A/Title: Evolution of the rabbit immunoglobulin kappa chain genes.
 A/Reference number: A53275; PMID:91372868; PMID:1909995

A/Accession: C53275
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-13 <AVA>
 A/Cross-references: UNIPARC:UPI000017C5D0
 A/Note: sequence extracted from NCBI backbone (NCBIN:56069, NCBI:P:56164)
 C/Comment: This J3 segment may not be functional because of substitutions in the 7 mer
 C/Keywords: heterotrimer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGSRL 9
 DB 5 PGTKL 9

RESULT 75

S33800
 chaperone, TCP1-related - oat
 C/Species: Avena sativa (oat)
 C/Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
 C/Accession: S33800
 R/Mummett, E.; Grimm, R.; Spehl, V.; Eckerskorn, C.; Schiltz, E.; Gatenby, A.A.; Schaeff
 Nature 363, 644-648, 1993
 A/Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its photo
 A/Reference number: S33800; PMID:93288140; PMID:8099715

A/Accession: S33800
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <MDM>
 A/Cross-references: UNIPROT:Q7M1G8; UNIPARC:UPI000017B0D5

Query Match 17.5%; Score 20; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6.8e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 10 GNPX 13
 DB 8 GNPS 11

RESULT 76

S60353
 amylopullulanase - Bacillus sp. (strain KSM-1378) (fragment)
 C/Species: Bacillus sp.
 A/Variety: strain KSM-1378
 C/Date: 24-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
 C/Accession: S60353
 R/Alra, K.; Saeki, K.; Igarashi, K.; Takaiwa, M.; Uemura, T.; Hagihara, H.; Kawai, S.; It
 Biochim. Biophys. Acta 1243, 315-324, 1995
 A/Title: Purification and characterization of an alkaline amylopullulanase with both al
 A/Reference number: S60353; PMID:95244580; PMID:7727505
 A/Accession: S60353
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <ARA>
 A/Cross-references: UNIPROT:P70983; UNIPARC:UPI000015219C
 C/Superfamily: pullulanase type debranching enzyme

Query Match 17.5%; Score 20; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 7.4e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 YKRP 20
 DB 11 YERP 14

RESULT 77
B60683
malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
C:Species: Panicum sp. (millet)
C:Date: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004
C:Accession: B60683
R:Murata, T.; Ikeda, J.; Takano, M.; Ohnagi, R.
Plant Cell Physiol. 30, 429-437, 1989
A:Title: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.
A:Reference number: A60683
A:Accession: B60683
A:Molecule type: protein
A:Residues: 1-14 <MUR>
A:Cross-references: UNIPROT:Q7MT9; UNIPARC:UPI000017B12P
C:Keywords: oxidoreductase; photosynthesis

Query Match 17.5%; Score 20; DB 2; Length 14;
Best Local Similarity 80.0%; Pred. No. 7.4e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 PKAPL 16
DB 6 PKAPL 10

RESULT 78
S24159
leukocyte elastase (EC 3.4.21.37) - sheep (fragment)
N:Alternate names: neutrophil elastase
C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C:Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C:Accession: S24159
R:Junger, W.G.; Hallstroem, S.; Liu, F.C.; Redl, H.; Schlag, G.
Biol. Chem. Hoppe-Seyler 373, 691-698, 1992
A:Title: The enzymatic and release characteristics of sheep neutrophil elastase: a comparison of the enzyme from sheep and human neutrophils
A:Reference number: S24159; PMID:93039751; PMID:1418684
A:Accession: S24159
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <JUN>
A:Cross-references: UNIPROT:Q9TRJ3; UNIPARC:UPI0000086FEA
C:Superfamily: trypsin; trypsin homology
C:Keywords: hydrolase; serine protease

Query Match 17.5%; Score 20; DB 2; Length 15;
Best Local Similarity 44.4%; Pred. No. 7.9e+03;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 GSRLGNPKA 14
DB 3 GGRARFPA 11

RESULT 79
S59492
formate dehydrogenase alpha chain - Alcaligenes eutrophus (fragment)
C:Species: Alcaligenes eutrophus
C:Date: 27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C:Accession: S59492
R:Friddlebold, J.; Meyer, F.; Bill, E.; Trautwein, A.X.; Bowlen, B.
Biol. Chem. Hoppe-Seyler 376, 561-568, 1995
A:Title: Structural and immunological studies on the soluble formate dehydrogenase from Alcaligenes eutrophus
A:Reference number: S59492; PMID:9615726; PMID:8651915
A:Accession: S59492
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <FRI>
A:Cross-references: UNIPROT:Q87815; UNIPARC:UPI000017AA0P
C:Superfamily: NAD-dependent formate dehydrogenase, alpha subunit

Query Match 17.5%; Score 20; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPAP 15
DB 10 GNPAP 15

RESULT 80
PA0002
photosystem II oxygen-evolving complex protein 3 - Arabidopsis thaliana (fragment)
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 18-Nov-1994 #sequence_revision 06-Jan-1995 #text_change 23-Mar-1995
C:Accession: PA0002
R:Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.
submitted to JIPID, July 1994
A:Description: Separation and characterization of Arabidopsis proteins by two-dimensional gel electrophoresis
A:Reference number: PA0001
A:Accession: PA0002
A:Molecule type: protein
A:Residues: 1-15 <KAM>
A:Cross-references: UNIPARC:UPI000017AFDB
A:Experimental source: stem
C:Keywords: photosynthesis; photosystem II

Query Match 17.5%; Score 20; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 7.9e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 LGNPKAP 15
DB 7 VGSPXP 13

RESULT 81
PL0143
carbon-monoxide dehydrogenase (EC 1.2.99.2) medium chain - Pseudomonas carboxydohydrogena
C:Species: Pseudomonas carboxydohydrogena
C:Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
C:Accession: PL0143
R:Kraut, M.; Hugendieck, I.; Herwig, S.; Meyer, O.
Arch. Microbiol. 152, 335-341, 1989
A:Title: Homology and distribution of CO dehydrogenase structural genes in carboxydohydrogena
A:Reference number: PL0138; PMID:90055678; PMID:2818128
A:Accession: PL0143
A:Molecule type: protein
A:Residues: 1-15 <KRA>
A:Cross-references: UNIPROT:P19917; UNIPARC:UPI0000128PDB
C:Comment: Carbon-monoxide dehydrogenase consists of three polypeptide chains: large, medium, and small
C:Keywords: oxidoreductase

Query Match 17.5%; Score 20; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 7.9e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DYEPGS 7
DB 8 DYHRPKS 14

RESULT 82
S36896
ribosomal protein S16 - Mycobacterium bovis (fragment)
C:Species: Mycobacterium bovis
C:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C:Accession: S36896
R:Ohara, N.; Kimura, M.; Higashi, Y.; Yamada, T.
FEBS Lett. 331, 9-14, 1993
A:Title: Isolation and amino acid sequence of the 30S ribosomal protein S19 from Mycobacterium bovis
A:Reference number: S36887; PMID:94009653; PMID:8405418
A:Accession: S36896
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-15 <OHA>
A:Cross-references: UNIPROT:Q9R544; UNIPARC:UPI0000087C39

C/Keywords: protein biosynthesis; ribosome

Query Match 17.5%; Score 20; DB 2; Length 15;

Best Local Similarity 44.4%; Pred. No. 7.9e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 SRLGNPAP 15
|:|:|:|:
DB 7 TRILAKINP 15

RESULT 83

S04586

NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 1 - common tobacco mitochondrion (fr

C/Species: mitochondrion Nicotiana tabacum (common tobacco)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: S04586

R/Brand, M.M.; Levings III, C.S.; Matzinger, D.F.

Mol. Gen. Genet. 204, 8-16, 1986

A/Title: The tobacco mitochondrial ATPase subunit 9 gene is closely linked to an open re

A/Reference number: S01427; MUID:86310310; PMID:2875379

A/Accession: S04586

A/Molecule type: DNA

A/Residues: 1-15 <BLA>

A/Cross-references: UNIPROT:Q35188; UNIPARC:UPI00000986C6; EMBL:X04019; NID:G13148; PIND

C/Genetics:

A/Genome: mitochondrion

C/Keywords: mitochondrion; NAD; oxidoreductase

Query Match 17.5%; Score 20; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 7.9e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 15 PLYKR 19
|:|:|:|:
DB 1 PLYSK 5

RESULT 84

B54877

alpha-conotoxin PnIB - cone shell (Conus pennaceus)

C/Species: Conus pennaceus

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: B54877

R/Painlifter, M.; Hasson, A.; Oren, R.; Burlingame, A.L.; Gordon, D.; Spira, M.B.; Zlock

Biochemistry 33, 9523-9529, 1994

A/Title: New mollusc-specific alpha-conotoxins block Aplysia neuronal acetylcholine rece

A/Reference number: A54877; MUID:94347719; PMID:8068627

A/Accession: B54877

A/Molecule type: protein

A/Residues: 1-16 <FAI>

A/Cross-references: UNIPROT:P50985; UNIPARC:UPI000004C0F6

C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynapt

C/Superfamily: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 8.5e+03;

Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
|:|:|:|:
DB 6 PCCALSNP 13

RESULT 85

T37075

hypothetical protein SCJ30.08 - Streptomyces coelicolor

C/Species: Streptomyces coelicolor

C/Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C/Accession: T37075

R/Sanders, D.C.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.

submitted to the EMBL Data Library, August 1999

A/Reference number: Z21621

A/Accession: T37075

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-16 <SAN>

A/Cross-references: UNIPARC:UPI000017ADCE; EMBL:AL109973; PIND:CAM53303.1; GSPDB:GN0007

A/Experimental source: strain A3(2)

C/Genetics:

A/Genome: SCODDB:SCJ30.08

Query Match 17.5%; Score 20; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 8.5e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
|:|:|:|:
DB 8 PRSALGIP 15

RESULT 86

G24304

ribosomal protein H [validated] - Haloarcula marismortui (fragment)

C/Species: Haloarcula marismortui

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 21-Jul-2000

C/Accession: G24304

R/Shoham, M.; Dijk, J.; Reinhardt, R.; Wilmann-Liebold, B.

FEBS Lett. 204, 323-330, 1986

A/Title: Purification and characterization of ribosomal proteins from the 30 S subunit

A/Reference number: A24304

A/Accession: G24304

A/Molecule type: protein

A/Residues: 1-16 <SHO>

A/Cross-references: UNIPARC:UPI000017ABZ2

C/Keywords: protein biosynthesis; ribosome

Query Match 17.5%; Score 20; DB 2; Length 16;

Best Local Similarity 33.3%; Pred. No. 8.5e+03;

Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPAPL 16
|:|:|:|:
DB 1 PGNKRYNDEGXL 12

RESULT 87

PT0237

Ig heavy chain CDR3 region (clone 2-94A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0237

J. Yamada, M.; Masserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222; MUID:91108337; PMID:1899102

A/Accession: PT0237

A/Molecule type: DNA

A/Residues: 1-16 <YAM>

A/Cross-references: UNIPARC:UPI000017C1D8

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 17.5%; Score 20; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 8.5e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYRYPG 6
|:|:|:|:
DB 8 DFEDYWG 13

RESULT 88

A42291
 tail fiber protein I - phage P2 (fragment)
 C/Species: phage P2
 C/Date: 10-Jul-1992 #sequence_revision 10-Jul-1992 #text_change 09-Jul-2004
 C/Accession: A42291
 R.Haggard-Ljungquist, B.; Halling, C.; Calendar, R.
 J. Bacteriol. 174, 1462-1477, 1992
 A/Title: DNA sequences of the tail fiber genes of bacteriophage P2: evidence for horizon
 A/Reference number: A42291, PMID:92165720, PMID:1531648
 A/Accession: A42291
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-16 <HAG>
 A/Cross-references: UNIPROT:P26701, UNIPARC:UPI000017A829, GB:M64677

Query Match 17.5%; Score 20; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 YPG 6
 |||
 Db 14 YPG 16

RESULT 89
 JTO609
 leukocyte chemoattractant peptide 6 - sheep
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 16-Sep-1992 #sequence_revision 16-Sep-1992 #text_change 09-Jul-2004
 C/Accession: JTO609
 R.Murdoch, W.J.; McCormick, R.J.
 Biochem. Biophys. Res. Commun. 184, 848-852, 1992
 A/Title: Sequence analysis of leukocyte chemoattractant peptides secreted by periovulato
 A/Reference number: JTO609, PMID:92246975, PMID:1575752
 A/Accession: JTO609
 A/Molecule type: protein
 A/Residues: 1-16 <MUR>
 A/Status: preliminary
 A/Cross-references: UNIPROT:Q7M2L0, UNIPARC:UPI000017C5AC
 C/Keywords: hydroxyproline
 F3,6,9,12,15/modified site: hydroxyproline (Pro) #status experimental

Query Match 17.5%; Score 20; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 8.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 GNPAP 15
 |||
 Db 4 GPPGAP 9

RESULT 90
 B61334
 trypsin (EC 3.4.21.4) 2 - starfish (Dermasterias imbricata) (fragment)
 C/Species: Dermasterias imbricata
 C/Date: 17-Jul-1994 #sequence_revision 17-Jul-1994 #text_change 09-Jul-2004
 C/Accession: B61334
 R.Estell, D.A.; Laskowski Jr., M.
 Biochemistry 19, 124-131, 1980
 A/Title: Dermasterias imbricata trypsin 1: an enzyme which rapidly hydrolyzes the reacti
 A/Reference number: A61334, PMID:80109692, PMID:7352972
 A/Accession: B61334
 A/Molecule type: protein
 A/Residues: 1-17 <EST>
 A/Cross-references: UNIPROT:Q7M433, UNIPARC:UPI0000175C3B
 C/Keywords: trypsin; trypsin homology
 C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match 17.5%; Score 20; DB 2; Length 17;
 Best Local Similarity 25.0%; Pred. No. 9e+03;
 Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;

QY 9 LGNPAPLYKRP 20
 :|:::|

Db 2 VQKESTASHRP 13

RESULT 91
 I49593
 cystic fibrosis transmembrane conductance regulator - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
 C/Accession: I49593
 R.Denamur, B.; Chehab, F.F.
 Hum. Mol. Genet. 3, 1089-1094, 1994
 A/Title: Analysis of the mouse and rat CFTR promoter regions.
 A/Reference number: I49593, PMID:95072572, PMID:7526924
 A/Accession: I49593
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPARC:UPI000016CC99, GB:L04873, NID:9414726, PIDN:AAAT3562.1, PID
 A/Status: preliminary
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPARC:UPI000016CC99, GB:L04873, NID:9414726, PIDN:AAAT3562.1, PID
 A/Status: preliminary
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPARC:UPI000016CC99, GB:L04873, NID:9414726, PIDN:AAAT3562.1, PID

Query Match 17.5%; Score 20; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 9e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KAPLYK 18
 |||
 Db 3 KSPLEK 8

RESULT 92
 I84733
 gene CFTR protein - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I84733
 R.Denamur, B.; Chehab, F.F.
 Hum. Mol. Genet. 3, 1089-1094, 1994
 A/Title: Analysis of the mouse and rat CFTR promoter regions.
 A/Reference number: I49593, PMID:95072572, PMID:7526924
 A/Accession: I84733
 A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPROT:P34158, UNIPARC:UPI000016CC99, GB:L26098, NID:9425185, PIDN
 A/Status: preliminary
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPROT:P34158, UNIPARC:UPI000016CC99, GB:L26098, NID:9425185, PIDN
 A/Status: preliminary
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPROT:P34158, UNIPARC:UPI000016CC99, GB:L26098, NID:9425185, PIDN

Query Match 17.5%; Score 20; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 9e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 KAPLYK 18
 |||
 Db 3 KSPLEK 8

RESULT 93
 B25348
 glycogen(starch) synthase (EC 2.4.1.11) P-2 peptide - rabbit (fragment)
 N/Alternate names: UDPglucose-glycogen glucosyltransferase
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 09-Jul-2004
 C/Accession: B25348
 J.Wang, Y.; Bell, A.W.; Hermodson, M.A.; Roach, P.J.
 J. Biol. Chem. 261, 16909-16915, 1986
 A/Title: Liver isozyme of rabbit glycogen synthase. Amino acid sequences surrounding p
 A/Reference number: A92570, PMID:87057401, PMID:3097016
 A/Accession: B25348
 A/Molecule type: protein
 A/Residues: 1-17 <WAN>

A/Cross-references: UNIPROT:Q7M2K1, UNIPARC:UPI000017C50C
C/Function: A:Description: catalyzes the alpha-1,4-glucosylation of glycogen by UDPglucose producing C/Keywords: glycogen/starch biosynthesis; glycocyltransferase; hexosyltransferase
Query Match 17.5%; Score 20; DB 2; Length 17;
Best Local Similarity 60.0%; Pred. No. 9e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 16 LYKRP 20
DB 1 MYPRP 5
RESULT 94
S47196
T-cell receptor J-alpha wnt.3 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C/Accession: S47196
R/Place: A.; Kono, D.H.; Theofilopoulos, A.N.
Submitted to the EMBL Data Library, February 1993
A/Reference number: S40133
A/Accession: S47196
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-18 <PLA>
A/Cross-references: UNIPARC:UPI000011611E; EMBL:X71027; NID:G506912; PIDN:CAA50344.1; PI
C/Keywords: T-cell receptor
Query Match 17.5%; Score 20; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 5 PGSRL 9
DB 2 PGNKL 6
RESULT 95
B44239
amine oxidase (copper-containing) (EC 1.4.3.6), serum - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: B44239
R/Name: S.M.; Peticic, M.M.; Scaman, C.H.; Smith, A.J.; Brown, D.E.; Dooley, D.M.; Mure, J.
Biochemistry 31, 12147-12154, 1992
A/Title: Identification of topaquinine and its consensus sequence in copper amine oxidase
A/Reference number: A44239; MUID:93090740; PMID:11457410
A/Accession: B44239
A/Molecule type: protein
A/Residues: 1-7, 'X', '9'-18 <JAN>
A/Cross-references: UNIPROT:Q9TRK5; UNIPARC:UPI00000871BF; PIDN:AB24427.1; PID:G261361
A/Experimental source: serum
A/Note: sequence extracted from NCBI backbone (NCBI:P.119896)
C/Keywords: oxidoreductase; quinoprotein; topaquinine
P/8/Modified site: topaquinine (Try) #status experimental
Query Match 17.5%; Score 20; DB 2; Length 18;
Best Local Similarity 25.0%; Pred. No. 9.6e+03;
Matches 3; Conservative 4; Mismatches 5; Indels 0; Gaps 0;
QY 1 DYKPSGRRLNP 12
DB 7 NYDYVXDMIRHP 18
RESULT 96
S25715
hypothetical protein - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Nov-1999

C/Accession: S25715; S21390
R/Bowtell, D.; Fu, P.; Simon, M.; Senior, P.
Proc. Natl. Acad. Sci. U.S.A. 89, 6511-6515, 1992
A/Title: Identification of murine homologues of the Drosophila Son of sevenless gene; p
A/Reference number: S25714; MUID:92335328; PMID:1631150
A/Accession: S25715
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-19 <BOM>
A/Cross-references: UNIPARC:UPI000016D049; EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PI
R/Bowtell, D.D.; Fu, P.; Simon, M.A.; Senior, P.V.
Submitted to the EMBL Data Library, January 1992
A/Description: Identification of murine homologues of the Drosophila Son of sevenless g
A/Reference number: S21390
A/Accession: S21390
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-19 <BOM>
A/Cross-references: UNIPARC:UPI000016D049; EMBL:Z11578; NID:G54132; PIDN:CAA77665.1; PI
Query Match 17.5%; Score 20; DB 2; Length 19;
Best Local Similarity 55.6%; Pred. No. 1e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 2; Gaps 1;
QY 12 PKAPLYKRP 20
DB 3 PPAP--RRP 9
RESULT 97
S43045
translational elongation factor EF-1 alpha - rabbit
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
C/Accession: S43045
R/Rosenberry, T.L.; Krall, J.A.; Dever, T.E.; Haas, R.; Louvard, D.; Merrick, W.C.
J. Biol. Chem. 264, 7096-7099, 1989
A/Title: Biosynthetic incorporation of [(3)H]ethanolamine into protein synthesis elonga
A/Reference number: A33048; MUID:89214136; PMID:2708357
A/Accession: S43045
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-19 <ROS>
A/Cross-references: UNIPROT:Q7M2K4; UNIPARC:UPI000017C5E8
Query Match 17.5%; Score 20; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 5 PGSRLG 10
DB 6 PGDNVG 11
RESULT 98
JP0059
ribosomal protein L30 - Thermactinomyces intermedius (fragment)
C/Species: Thermactinomyces intermedius
C/Date: 10-Mar-1994 #sequence_revision 28-Oct-1994 #text_change 05-Oct-2004
C/Accession: JP0059
R/Ochi, K.
Submitted to JIPID, February 1994
A/Description: Phylogenetic diversity in the genus Bacillus and comparative ribosomal p
A/Reference number: JP0042
A/Accession: JP0059
A/Molecule type: protein
A/Residues: 1-20 <OCH>
A/Cross-references: UNIPROT:Q7M167; UNIPARC:UPI0000177345
C/Suprafamily: Ribosomal protein L30p
C/Keywords: protein biosynthesis; ribosome
Query Match 17.5%; Score 20; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 1.1e+04;

Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 SRLGNPKA 14
|:|:|:
Db 11 SMIGRPES 18

RESULT 99

B46174
RNA-binding protein TIR - human (fragment)
N/Alternate names: cytotoxic granule-associated RNA-binding protein; TIR-1 related prote
C/Species: Homo sapiens (man)
C/Date: 21-Sep-1993 #sequence_rev18-Nov-1994 #text_change 31-Dec-2004
C/Accession: B46174
R/Kawakami, A.; Tian, O.; Duan, X.; Streuli, M.; Schlossman, S.F.; Anderson, P.
Proc. Natl. Acad. Sci. U.S.A. 89, 8681-8685, 1992
A/Title: Identification and functional characterization of a TIR-1-related nucleolytin.
A/Reference number: A46174; MUID:92409580; PMID:1326761
A/Accession: B46174
A/Status: preliminary
A/Molecule type: nucleic acid
A/Residues: 1-20 <KAW>
A/Cross-references: UNIPARC:UPI000017A36B
A/Note: sequence extracted from NCBI backbone (NCBIN:114067, NCBIIP:114068)

Query Match 17.5%; Score 20; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 EYPSRLGN 11
|:|:|:
Db 2 EQPDSRRVN 10

RESULT 100

S38292
30K allergen - rye (fragment)
C/Species: Secale cereale (rye)
C/Date: 19-May-1994 #sequence_rev18-Nov-1994 #text_change 09-Jul-2004
C/Accession: S38292
R/Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.
Biol. Chem. Hoppe-Seyler 374, 855-861, 1993
A/Title: Comparison of four grass pollen species concerning their allergens of grass gro
A/Reference number: S38288; MUID:94092339; PMID:7505588
A/Accession: S38292
A/Molecule type: protein
A/Residues: 1-16 <PPT>
A/Cross-references: UNIPROT:Q7M263; UNIPARC:UPI000017B131

Query Match 17.1%; Score 19.5; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 5; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

QY 5 PGSRLGNPKA 14
|:|:|:
Db 10 PGTO---PKA 16

Search completed: January 20, 2006, 19:12:10
Job time : 12.3462 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 66.5385 Seconds
(without alignments)
212.066 Million cell updates/sec

Title: US-09-662-293-2

Perfect score: 114
Sequence: 1 DYVEPGSRILGNPKAPLYKRP 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	28.9	16	2	Q7DLV3 SOLTU
2	33	28.9	18	2	Q7DLV3 SOLTU
3	32	28.1	13	2	P90442_NPVS
4	31	27.2	12	2	Q4Y8T5_PLABR
5	30	26.3	12	1	GRAR_RANRU
6	30	26.3	13	2	Q6LDV4_BOVIN
7	29	25.4	14	2	O50268_9MOU
8	29	25.4	19	2	Q7M1M6_PHAVU
9	29	25.4	20	2	Q5KR93_CRIGR
10	28	24.6	20	1	M117_BOVIN
11	28	24.6	20	2	P82163_SPIOL
12	27.5	24.1	18	2	Q79B85_9ZZZ
13	27	23.7	15	1	K10M_LITME
14	27	23.7	18	2	Q9UCT9_HUMAN
15	26.5	23.2	19	2	Q9S8G9_PSORP
16	26.5	23.2	20	2	Q9S8H0_PSORP
17	26	22.8	13	2	Q43174_SOLTU
18	26	22.8	19	2	Q9OV88_9MURI
19	26	22.8	20	1	P1BB_ELEMA
20	26	22.8	20	1	PYRH_PYRAP
21	26	22.8	20	2	Q4XKQ4_PLACH
22	26	22.8	20	2	Q9TR50_BOVIN
23	26	22.8	20	2	Q9R4V6_PORGI
24	25.5	22.4	14	2	Q8JDM0_9HIV1
25	25.5	22.4	14	2	Q8JDM3_9HIV1
26	25.5	22.4	14	2	Q8JDM7_9HIV1
27	25	21.9	9	2	Q9UC36_HUMAN
28	25	21.9	13	2	Q9P116_HUMAN
29	25	21.9	13	2	Q7X9Y2_LYCER
30	25	21.9	14	2	Q98Y97_9HIV1
31	25	21.9	15	2	Q9TWE9_GALME

32	25	21.9	15	2	Q7X9Y4_CUCSA	Q7X9Y4 cucumis sat
33	25	21.9	15	2	Q9R564_ECOLI	Q9R564 escherichia
34	25	21.9	15	2	Q9R501_MICON	Q9R501 micropogoni
35	25	21.9	17	2	Q9EBB8_9HIV1	Q9EBB8 human immun
36	25	21.9	17	2	Q9ERK3_9HIV1	Q9ERK3 human immun
37	25	21.9	17	2	Q9BL24_9HIV1	Q9BL24 human immun
38	25	21.9	18	2	Q9TWK3_MYTED	Q9TWK3 mytilus edu
39	25	21.9	18	2	Q38573_BPKU1	Q38573 bacterioph
40	25	21.9	19	1	CKAD_CONGE	CKAD271 cone geogr
41	25	21.9	19	2	Q9TWY2_LEIME	Q9TWY2 leishmania
42	25	21.9	20	2	Q4Z0Y4_PLAEM	Q4Z0Y4 plasmodium
43	25	21.9	20	2	Q69176_CHLTR	Q69176 chlamydia t
44	25	21.9	20	2	O85509_CHLTR	O85509 chlamydia t
45	25	21.9	20	2	O85510_CHLTR	O85510 chlamydia t
46	25	21.9	20	2	O85512_CHLTR	O85512 chlamydia t
47	25	21.9	20	2	O85514_CHLTR	O85514 chlamydia t
48	25	21.9	20	2	O85517_CHLTR	O85517 chlamydia t
49	25	21.9	20	2	O85519_CHLTR	O85519 chlamydia t
50	25	21.9	20	2	O85520_CHLTR	O85520 chlamydia t
51	25	21.9	20	2	O85521_CHLTR	O85521 chlamydia t
52	25	21.9	20	2	O85522_CHLTR	O85522 chlamydia t
53	25	21.9	20	2	O85523_CHLTR	O85523 chlamydia t
54	25	21.9	20	2	O85525_CHLTR	O85525 chlamydia t
55	25	21.9	20	2	O85526_CHLTR	O85526 chlamydia t
56	25	21.9	20	2	O85528_CHLTR	O85528 chlamydia t
57	25	21.9	20	2	O85530_CHLTR	O85530 chlamydia t
58	25	21.9	20	2	O85531_CHLTR	O85531 chlamydia t
59	25	21.9	20	2	O85533_CHLTR	O85533 chlamydia t
60	25	21.9	20	2	Q53520_CHLTR	Q53520 chlamydia t
61	25	21.9	20	2	Q9R8N0_CHLTR	Q9R8N0 chlamydia t
62	25	21.9	20	2	Q9R8N4_CHLTR	Q9R8N4 chlamydia t
63	25	21.9	20	2	Q9R8P4_CHLTR	Q9R8P4 chlamydia t
64	25	21.9	20	2	Q61871_MOUSE	Q61871 mus musculu
65	25	21.9	20	2	Q9PRV5_XENLA	Q9PRV5 xenopus lae
66	25	21.9	8	2	Q6BC29_HUMAN	Q6BC29 homo sapien
67	24	21.1	9	2	O12096_CAEV	O12096 caprine art
68	24	21.1	9	2	O12098_CAEV	O12098 caprine art
69	24	21.1	9	2	O12100_CAEV	O12100 caprine art
70	24	21.1	9	2	O12102_CAEV	O12102 caprine art
71	24	21.1	9	2	O12104_CAEV	O12104 caprine art
72	24	21.1	10	2	Q7M500_9EUBO	Q7M500 aspergillus
73	24	21.1	11	2	Q9C057_HUMAN	Q9C057 homo sapien
74	24	21.1	12	2	O12074_CAEV	O12074 caprine art
75	24	21.1	12	2	O12076_CAEV	O12076 caprine art
76	24	21.1	12	2	O12078_CAEV	O12078 caprine art
77	24	21.1	12	2	O12080_CAEV	O12080 caprine art
78	24	21.1	12	2	O12082_CAEV	O12082 caprine art
79	24	21.1	12	2	O12084_CAEV	O12084 caprine art
80	24	21.1	12	2	O12086_CAEV	O12086 caprine art
81	24	21.1	12	2	O12088_CAEV	O12088 caprine art
82	24	21.1	12	2	O12090_CAEV	O12090 caprine art
83	24	21.1	12	2	O12092_CAEV	O12092 caprine art
84	24	21.1	12	2	O12094_CAEV	O12094 caprine art
85	24	21.1	12	2	O12106_CAEV	O12106 caprine art
86	24	21.1	12	2	O12108_CAEV	O12108 caprine art
87	24	21.1	12	2	O12110_CAEV	O12110 caprine art
88	24	21.1	12	2	O12112_CAEV	O12112 caprine art
89	24	21.1	12	2	O12114_CAEV	O12114 caprine art
90	24	21.1	12	2	O12116_CAEV	O12116 caprine art
91	24	21.1	12	2	O12118_CAEV	O12118 caprine art
92	24	21.1	13	2	Q9UDC6_HUMAN	Q9UDC6 homo sapien
93	24	21.1	15	2	Q6LAT1_DROME	Q6LAT1 drosophila
94	24	21.1	16	2	Q9NPQ7_HUMAN	Q9NPQ7 homo sapien
95	24	21.1	18	2	Q4TZV7_PAPPA	Q4TZV7 papio hamad
96	24	21.1	18	2	O5UTR3_RAT	O5UTR3 rattus norv
97	24	21.1	19	1	HB82_UROHA	HB822 uronasteyx h
98	24	21.1	19	2	Q8WTX6_HUMAN	Q8WTX6 homo sapien
99	24	21.1	20	2	Q51XB0_MAGR	Q51XB0 magnapothec
100	24	21.1	20	2	Q9T3Q9_SOLTU	Q9T3Q9 solanum tub

ALIGNMENTS

```

RESULT 1
07DLV3 SOLUTU
ID 07DLV3_SOLUTU PRELIMINARY; PRT; 16 AA.
AC 07DLV3;
DT 05-JUL-2004 (TRENBLREL. 27, Created)
DT 05-JUL-2004 (TRENBLREL. 27, Last sequence update)
DT 05-JUL-2004 (TRENBLREL. 27, Last annotation update)
DE Beta-fructofuranosidase (Invertase) (EC 3.2.1.26) (Fragment).
OS Solanum tuberosum (Potato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4113;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96279736; PubMed=8710506; DOI=10.1093/nar/24.12.2347;
RA Bourray A.S., Hedley P.E., Maddison A., Waugh R., Machray G.C.;
RT "Exon skipping induced by cold stress in a potato invertase gene
transcript."
RL Nucleic Acids Res. 24:2347-2351(1996).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Maddison A.L.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; X95820; CAA65086.1; -; Genomic DNA.
DR GO; GO:0004564; P:beta-fructofuranosidase activity; IEA.
DR GO; GO:0016798; P:hydrolase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
KW Glycosidase; Hydrolase.
FT NON TER 1
FT NON TER 16
SQ SEQUENCE 16 AA; 1894 MW; 003053E73810C36 CRC64;

Query Match 28.9%; Score 33; DB 2; Length 16;
Best Local Similarity 38.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAPLY 17
| : : : | : |
DB 1 PKMWINDPNHMY 13

RESULT 2
AGI_EUPMA
ID AGI_EUPMA STANDARD; PRT; 18 AA.
AC P33889;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Galactose-inhibitable lectin [Contains: Galactose-inhibitable lectin
isoform Ala-1 del] (Fragment).
OS Euphorbia marginata (Snow-on-the-mountain).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Rosids; eurosids I; Malpighiales; Euphorbiaceae; Euphorbioidae;
OC Euphorbiaceae; Euphorbia.
OX NCBI_TaxID=28955;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93357266; PubMed=8351129; DOI=10.1016/0304-4165(93)90093-N;
RA Stipe P., Licastro F., Morini M.C., Parente A., Savino G.,
RA Abbondanza A., Bolognesi A., Falasca A.I., Rossi C.A.;
RT "Purification and partial characterization of a mitogenic lectin from
the latex of Euphorbia marginata."
RL Biochim. Biophys. Acta 1158:33-39(1993).
-1- FUNCTION: Lectin that binds galactose, galactose-containing sugars
and gentiobiose. It is strongly mitogenic for human T lymphocytes
and induces the release of interleukin-1 beta and tumor necrosis
factor alpha from cultured mononuclear cells. It has a strong
hemagglutinating activity.
-1- SUBUNIT: Homodimer.

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CC -1- DEVELOPMENTAL STAGE: The production of this lectin varies with
CC seasons being higher in late spring.
CC -1- PTM: N-glycosylated.
CC -1- PTM: An isoform with Ala-1 missing is found in 20% of the samples.
CC -1- SIMILARITY: Contains 1 ricin B-type lectin domain.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
-----
CC PIR; S36120; S36120.
DR InterPro; IPR000772; Ricin_B_Lectin; PARTIAL.
DR PROSITE; PS50231; Ricin_B_Lectin; PARTIAL.
KW Direct protein sequencing; Glycoprotein; Lectin.
FT CHAIN 1 >18 Galactose-inhibitable lectin.
FT CHAIN 2 >18 Galactose-inhibitable lectin isoform Ala-
FT 1 del.
FT NON TER 18
FT NON TER 18
SQ SEQUENCE 18 AA; 1888 MW; 6F79E053BC740AA CRC64;

Query Match 28.9%; Score 33; DB 1; Length 18;
Best Local Similarity 55.6%; Pred. No. 6.7e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSLGNP 12
| | | | : |
DB 2 YPGSHISGP 10

RESULT 3
P90442.NPVSL PRELIMINARY; PRT; 13 AA.
ID P90442.NPVSL PRELIMINARY; PRT; 13 AA.
AC P90442;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-JUN-2003 (TRENBLREL. 24, Last annotation update)
DE Polyhedrin (Fragment).
OS Spodoptera littoralis nuclear polyhedrosis virus (SLNPV).
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10456;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97300849; PubMed=9155869; DOI=10.1007/s007050050055;
RA Faktor O., Tolster-Achituv M., Nachum O.;
RT "Enhanced element, repetitive sequences and gene organization in an 8-
RT kbp region containing the polyhedrin gene of the Spodoptera littoralis
RT nucleopolyhedrovirus."
RL Arch. Virol. 142:1-15(1997).
DR EMBL; X99711; CAA68046.1; -; Genomic RNA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR001746; Polyhedrin.
DR Pfam; PF00738; Polyhedrin; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 13 AA; 1383 MW; 2B0CD62832655737 CRC64;

Query Match 28.1%; Score 32; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 6.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
| | | | | |
DB 3 PDAPLYTGP 11

RESULT 4
Q4YET5.PLABE PRELIMINARY; PRT; 12 AA.
ID Q4YET5.PLABE PRELIMINARY; PRT; 12 AA.
AC Q4YET5;
DT 13-SEP-2005 (TRENBLREL. 31, Created)
DT 13-SEP-2005 (TRENBLREL. 31, Last sequence update)

```


DT 13-SEP-2005 (TrEMBL:rel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB405057.00.0;
 OS Plasmodium berghei
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NC NCBL_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,
 RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Duggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAI01005850; CAI03484.1; -; Genomic_DNA.
 KW Hypothetical protein.
 PT NON_TER 1
 SQ SEQUENCE 12 AA; 1468 MW; 9ATC7B45DB5B0B5A CRC64;
 Query Match 27.2%; Score 31; DB 2; Length 12;
 Best local similarity 71.4%; Pred. No. 8.7e+02;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYEPGS 7
 Db 5 DYEVAGN 11

RESULT 5
 GRAR_RANRU STANDARD; PRT; 12 AA.
 ID GRAR_RANRU
 AC PA0754;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Granulibertin-R.
 OS Rana rugosa (Winkled frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranae;
 OC Ranae;
 NC NCBL_TaxID=8410;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Skin secretion;
 RX MEDLINE=78062810; PubMed=589733;
 RA Nakajima T., Yasuhara T.;
 RT "A new mast cell degranulating peptide, granulibertin-R, in the frog
 RT (Rana rugosa) skin."
 RL Chem. Pharm. Bull. 25:2464-2465(1977).
 RN [2]
 RP SYNTHESIS.
 RX MEDLINE=78189201; PubMed=657408;
 RA Nakajima T., Yasuhara T., Hirai Y., Kikada C., Fujino M., Takeyama M.,
 RA Koyama K., Yajima H.;
 RT "Synthesis of the dodecapeptide amide corresponding to the entire
 RT amino acid sequence of granulibertin-R, a new frog skin peptide from
 RT Rana rugosa."
 RL Chem. Pharm. Bull. 26:1222-1230(1978).
 CC -1- FUNCTION: Mast cell degranulating peptide.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
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CC -----
 KW Amidation; Amphibian defense peptide; Direct protein sequencing;
 KM Mast cell degranulation.
 FT MOD_RES 12
 FT SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;
 SQ SEQUENCE 12 AA; 1424 MW; 2B974EB9CA1B5047 CRC64;
 Query Match 26.3%; Score 30; DB 1; Length 12;
 Best local similarity 66.7%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 PLYKRP 20
 Db 5 PLYRRP 10

RESULT 6
 Q6LDV4_BOVIN PRELIMINARY; PRT; 13 AA.
 ID Q6LDV4_BOVIN
 AC Q6LDV4;
 DT 05-JUL-2004 (TrEMBL:rel. 27, Created)
 DT 05-JUL-2004 (TrEMBL:rel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBL:rel. 27, Last annotation update)
 DE Thyroglobulin (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eureleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 NC NCBL_TaxID=9913;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=87204101; PubMed=3472203;
 RA Ricketts M.H., Simons M.-U., Parma J., Mercken L., Dong Q.,
 RA Vassart G.;
 RT "A nonsense mutation causes hereditary goitre in the Afrikaner cattle
 RT and ummaaks alternative splicing of thyroglobulin transcripts";
 RL Proc. Natl. Acad. Sci. U.S.A. 84:3181-3184(1987).
 DR EMBL; M16448; AAA30777.2; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 13
 SQ SEQUENCE 13 AA; 1354 MW; 8BB974B525A2DC5 CRC64;
 Query Match 26.3%; Score 30; DB 2; Length 13;
 Best local similarity 63.6%; Pred. No. 1.4e+03;
 Matches 7; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 5 PGSR--LGMPK 13
 Db 2 PGTRSLGSRK 12

RESULT 7
 Q50268_9MOLU
 ID Q50268_9MOLU PRELIMINARY; PRT; 14 AA.
 AC Q50268;
 DT 01-NOV-1996 (TrEMBL:rel. 01, Created)
 DT 01-JAN-1999 (TrEMBL:rel. 09, Last sequence update)
 DT 01-DEC-2001 (TrEMBL:rel. 19, Last annotation update)
 DE Rpl16 protein (Fragment).
 GN Name=rpl16;
 OS Phytolacca sp.
 OC Bacteria; Firmicutes; Mollicutes; Acholoplasmatales;
 OC Acholoplasmataceae; Candidatus Phytolacca.
 NC NCBL_TaxID=2155;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Lim P.-O., Sears B.B.;
 RT "DNA sequence of the ribosomal protein genes rpl2 and rpl3 from a
 RT plant-pathogenic mycoplasma-like organism."
 RL FEMS Microbiol. Lett. 84:71-74(1991).
 CC -1- FUNCTION: Ribosomal protein.
 CC -1- SUBCELLULAR LOCATION: Cytoplasm.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
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RT "Evolutionary relationships of a plant-pathogenic mycoplasma-like
 RT organism and Acholeplasma laidlawii deduced from two ribosomal protein
 RT gene sequences";
 RL J. Bacteriol. 174:2606-2611(1992).
 DR EMBL, M74770; AAA2531.1; -; Genomic DNA.
 FT NON_TER 14 14
 SQ SEQUENCE 14 AA; 1870 MW; 87C315B73386A21 CRC64;

Query Match 25.4%; Score 29; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 2.1e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
 Db 4 PKRTKTRRP 12

RESULT 8
 Q7M1M8 PHAVU
 ID 07M1M8 PHAVU PRELIMINARY; PRT; 19 AA.

AC 07M1M8_1
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Hydroxyproline-rich cell wall glycoprotein (42K and others)
 DE (Fragment).
 OS Phaseolus vulgaris (Kidney bean) (French bean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid1; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Phaseolus.
 OX NCBI_TaxID=3885;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96011753; PubMed=7548825;
 RA Wojtasek P., Trethowan J., Bolwell G.P.;
 RT "Specificity in the immobilisation of cell wall proteins in response
 RT to different elicitor molecules in suspension-cultured cells of French
 RT bean (Phaseolus vulgaris L.).";
 RL Plant Mol. Biol. 28:1075-1087(1995).
 DR PIR, S59485; S59485.
 FT NON_TER 1 19
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2225 MW; 53AB9D0984A87E0A CRC64;

Query Match 25.4%; Score 29; DB 2; Length 19;
 Best Local Similarity 62.5%; Pred. No. 2.9e+03;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 KAPLYKRP 20
 Db 9 KPPVYKRP 16

RESULT 9
 Q5KR93 CRIGR
 ID 05KR93 CRIGR PRELIMINARY; PRT; 20 AA.

AC 05KR93_1
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Ovcal (Fragment).
 DE Name=ovcal;
 OS Cricetus griseus (Chinese hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Cricetulus.
 OX NCBI_TaxID=10029;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15637051; DOI=10.1074/jbc.M13017200;
 RA Nobukuni Y., Kohno K., Miyagawa K.;
 RT "Gene Trap Mutagenesis-based Forward Genetic Approach Reveals That the
 RT Tumor Suppressor OVCA1 Is a Component of the Biosynthetic Pathway of

RT Dipthamide on Elongation Factor 2.";
 RL J. Biol. Chem. 280:10572-10577(2005).
 DR EMBL, AB194396; BAD86738.1; -, mRNA.
 FT NON_TER 1 20
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 1984 MW; 85701624F2B38874 CRC64;

Query Match 25.4%; Score 29; DB 2; Length 20;
 Best Local Similarity 83.3%; Pred. No. 3.1e+03;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PGSRLG 10
 Db 12 PGSRVG 17

RESULT 10
 M17_BOVIN
 ID M17_BOVIN STANDARD; PRT; 20 AA.

AC P35451;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE 17 kDa milk glycoprotein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]

RP PROTEIN SEQUENCE.
 RC TISSUE=Milk;
 RX MEDLINE=93308294; PubMed=8320368;
 RA Soerensen B.S., Petersen T.B.;
 RT "Purification and characterization of three proteins isolated from the
 RT proteose peptone fraction of bovine milk.";
 RL J. Dairy Res. 60:189-197(1993).
 CC -1- PTM: N-glycosylated.
 CC -1- SIMILARITY: To camel whey protein.

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 CC removed.

CC Direct protein sequencing; Glycoprotein; Milk.

KW Direct protein sequencing; Glycoprotein; Milk.
 FT NON_TER 1 20
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2234 MW; 4CCA589404C62C27 CRC64;

Query Match 24.6%; Score 28; DB 1; Length 20;
 Best Local Similarity 83.3%; Pred. No. 4.4e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPKAPL 16
 Db 9 NPKLPL 14

RESULT 11
 P82163 SPIOL
 ID P82163 SPIOL PRELIMINARY; PRT; 20 AA.

AC P82163_1
 DT 01-JUN-2000 (TREMBlrel. 14, Created)
 DT 01-JUN-2000 (TREMBlrel. 14, Last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
 DE Chloroplast 30S ribosomal protein S13 (Fragment).
 OS Spinacia oleracea (Spinach).

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Caryophyllales; Amaranthaceae; Spinacia.
 OX NCBI_TaxID=3562;

```

RN [1]
RP PROTEIN SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
RC STRAIN=CV, ALMARO, TISSUE=leaf,
RX MEDLINE=20435797; PubMed=10874039, DOI=10.1074/jbc.M004350200;
RA Yamaguchi K., von Knoblauch K., Subramanian A.R.;
RT "The plastid ribosomal proteins. Identification of all the proteins in
RT the 30S subunit of an organelle ribosome (chloroplast).";
RL J. Biol. Chem. 275:28455-28465(2000).
CC -1- FUNCTION. THIS PROTEIN BINDS DIRECTLY TO 16S RIBOSOMAL RNA.
CC -1- SUBCELLULAR LOCATION: CHLOROPLAST.
CC -1- TISSUE SPECIFICITY: EXPRESSED IN ALL PLANT TISSUES.
CC -1- MASS SPECTROMETRY: MM=14900; METHOD=MALDI.
CC -1- MISCELLANEOUS: ON THE 2D-GEL, ITS MW IS: 15.5 kDa.
CC -1- SIMILARITY: BELONGS TO THE S13P FAMILY OF RIBOSOMAL PROTEINS.
DR GO: GO:0009507; C:chloroplast; IEA.
DR GO: GO:0019843; F:rRNA binding; IEA.
DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
DR InterPro: IPR001892; Ribosomal S13.
DR PROSITE: PS00646; RIBOSOMAL_S13_1; PARTIAL.
KM Chloroplast; Ribosomal protein, rRNA-binding.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2401 MW; 96AEFF51BE1035106 CRC64;

Query Match 24.6%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.4e+03;
Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 RLGNPKAPLYKR 19
DB 2 RVGNVEIPNNKR 13

RESULT 12
QY9EB5_9222Z
ID QY9EB5_9222Z PRELIMINARY; PRT; 18 AA.
AC QY9EB5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE NodQ1 protein (fragment).
GN Name=nodQ1;
OG Megaplasmaid pSym-a.
OC other sequences; plasmids.
OX NCB1_TaxID=28391;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94220739; PubMed=8167368;
RA Schwedock J., Long S.R.;
RT "An open reading frame downstream of Rhizobium meliloti nodQ1 shows
RT nucleotide sequence homology to an Agrobacterium tumefaciens insertion
RT sequence.";
RL Mol. Plant Microbe Interact. 7:151-153(1994).
DR EMBL: L08667; AAA25332.1; -; Genomic_DNA.
KM plasmid.
FT NON_TER 1
SQ SEQUENCE 18 AA; 2115 MW; 9482F267BDEABFAC CRC64;

Query Match 24.1%; Score 27.5; DB 2; Length 18;
Best Local Similarity 38.9%; Pred. No. 4.7e+03;
Matches 7; Conservative 3; Mismatches 7; Indels 1; Gaps 1;

QY 3 EYEGSRIGNPKAPLYKRP 20
DB 1 EFLDRRIGGQMTPL-QRP 17

RESULT 13
KLOM_LUMTB
ID KLOM_LUMTB STANDARD; PRT; 15 AA.
AC P11918;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)

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DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Lombricine kinase (EC 2.7.3.5) (LK) (Fragment).
OS Lumbicus terrestris (Common earthworm).
OC Eukaryota; Metazoa; Annelida; Clitellata; Oligochaeta; Nematoda;
OC Lumbicinae; Lumbicidae; Lumbicus.
OX NCB1_TaxID=6398;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=72065544; PubMed=5128744;
RA der Terrosian E., Desvages G., Pradel L.A., Kaseab R., van Thoi N.;
RT "Comparative structural studies of the active site of ATP: guanidine
RT phosphotransferase. The essential cysteine tryptic peptide of
RT lombricine kinase from lumbicus terrestris muscle.";
RL Eur. J. Biochem. 22:585-592(1971).
CC -1- CATALYTIC ACTIVITY: ATP + lombricine = ADP + N-phospholombricine.
CC -1- SUBUNIT: Homodimer.
CC -1- SIMILARITY: Belongs to the ATP:guanine phosphotransferase family.
CC -----
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CC removed.
CC -----
DR PIR: A08416; A08416.
DR InterPro: IPR000749; ATP-gua_Ptrans.
DR PROSITE: PS00112; GUANIDO_KINASE; 1.
KM Direct protein sequencing; Kinase; Transferase.
FT ACT SITE 6
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1565 MW; 2A45FE6140B90C4 CRC64;

Query Match 23.7%; Score 27; DB 1; Length 15;
Best Local Similarity 83.3%; Pred. No. 4.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PGSRIG 10
DB 7 PGSRIG 12

RESULT 14
QY0UCT9_HUMAN
ID QY0UCT9_HUMAN PRELIMINARY; PRT; 18 AA.
AC QY0UCT9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE PG=PROLINE-rich glycoprotein (fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Barchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCB1_TaxID=9606;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=91373355; PubMed=1894623;
RA Gillette-Castro B.L., Prakobphol A., Burlingame A.L., Leffler H.,
RA Fisher S.J.;
RT "Structure and bacterial receptor activity of a human salivary
RT proline-rich glycoprotein.";
RL J. Biol. Chem. 266:17358-17368(1991).
DR GO: GO:0005576; C:extracellular region; NAS.
DR GO: GO:0008368; P:gram-negative bacterial binding; NAS.
DR GO: GO:0009618; P:response to pathogenic bacteria; NAS.
FT NON_TER 1
FT NON_TER 18
SQ SEQUENCE 18 AA; 1780 MW; 961F6F0A83D2E40 CRC64;

Query Match 23.7%; Score 27; DB 2; Length 18;
Best Local Similarity 45.5%; Pred. No. 5.7e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

```

Qy 5 PGSRLGNPKAP 15
 Db 4 PPPRPCKPCKP 14

RESULT 15

Q958G9_PSOTE PRELIMINARY; PRT; 19 AA.

AC Q958G9_PSOTE PRELIMINARY; PRT; 19 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Proline-rich protein (Fragment).
 OS Psophocarpus tetragonolobus (Goa bean) (Asparagaceae).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Psophocarpus.
 OC NCBI_Taxid=3891;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95277008; PubMed=7757337;
 RA Esaka M., Hayakawa H.;
 RT "Specific secretion of proline-rich proteins by salt-adapted winged
 bean cells.";
 RL Plant Cell Physiol. 36:441-446(1995).
 SQ SEQUENCE 19 AA; 2118 MW; 59ED45C4F0F8779A CRC64;

Query Match 23.2%; Score 26.5; DB 2; Length 19;

Best Local Similarity 42.9%; Pred. No. 7.2e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 10 GNP--KAPLYKRP 20
 Db 3 GKRPVKKPVPVKKP 16

RESULT 16

Q958H0_PSOTE PRELIMINARY; PRT; 20 AA.

AC Q958H0_PSOTE PRELIMINARY; PRT; 20 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Proline-rich protein (Fragment).
 OS Psophocarpus tetragonolobus (Goa bean) (Asparagaceae).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eurosid 1; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 OC Psophocarpus.
 OC NCBI_Taxid=3891;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95277008; PubMed=7757337;
 RA Esaka M., Hayakawa H.;
 RT "Specific secretion of proline-rich proteins by salt-adapted winged
 bean cells.";
 RL Plant Cell Physiol. 36:441-446(1995).
 SQ SEQUENCE 20 AA; 2246 MW; AEE9ED45C4F0F877 CRC64;

Query Match 23.2%; Score 26.5; DB 2; Length 20;

Best Local Similarity 42.9%; Pred. No. 7.6e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 3; Gaps 1;

Qy 10 GNP--KAPLYKRP 20
 Db 3 GKRPVKKPVPVKKP 16

RESULT 17

Q43174_SOLTU PRELIMINARY; PRT; 13 AA.

AC Q43174;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Beta-fructofuranosidase (Invertase) (EC 3.2.1.26) (Fragment).
 OS Solanum tuberosum (Potato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum.
 OC NCBI_Taxid=4113;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=96279736; PubMed=8710506; DOI=10.1093/nar/24.12.2347;
 RA Bounay A.S., Hedley P.B., Maddison A., Maugh R., Machray G.C.;
 RT "Exon skipping induced by cold stress in a potato invertase gene
 transcript.";
 RL Nucleic Acids Res. 24:2347-2351(1996).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Maddison A.L.;
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; X95821; CAA65087.1; -; Genomic DNA.
 DR GO; GO:0004564; F-beta-fructofuranosidase activity; IEA.
 DR GO; GO:0016798; F-hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P-carbohydrate metabolism; IEA.
 KW Glycosidase; Hydrolase.
 FT NON_TER 1 1
 FT NON_TER 13 13
 SQ SEQUENCE 13 AA; 1541 MW; 1B3053E7384C6874 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 13;

Best Local Similarity 33.3%; Pred. No. 5.6e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 9 LGNPKAPLY 17
 Db 2 INDPNGPMY 10

RESULT 18

Q9QVB8_9MURI PRELIMINARY; PRT; 19 AA.

AC Q9QVB8_9MURI PRELIMINARY; PRT; 19 AA.
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE TRUE classse kallikrein (EC 3.4.21.35) (Fragment).
 OS Mus sp. .
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OC NCBI_Taxid=10095;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92348355; PubMed=1639762;
 RA Peters J., Takahashi S., Tada M., Miyake Y.;
 RT "MGK-6-derived true tissue kallikrein is synthesized, processed, and
 targeted through a regulated secretory pathway in mouse pituitary ACT-
 20 cells.";
 RL J. Biochem. 111:643-648(1992).
 DR GO; GO:0004293; F:ctlease kallikrein activity; IEA.
 SQ SEQUENCE 19 AA; 2296 MW; 250436479C0B6626 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 8.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 2 YEYP 5
 Db 1 YEYP 4

RESULT 19

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FIBB_ELEMA
ID FIBB_ELEMA STANDARD; PRT; 20 AA.
AC P14536;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen beta chain [Contains: Fibrinopeptide B] (Fragment).
GN Name=FGB;
OS Elephas maximus (Indian elephant).
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Afrotheria; Proboscidea; Elephantidae; Elephas.
OX NCBI_TaxID=9783;
RN [1]
RP PROTEIN SEQUENCE.
RA O'Neill P.B., Doolittle R.F.;
RT "Mammalian phylogeny based on fibrinopeptide amino acid sequences.";
RL Synt. 2001. 22:590-595(1973).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterocliners
CC are in head to head conformation with the N-termini in a small
CC central domain (By similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central module to the C-terminal domains
CC (distal modules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
CC -----
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CC -----
CC InterPro; IPR002181; Fibrinogen C.
CC PROSITE; PS00514; FIBRIN AG C DOMAIN; PARTIAL.
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma;
CC Sulfation.
CC PEPTIDE 1 20 Fibrinopeptide B.
CC MOD_RES 4 4 Sulfotyrosine.
CC FT NON_TER 20
CC SQ SEQUENCE 20 AA; 2107 MW; BAF52B95993273 CRC64;

Query Match 22.8%; Score 26; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 9.1e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DVEYPSG 7
| | | | |
Db 6 DEEPFGA 12

RESULT 20
PYRRH PYRAP STANDARD; PRT; 20 AA.
AC P3736Z; P80307;
DT 01-OCT-1994 (Rel. 30, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Pyrrhocorin.
OS Pyrrhocoris apterus (8sp sucking bug).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Paraneoptera; Hemiptera; Euhemiptera; Heteroptera;
OC Pentheteroptera; Pentatomomorpha; Pyrrhocoroidea; Pyrrhocoridae;
OC Pyrrhocoridae.
OX NCBI_TaxID=37000;
RN [1]

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RP PROTEIN SEQUENCE.
RC TISSUE=Hemolymph;
RX MEDLINE=94271176; PubMed=8002963;
RA Cocciandich S., Dupont A., Hegy G., Ianot R., Holder F., Helru C.,
RA Hoffmann J.A., Bulot P.;
RT "Novel inducible antibacterial peptides from a hemipteran insect, the
RT 8sp-sucking bug Pyrrhocoris apterus.";
RL Biochem. J. 300:567-575(1994).
RN [2]
RP CARBOHYDRATE-LINKAGE SITE THR-11.
RX MEDLINE=99177428; PubMed=10076062; DOI=10.1016/S0304-4165(98)00169-X;
RA Hoffmann R., Bulot P., Urges L., Otyoes L. Jr.;
RT "Range of activity and metabolic stability of synthetic antibacterial
RT glycopeptides from insects.";
RL Biochim. Biophys. Acta 1426:459-467(1999).
CC -1- FUNCTION: Antibacterial peptide. Affects Gram-negative bacteria
CC B.coil 1106, P.aeruginosa, B.coil D22 and E.cloacae and Gram-
CC positive bacteria M.luteus and B.subtilis.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- PTM: O-linked glycan consists of a Gal-GalNAc disaccharide, O-
CC glycosylation is essential for full biological activity.
CC -----
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CC -----
CC PIR; S44465; S44465.
CC Antitoxic; Antimicrobial; Direct protein sequencing; Glycoprotein;
CC Hemolymph; Immune response; Innate immunity.
CC O-linked (GalNAc. .).
CC FT CARBOHYD 11
CC SQ SEQUENCE 20 AA; 2341 MW; FA320BC2FF29462C CRC64;

Query Match 22.8%; Score 26; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 9.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 PKAPLYR 19
| | | | |
Db 12 PPRPYNR 19

RESULT 21
Q4XKQ4_PLACH PRELIMINARY; PRT; 20 AA.
AC Q4XKQ4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC400091.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5825;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Koolij T.W.A.,
RA Bertran M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris B., Churche C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
CC DR EMBL; CAJ01005069; CAH82508.1; -; Genomic_DNA.
CC KM Hypothetical protein.
CC FT NON_TER 1
CC SQ SEQUENCE 20 AA; 2345 MW; 0C1C6A76C57D4C65 CRC64;

```

Query Match 22.8%; Score 26; DB 2; Length 20;
Best Local Similarity 71.4%; Pred. No. 9.1e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PGSRLCN 11
|:|:|:|
DB 3 PTOURLCN 9

RESULT 22

Q9TR50_BOVIN PRELIMINARY; PRT; 20 AA.
AC Q9TR50;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
OS Amphoterin homolog (Fragment).
OS Bos taurus (Bovine).
OC Bukaryoca; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96029671; PubMed=7592757; DOI=10.1074/jbc.270.43.25752;
RA Horl O., Brett J., Slattery T., Cao R., Zhang J., Chen J.X.,
RA Nagashima M., Lunsh E.R., Vijay S., Nitecki D.;
RT "The receptor for advanced glycation end products (RAGE) is a cellular
binding site for amphoterin. Mediation of neurite outgrowth and co-
RT expression of rage and amphoterin in the developing nervous system.";
RL J. Biol. Chem. 270:25752-25761(1995).
DR HSSP; P07155; 1AAB.
SQ SEQUENCE 20 AA; 2229 MW; 9B615F547CD3B518 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 9.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GNPKAPLYK 18
|:|:|:|
DB 3 GNPKAPXGK 11

RESULT 23

Q9R4Y6_PORCI PRELIMINARY; PRT; 20 AA.
AC Q9R4Y6;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
OS Major outer membrane protein (Fragment).
OC Porphyromonas gingivalis (Bacteroides gingivalis).
OC Bacteri; Bacteroidetes; Bacteroides (class); Bacteroidales;
OC Porphyromonadaceae; Porphyromonas.
OX NCBI_TaxID=837;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94268318; PubMed=8208139;
RA Kokeguchi S., Miyamoto M., Oniyama H., Hongyo H., Takigawa M.,
RA Kurihara H., Murayama Y., Kato K.;
RT "Biochemical properties of the major outer membrane proteins of
RT Porphyromonas gingivalis.";
RL Microbios 77:247-252(1994).
SQ SEQUENCE 20 AA; 2150 MW; FD89405CE853DA41 CRC64;

Query Match 22.8%; Score 26; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 9.1e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DYEPYPSRLG 10
|:|:|:|
DB 11 DYHYGVEMAG 20

RESULT 24
Q8UDM0_9H1V1 PRELIMINARY; PRT; 14 AA.
ID Q8UDM0_9H1V1
AC Q8UDM0;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OS Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922020753747914;
RA Long E.M., Rainwater S.M., Laveys L., Mandalia K., Overbaugh J.;
RT "HIV type 1 variants transmitted to women in Kenya require the CCR5
RT coreceptor for entry, regardless of the genetic complexity of the
RT infecting virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407150; AAM66205.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 22.4%; Score 25.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 PGSRL-GNPKAP 15
|:|:|:|
DB 1 PSSQLRGDPTGP 12

RESULT 25
Q8UDM3_9H1V1 PRELIMINARY; PRT; 14 AA.
ID Q8UDM3_9H1V1
AC Q8UDM3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Truncated tat protein (Fragment).
GN Name=tat;
OS Human immunodeficiency virus 1.
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922020753747914;
RA Long E.M., Rainwater S.M., Laveys L., Mandalia K., Overbaugh J.;
RT "HIV type 1 variants transmitted to women in Kenya require the CCR5
RT coreceptor for entry, regardless of the genetic complexity of the
RT infecting virus.";
RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
DR EMBL; AF407149; AAM66202.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 14 AA; 1442 MW; 37C58F7BF82D7AA8 CRC64;

Query Match 22.4%; Score 25.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 7.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 5 PGSRL-GNPKAP 15
|:|:|:|
DB 1 PSSQLRGDPTGP 12

RESULT 26
Q8UDM7_9H1V1 PRELIMINARY; PRT; 14 AA.
ID Q8UDM7_9H1V1

AC Q8JDM7,
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Truncated tat protein (Fragment).
 GN Name=tat;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OC NCBI_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22032414; PubMed=12036486; DOI=10.1089/08922202753747914;
 RA Long B.M., Rainwater S.M., Lavrey L., Mandalia K., Overbaugh J.;
 RT "HIV type 1 variants transmitted to women in Kenya require the CCR5
 RT coreceptor for entry, regardless of the genetic complexity of the
 RT infecting virus."
 RL AIDS Res. Hum. Retroviruses 18:567-576(2002).
 DR EMBL; AF407148; AAM66198.1; -; Genomic_DNA.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1442 MW; 37C58F7B82D7AA8 CRC64;

Query Match 22.4%; Score 25.5; DB 2; Length 14;
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;
 Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

OY 5 PGSRL-GNPKAP 15
 DB 1 PSSQLRNDPTGP 12

RESULT 27

Q9UC36 HUMAN
 ID Q9UC36_HUMAN PRELIMINARY; PRT; 9 AA.

AC Q9UC36,
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE 28 kDa heat shock protein homolog fragment 1 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92218434; PubMed=1560006;
 RA Kato K., Shinohara H., Goto S., Inaguma Y., Morishita R., Asano T.;
 RT "Copurification of small heat shock protein with alpha B crystallin
 RT from human skeletal muscle." (1992).
 RL J. Biol. Chem. 267:7718-7725(1992).
 DR GO; GO:0006986; P:response to unfolded protein; NAS.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 9 AA; 1220 MW; 26933415B1F77B43 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 9;
 Best Local Similarity 83.3%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 4 YPGSRL 9
 DB 3 YPGSRL 8

RESULT 28

O9P16 HUMAN
 ID O9P16_HUMAN PRELIMINARY; PRT; 12 AA.

AC O9P16,
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Apolipoprotein B receptor 2 (Fragment).

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Korschinek I., Charehbaghi-schnell E., Lang I., Binder R.B.;
 RL Submitted (FEBS-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF129170; AAF66440.1; -; Genomic_DNA.
 DR GO; GO:0004872; P:receptor activity; IEA.
 KW Lipoprotein; Receptor.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 12 AA; 1467 MW; 4B8935410404877 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 12;
 Best Local Similarity 45.5%; Pred. No. 7.4e+03;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15
 DB 1 PPTFLGNRRRP 11

RESULT 29

Q7X9Y2 LYCES
 ID Q7X9Y2_LYCES PRELIMINARY; PRT; 13 AA.

AC Q7X9Y2,
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE TAG1 (Fragment).
 GN Name=TAG1;
 OS Lycopersicon esculentum (Tomato).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
 OC NCBI_TaxID=4081;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22667639; PubMed=12782724; DOI=10.1105/tpc.009548;
 RA Hong R.L., Hamaguchi L., Busch M.A., Weigel D.;
 RT "Regulatory elements of the floral homeotic gene AGAMOUS identified by
 RT phylogenetic footprinting and shadowing."
 RL Plant Cell 15:1296-1309(2003).
 DR EMBL; AY254705; AAP35239.1; -; Genomic_DNA.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 13 AA; 1598 MW; CA858C01BF9E444D CRC64;

Query Match 21.9%; Score 25; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 8e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 2 YEPGSRL 9
 DB 3 YEVANNRV 10

RESULT 30

O98Y97 SHIV1
 ID O98Y97_SHIV1 PRELIMINARY; PRT; 14 AA.

AC O98Y97,
 DT 01-JUN-2001 (TrEMBLrel. 17, Created)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Truncated pol protein (Fragment).
 GN Name=pol;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrod viruses; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 OC NCBI_TaxID=11676;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22056123; PubMed=12060770; DOI=10.1073/pnas.112177799;
RA Beerenwinkel N., Schmidt B., Walter H., Kaiser R., Lengauer T.,
RT Hoffmann D., Korn K., Selbig U.;
RT "Diversity and complexity of HIV-1 drug resistance: a bioinformatics
RT approach to predicting phenotype from genotype."
RT Proc. Natl. Acad. Sci. U.S.A. 99:8271-8276(2002).
DR EMBL; AF347572; AK32648.1; -; Genomic_RNA.
FT NON_TER
SQ SEQUENCE 14 AA; 1748 MW; C2921F7CAB276416 CRC64;

Query Match
Best Local Similarity 44.4%; Pred. No. 8.7e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PRAPLYKRP 20
DB 1 POTTLMQRP 9

RESULT 31
Q9TWE9_GALME PRELIMINARY; PRT; 15 AA.
ID Q9TWE9;
AC Q9TWE9;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PROPHENOLOXIDASE (fragment).
OS Galleria mellonella (Wax moth).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictysta; Pyraloidea;
OC Pyralidae; Galleriinae; Galleria.
NCBI_TaxID=7137;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=96137142; PubMed=8580908; DOI=10.1016/0955-1748(95)00040-2;
RA Kopacek P., Weise C., Goez P.;
RT "The prophenoloxidase from the wax moth Galleria mellonella:
RT purification and characterization of the proenzyme."
RT Insect Biochem. Mol. Biol. 25:1081-1091(1995).
SQ SEQUENCE 15 AA; 1695 MW; C78B5B2430AFD4A CRC64;

Query Match
Best Local Similarity 66.7%; Pred. No. 9.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EYPSGR 8
DB 10 DYFGIR 15

RESULT 32
Q7X9Y4_CUCSA PRELIMINARY; PRT; 15 AA.
ID Q7X9Y4;
AC Q7X9Y4;
DT 01-OCT-2003 (TREMBlrel. 25, Created)
DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)
DE CAG2 (Fragment).
OS Cucumis sativus (Cucumber).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside 1; Cucurbitales; Cucurbitaceae; Cucumis.
NCBI_TaxID=3659;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22667639; PubMed=12782724; DOI=10.1105/epc.009548;
RA Hong R.L., Hamaguchi U., Buesch M.A., Weigel D.;
RT "Regulatory elements of the floral homeotic gene AGAMOUS identified by
RT phylogenetic footprinting and shadowing."
RT Plant Cell 15:1296-1309(2003).

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DR EMBL; AY254703; AAP35237.1; -; Genomic_DNA.
FT NON_TER
SQ SEQUENCE 15 AA; 1825 MW; 159B31EFC989114 CRC64;

Query Match
Best Local Similarity 50.0%; Pred. No. 9.4e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 YEYPSRL 9
DB 6 YEXANNRV 13

RESULT 33
Q9R564_ECOLI PRELIMINARY; PRT; 15 AA.
ID Q9R564;
AC Q9R564;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
DE 36 kDa porin homolog (Outer membrane protein) (fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
NCBI_TaxID=562;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93328296; PubMed=8392972;
RA Dytoc M., Soni R., Cockcroft F.II., De Azavedo J., Louie M.,
RT "Multiple determinants of verotoxin-producing Escherichia coli O157:H7
RT attachment-effacement."
RT Infect. Immun. 61:3382-3391(1993).
DR HSP; P02934; I0UP.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0008279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
DR Pfam; PF01389; OmpA membrane; 1.
SQ SEQUENCE 15 AA; 1708 MW; 1DF32F8131A21BE CRC64;

Query Match
Best Local Similarity 57.1%; Pred. No. 9.4e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 YPSRLG 10
DB 8 YTGAKLG 14

RESULT 34
Q9PS01_MITCN PRELIMINARY; PRT; 15 AA.
ID Q9PS01;
AC Q9PS01;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE Gonadotropin alpha subunit (fragment).
OS Microgononias undulatus (Atlantic croaker).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percormorpha; Perciformes; Percoidae;
OC Sciadenidae; Microgononias.
NCBI_TaxID=29154;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94010173; PubMed=8405898; DOI=10.1006/gen.1993.1112;
RA Copeland P.A., Thomas P.;
RT "Isolation of gonadotropin subunits and evidence for two distinct
RT gonadotropins in Atlantic croaker (Microgononias undulatus)."
RT Gen. Comp. Endocrinol. 91:115-125(1993).
DR GO; GO:0005576; C:extracellular region; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.

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DR InterPro; IPR000476; Glyco hormone.
DR PRODOM; PD002047; Glyco hormone; 1.
SQ SEQUENCE 15 AA; 1691 MW; 012P924A460B28B9 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 15;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 YPGSRIGN 11
DB 1 YPNTLSN 8

RESULT 35
Q9EBE8_9HIV1
ID Q9EBE8_9HIV1 PRELIMINARY; PRT; 17 AA.
AC Q9EBE8;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=039D12;
RX DOI=10.1128/AAC.44.9.2475-2484.2000;
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,
RA Krakowski K., Bolling L., Aujoy M., Wang X.V., Ellis D., Becker M.F.,
RA Laeute A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;
RT "Human immunodeficiency virus type 1 mutations selected in patients
RT failing efavirenz combination therapy.";
RL Antimicrob. Agents Chemother. 44:2475-2484(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=039D12;
RA Abremski K.B., Bacheler L.T., Li J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY003625; AAC03309.1; -; Genomic_RNA.
FT CHAIN <1 17 protease.
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 1906 MW; 1B34A845B7DEBCA9 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 17;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
DB 1 PQTLMQRP 9

RESULT 36
Q9EKP3_9HIV1
ID Q9EKP3_9HIV1 PRELIMINARY; PRT; 17 AA.
AC Q9EKP3;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=037G06;
RX DOI=10.1128/AAC.44.9.2475-2484.2000;
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,
RA Krakowski K., Bolling L., Aujoy M., Wang X.V., Ellis D., Becker M.F.,
RA Laeute A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;
RT "Human immunodeficiency virus type 1 mutations selected in patients
RT failing efavirenz combination therapy.";
RL Antimicrob. Agents Chemother. 44:2475-2484(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=037G06;
RA Abremski K.B., Bacheler L.T., Li J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY000247; AAF88276.1; -; Genomic_RNA.
FT CHAIN <1 17 protease.
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 1978 MW; 5A37CE45B7DEBCA9 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 17;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
DB 1 PQTLMQRP 9

RESULT 37
Q9EL24_9HIV1
ID Q9EL24_9HIV1 PRELIMINARY; PRT; 17 AA.
AC Q9EL24;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=095C04;
RX DOI=10.1128/AAC.44.9.2475-2484.2000;
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,
RA Krakowski K., Bolling L., Aujoy M., Wang X.V., Ellis D., Becker M.F.,
RA Laeute A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;
RT "Human immunodeficiency virus type 1 mutations selected in patients
RT failing efavirenz combination therapy.";
RL Antimicrob. Agents Chemother. 44:2475-2484(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=095C04;
RA Abremski K.B., Bacheler L.T., Li J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY000247; AAF88276.1; -; Genomic_RNA.
FT CHAIN <1 17 protease.
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 1978 MW; 5A37CE45B7DEBCA9 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 17;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
DB 1 PQTLMQRP 9

RESULT 38
Q9TWK3_MYTEB
ID Q9TWK3_MYTEB PRELIMINARY; PRT; 18 AA.
AC Q9TWK3;

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RX DOI=10.1128/AAC.44.9.2475-2484.2000;
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,
RA Krakowski K., Bolling L., Aujoy M., Wang X.V., Ellis D., Becker M.F.,
RA Laeute A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;
RT "Human immunodeficiency virus type 1 mutations selected in patients
RT failing efavirenz combination therapy.";
RL Antimicrob. Agents Chemother. 44:2475-2484(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=037G06;
RA Abremski K.B., Bacheler L.T., Li J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY000379; AAF88407.1; -; Genomic_RNA.
FT CHAIN <1 17 protease.
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 1963 MW; 6C34A845A57DEBCD CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 17;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
DB 1 PQTLMQRP 9

RESULT 37
Q9EL24_9HIV1
ID Q9EL24_9HIV1 PRELIMINARY; PRT; 17 AA.
AC Q9EL24;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Truncated pol protein (Fragment).
GN Name=pol;
OS Human immunodeficiency virus 1.
OC Viruses; Retro-transcribing viruses; Retroviridae; Orthoretrovirinae;
OC Lentivirus; Primate lentivirus group.
OX NCBI_TaxID=11676;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=095C04;
RX DOI=10.1128/AAC.44.9.2475-2484.2000;
RA Bacheler L.T., Anton E., Kudish P., Baker D., Bunville J.,
RA Krakowski K., Bolling L., Aujoy M., Wang X.V., Ellis D., Becker M.F.,
RA Laeute A.L., George H.V., Spalding D.R., Hollis G., Abremski K.;
RT "Human immunodeficiency virus type 1 mutations selected in patients
RT failing efavirenz combination therapy.";
RL Antimicrob. Agents Chemother. 44:2475-2484(2000).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=095C04;
RA Abremski K.B., Bacheler L.T., Li J.;
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY000247; AAF88276.1; -; Genomic_RNA.
FT CHAIN <1 17 protease.
FT NON_TER 1 17
SQ SEQUENCE 17 AA; 1978 MW; 5A37CE45B7DEBCA9 CRC64;

Query Match
Best Local Similarity 21.9%; Score 25; DB 2; Length 17;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 12 PKAPLYKRP 20
DB 1 PQTLMQRP 9

RESULT 38
Q9TWK3_MYTEB
ID Q9TWK3_MYTEB PRELIMINARY; PRT; 18 AA.
AC Q9TWK3;

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DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TrEMBLrel. 13, Last annotation update)
DE Proximal collagen (Fragment).
OS Mytilus edulis (Blue mussel).
OC Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorpha; Mytiloida;
OC Mytiloidae; Mytilidae; Mytilinae; Mytilus.
OC NCBI_TaxID=6550;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95230211; PubMed=77144453;
RA Qin X., Waite J.H.;
RT "Exotic collagen gradients in the byssus of the mussel Mytilus
RT edulis."
RL J. Exp. Biol. 198;633-644(1995).
SQ SEQUENCE 18 AA; 1643 MW; D27B5EAF64C6BA04 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 18;
Best Local Similarity 46.2%; Pred. No. 1.2e+04;
Matches 6; Conservative 2; Mismatches 3; Indels 2; Gaps 1;

QY 5 PGS--RLGNPKAP 15
DB 4 PGNGQPGNGPGR 16

RESULT 39
ID Q38573_BPKUI PRELIMINARY; PRT; 18 AA.
AC Q38573;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Coat protein (Fragment).
OS Bacteriophage KUI.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Leviviridae;
OC Levivirus; Levivirus subgroup II.
OC NCBI_TaxID=12021;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96207403; PubMed=8615017; DOI=10.1006/viro.1996.0174;
RA Groenewald H., Oudot F., van Duin J.V.;
RT "RNA phage KUI has an insertion of 18 nucleotides in the start codon
RT of its lysis gene."
RL Virology 218:141-147(1996).
DR EMBL: S81763; AAD14371.1; -; Genomic_RNA.
DR HSSP: P07234; IUNA.
KW Capsid protein.
FT NON TER 1
SQ SEQUENCE 18 AA; 1825 MW; 2D402DC226D8904 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 RLGNPKA 14
DB 1 KIGNPVA 7

RESULT 40
ID CXAD_CONGE STANDARD; PRT; 19 AA.
AC P60274;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Alpha-conotoxin GID.
OS Conus geographus (Geography cone) (Nubecula geographus).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbecomha; Hyposogastropoda;
OC Neogastropoda; Conoidea; Conidae; Conus.
OC NCBI_TaxID=6491;

```

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RN [1]
RP PROTEIN SEQUENCE, STRUCTURE BY NMR, SYNTHESIS, MASS SPECTROMETRY, AND
RP MUTAGENESIS OF ARG-12.
RC TISSUE=Venom;
RX PubMed=12419800; DOI=10.1074/jbc.M210280200;
RA Nicke A., Loughman M.L., Millard E.L., Alewood P.F., Adams D.J.,
RA Daly N.L., Craik D.J., Lewis R.J.;
RT "Isolation, structure, and activity of GID, a novel alpha 4/7-
RT conotoxin with an extended N-terminal sequence."
RL J. Biol. Chem. 278:3137-3144(2003).
CC -1- FUNCTION: Alpha-conotoxins act on postsynaptic membranes, they
CC bind to the nicotinic acetylcholine receptors (nAChR) and thus
CC inhibit them. This peptide reversibly inhibits alpha-7, alpha-
CC 3/beta-2, and alpha-4/beta-2 subunits.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -1- MASS SPECTROMETRY: MW=2184.9; METHOD=UNKNOWN; RANGE=1-19;
CC NOTE=Ref.1.
CC -1- SIMILARITY: Belongs to the conotoxin A superfamily. Alpha-type
CC family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PDB; 1MTQ; NMR; -
DR InterPro; IPR013007; Alpha_conotoxin.
DR PROSITE; PS60014; ALPHA_CONOTOXIN; 1.
KW 3D-structure; Acetylcholine receptor inhibitor;
KW Direct protein sequencing; Gamma-carboxyglutamic acid; Hydroxylation;
KW Neurotoxin; Postsynaptic neurotoxin; Toxin.
FT MOD_RES 4 4
FT MOD_RES 16 16
FT DISULFID 5 11
FT DISULFID 6 19
FT MUTAGEN 1 4
SQ SEQUENCE 12 12
MUTAGEN 19 AA; 2130 MW; 0D14E58724C98F0E CRC64;

Query Match 21.9%; Score 25; DB 1; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PGSRLGNP 12
DB 9 PACRYVNP 16

RESULT 41
ID G9TWY2_LEIME PRELIMINARY; PRT; 19 AA.
AC G9TWY2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Membrane-bound acid phosphatase (Fragment).
OS Leishmania mexicana.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OC NCBI_TaxID=5665;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=91312388; PubMed=1857378; DOI=10.1016/0166-6851(91)90152-V;
RA Menz B., Winter G., Ilg T., Lottspeich F., Overath P.;
RT "Purification and characterization of a membrane-bound acid
RT phosphatase of Leishmania mexicana."
RL Mol. Biochem. Parasitol. 47:101-108(1991).
DR InterPro; IPR000560; HisAc_phosphatase.
DR Pfam; PF00328; Acid_phosphat_A; 1.

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FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2178 MW; EC44360F28A7D71B CRC64;

Query Match
 Best Local Similarity 21.9%; Score 25; DB 2; Length 19;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 14 APLVK 18
 DB 1 APMYK 5

RESULT 42

0420Y4_PLABE PRELIMINARY; PRT; 20 AA.
 AC 0420Y4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PB103079.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_Taxid=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,
 RA Britman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza J.,
 RA Bidwell S.L., Rejzender M.A., Carnucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT transcritomic, and proteomic analyses.";
 RT Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 KW Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2219 MW; B923157975PEF7 CRC64;

Query Match
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 12 PKAPLYR 19
 DB 3 PKGPNMKR 10

RESULT 43

069176_CHLTR PRELIMINARY; PRT; 20 AA.
 AC 069176;
 DT 01-AUG-1998 (TrEMBLrel. 07, Created)
 DT 01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Heileh Y.-H., Bobo L.D.;
 RA Submitted (May-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF065436; AAC17176.1; -, Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15
 DB 3 PTATGNAAAP 13

RESULT 44

085509_CHLTR PRELIMINARY; PRT; 20 AA.
 AC 085509;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Heileh Y.-H., Bobo L.D.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF070235; AAC25205.1; -, Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15
 DB 3 PTATGNAAAP 13

RESULT 45

085510_CHLTR PRELIMINARY; PRT; 20 AA.
 AC 085510;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Heileh Y.-H., Bobo L.D.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF070239; AAC25209.1; -, Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1957 MW; 504C9B32B19AF1F3 CRC64;

Query Match
 Best Local Similarity 21.9%; Score 25; DB 2; Length 20;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 5 PGSRLGNPKAP 15
 DB 3 PTATGNAAAP 13

RESULT 46

085510_CHLTR PRELIMINARY; PRT; 20 AA.
 AC 085510;
 DT 01-NOV-1998 (TrEMBLrel. 08, Created)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 OX NCBI_Taxid=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Heileh Y.-H., Bobo L.D.;
 RA Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF070239; AAC25209.1; -, Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1957 MW; 504C9B32B19AF1F3 CRC64;

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085512 CHLTR
ID 085512 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085512;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2a;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070251; AAC25221.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNAAAP 13

RESULT 47
085514 CHLTR
ID 085514 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085514;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B24a;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070255; AAC25225.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNAAAP 13

RESULT 48
085517 CHLTR
ID 085517 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085517;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
```

```
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2b;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070259; AAC25229.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNAAAP 13

RESULT 49
085519 CHLTR
ID 085519 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085519;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2c;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070263; AAC25233.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PGSRLGNPKAP 15
Db 3 PTATTGNAAAP 13

RESULT 50
085520 CHLTR
ID 085520 CHLTR PRELIMINARY; PRT; 20 AA.
AC 085520;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2d;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070267; AAC25237.1; -, Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
```

Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PRTATGNAAP 13

RESULT 51

085521_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085521;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B24b;
RA HeiJeh Y.-H.; Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070271; AAC25241.1; -; Genomic_DNA.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PRTATGNAAP 13

RESULT 52

085522_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085522;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B23a;
RA HeiJeh Y.-H.; Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070275; AAC25245.1; -; Genomic_DNA.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PRTATGNAAP 13

RESULT 53
085523_CHLTR
ID 085523_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085523;

DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2e;
RA HeiJeh Y.-H.; Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070279; AAC25249.1; -; Genomic_DNA.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PRTATGNAAP 13

RESULT 54

085525_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085525;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B2f;
RA HeiJeh Y.-H.; Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070283; AAC25253.1; -; Genomic_DNA.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PRTATGNAAP 13

RESULT 55

085526_CHLTR PRELIMINARY; PRT; 20 AA.

AC 085526;
DT 01-NOV-1998 (TReMBLrel. 08, Created)
DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
DT 01-NOV-1998 (TReMBLrel. 08, Last annotation update)
DE Major outer membrane protein (Fragment).
GN Name=omp-1;
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxId=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B3a;
RA Heish Y.-H., Bobo L.D.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070287; AAC25257.1; -, Genomic_DNA.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PTATTGNAAP 13

RESULT 56
ID 085528_CHLTR PRELIMINARY; PRT; 20 AA.
AC 085528;

DT 01-NOV-1998 (TREMBlrel. 08, Created)
DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
DE Major outer membrane protein (Fragment).

OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OX NCBI_TaxID=813;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B4a;

RA Heish Y.-H., Bobo L.D.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070291; AAC25261.1; -, Genomic_DNA.

FT NON_TER 1
FT NON_TER 20

SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PTATTGNAAP 13

RESULT 57

ID 085530_CHLTR PRELIMINARY; PRT; 20 AA.
AC 085530;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE Major outer membrane protein (Fragment).

GN Name=omp-1;

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B4b;

RA Heish Y.-H., Bobo L.D.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070295; AAC25265.1; -, Genomic_DNA.

FT NON_TER 1
FT NON_TER 20

SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PTATTGNAAP 13

RESULT 58
ID 085531_CHLTR PRELIMINARY; PRT; 20 AA.
AC 085531;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE Major outer membrane protein (Fragment).

GN Name=omp-1;

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B4c;

RA Heish Y.-H., Bobo L.D.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070299; AAC25269.1; -, Genomic_DNA.

FT NON_TER 1
FT NON_TER 20

SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PTATTGNAAP 13

RESULT 59

ID 085533_CHLTR PRELIMINARY; PRT; 20 AA.
AC 085533;

DT 01-NOV-1998 (TREMBlrel. 08, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DE Major outer membrane protein (Fragment).

GN Name=omp-1;

OS Chlamydia trachomatis.

OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.

OX NCBI_TaxID=813;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B4d;

RA Heish Y.-H., Bobo L.D.;

RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF070303; AAC25273.1; -, Genomic_DNA.

FT NON_TER 1
FT NON_TER 20

SQ SEQUENCE 20 AA; 1929 MW; 504C8985119AF1F3 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.3e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 5 PGSRLGNPKAP 15
| : || ||
Db 3 PTATTGNAAP 13

RESULT 60

ID 053520_CHLTR PRELIMINARY; PRT; 20 AA.
AC 053520;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxId=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=95318541; PubMed=7797929;
 RA Hayes L.J., Pecharatana S., Bailey R.L., Hampton T.J., Pickett M.A.,
 RA Mabey D.C., Watt P.J., Ward M.E.;
 RT "Extent and kinetics of genetic change in the omp1 gene of Chlamydia
 trachomatis in two villages with endemic trachoma."
 RT J. Infect. Dis. 172:268-272(1995).
 DR EMBL, 877980; AAB34695.1; -; Genomic_DNA.
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1959 MW; 51FC8985119AF1E3 CRC64;
 Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 5 PGSRGNPKAP 15
 DB 3 PTTTGNATAP 13

RESULT 61
 Q9R8N0 CHLTR
 ID Q9R8N0 CHLTR PRELIMINARY; PRT; 20 AA.
 AC Q9R8N0
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxId=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B124a;
 RA Heileh Y.-H., Bobo L.D.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF070247; AAC25217.1; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1959 MW; 505C8885119AF1F3 CRC64;
 Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 5 PGSRGNPKAP 15
 DB 3 PTTTGNATAP 13

RESULT 62
 Q9R8N4 CHLTR
 ID Q9R8N4 CHLTR PRELIMINARY; PRT; 20 AA.
 AC Q9R8N4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxId=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC STRAIN=B12a;
 RA Heileh Y.-H., Bobo L.D.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF070243; AAC25213.1; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1959 MW; 505C8885119AF1F3 CRC64;
 Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 5 PGSRGNPKAP 15
 DB 3 PTTTGNATAP 13

RESULT 63
 Q9R8P4 CHLTR
 ID Q9R8P4 CHLTR PRELIMINARY; PRT; 20 AA.
 AC Q9R8P4
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 DE Major outer membrane protein (Fragment).
 GN Name=omp-1;
 OS Chlamydia trachomatis.
 OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 ON NCBI_TaxId=813;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Ref Ba;
 RA Heileh Y.-H., Bobo L.D.;
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF070231; AAC25201.1; -; Genomic_DNA.
 FT NON_TER 1
 FT NON_TER 20
 SQ SEQUENCE 20 AA; 1959 MW; 505C8885119AF1F3 CRC64;
 Query Match 21.9%; Score 25; DB 2; Length 20;
 Best Local Similarity 45.5%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 5 PGSRGNPKAP 15
 DB 3 PTTTGNATAP 13

RESULT 64
 Q61871 MOUSE
 ID Q61871 MOUSE PRELIMINARY; PRT; 20 AA.
 AC Q61871
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Envelope protein (Fragment).
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 ON NCBI_TaxId=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AKR; TISSUE=Thymus;
 RX MEDLINE=88091045; PubMed=2826802;
 RA Laigret P., Repaske R., Boulukos K., Rabson A.B., Khan A.S.;
 RT "Potential progenitor sequences of mink cell focus-forming (MCF)
 murine leukemia viruses: ecotropic, xenotropic, and MCF-related viral
 RNAs are detected concurrently in thymus tissues of AKR mice."
 RL J. Virol. 62:376-386(1988).
 DR EMBL, M19049; AAA18408.1; -; mRNA.
 DR GO; GO:0019028; C:viral capsid; IEA.
 DR GO; GO:0019031; C:viral envelope; IEA.

DR GO; GO:0005198; P:structural molecule activity; IEA.
DR InterPro; IPR002050; Env polypeptoid.
DR Pfam; PF00429; Tlv_coat; 1.
KW Envelope protein.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2240 MW; 285338B2EB5C9DD CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.3e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPXAPL 16
DB 15 NPWAPL 20

RESULT 65
Q9PRV5_XENLA PRELIMINARY; PRT; 20 AA.
AC Q9PRV5;
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DE NI(2+)-binding protein, PNIX (Fragment).
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
OC Xenopodinae; Xenopus; Xenopus.
NCBI_Taxid=8335;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=95000642; PubMed=7917276;
RA Grbac-Ivanovic S., Antonijczuk K., Varghese A.H., Plozman M.C.,
Antonijczuk A., Korza G., Ozols J., Sunderman F.W.Tr.;
RT "Lipovitelin 2 beta is the 31 kD NI(2+)-binding protein (pnixb) in
Xenopus oocytes and embryos.";
RL Mol. Reprod. Dev. 38:256-263(1994).
SQ SEQUENCE 20 AA; 2318 MW; 9681AB6C0E5BAE44 CRC64;

Query Match 21.9%; Score 25; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 1.3e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 EYPSRLGN 11
DB 12 EHRGRLSS 20

RESULT 66
O6BC29_HUMAN PRELIMINARY; PRT; 8 AA.
AC O6BC29;
DT 25-OCT-2004 (TReMBLrel. 28, Created)
DT 25-OCT-2004 (TReMBLrel. 28, Last sequence update)
DT 25-OCT-2004 (TReMBLrel. 28, Last annotation update)
DE Protein S (Fragment).
GN Name=PROS1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hamada N.;
RT "Protein S variant in Exon3.";
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB162156; BAD36740.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 8 AA; 1108 MW; D33B5377B59DB5A CRC64;

Query Match 21.1%; Score 24; DB 2; Length 8;

Best Local Similarity 80.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DYFYP 5
DB 1 DYFYP 5

RESULT 67
O12096_CAEV PRELIMINARY; PRT; 9 AA.
AC O12096;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_Taxid=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81439; AAB60832.1; -; Genomic_RNA.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644B7340B8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GSRLGNP 8

RESULT 68
O12098_CAEV PRELIMINARY; PRT; 9 AA.
AC O12098;
DT 01-JUL-1997 (TReMBLrel. 04, Created)
DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_Taxid=11660;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81440; AAB60835.1; -; Genomic_RNA.
FT NON_TER 1
SQ SEQUENCE 9 AA; 922 MW; 21B8644B7340B8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
Best Local Similarity 71.4%; Pred. No. 2.2e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GSRLGNP 8

RESULT 69
O12100_CAEV PRELIMINARY; PRT; 9 AA.
AC O12100;
DT 01-JUL-1997 (TReMBLrel. 04, Created)

DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxId=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81441; AAB60836.1; -; Genomic_RNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 922 MW; 21B8644BB7340EB8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
 DB 2 GCRLCNP 8

RESULT 70
 012102 CAEV PRELIMINARY; PRT; 9 AA.
 AC 012102;
 DT 01-JUL-1997 (TEMBLrel. 04, Created)
 DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxId=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81442; AAB60838.1; -; Genomic_RNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 922 MW; 21B8644BB7340EB8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
 DB 2 GCRLCNP 8

RESULT 71
 012104 CAEV PRELIMINARY; PRT; 9 AA.
 AC 012104;
 DT 01-JUL-1997 (TEMBLrel. 04, Created)
 DT 01-JUL-1997 (TEMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TEMBLrel. 19, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroviridae; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxId=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81443; AAB60840.1; -; Genomic_RNA.

FT NON TER 1
 SQ SEQUENCE 9 AA; 922 MW; 21B8644BB7340EB8 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 9;
 Best Local Similarity 71.4%; Pred. No. 2.2e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
 DB 2 GCRLCNP 8

RESULT 72
 07M500 SEURO PRELIMINARY; PRT; 10 AA.
 ID 07M500;
 AC 07M500;
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE Polysialacturonase (EC 3.2.1.15) IV (Fragment).
 OS Aspergillus sp.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Eurotiales; Trichocomaceae; mitosporic Trichocomaceae; Aspergillus.
 OX NCBI_TaxId=5065;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Strailova B., Dzurowa M., Markovic O., Joernvall H.;
 RT "An essential tyrosine residue of Aspergillus polysialacturonase."
 RL FEBS Lett. 382:164-166 (1996).
 RN [2]
 RP PROTEIN SEQUENCE.
 RX PubMed=6612742;
 RA Strailova B., Dzurowa M., Markovic O., Joernvall H.;
 RT "An essential tyrosine residue of Aspergillus polysialacturonase."
 RL FEBS Lett. 382:164-166 (1996).
 DR PIR; S62880; S62880.
 DR GO; GO:0004650; F:polysialacturonase activity; IEA.
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1146 MW; D58E3F133861BB5D CRC64;

Query Match 21.1%; Score 24; DB 2; Length 10;
 Best Local Similarity 66.7%; Pred. No. 8.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DYEYPG 6
 DB 1 DYAYTG 6

RESULT 73
 09C057 HUMAN PRELIMINARY; PRT; 11 AA.
 ID 09C057;
 AC 09C057;
 DT 01-JUN-2001 (TEMBLrel. 17, Created)
 DT 01-JUN-2001 (TEMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TEMBLrel. 17, Last annotation update)
 DE HEX (Fragment).
 GN Name=HEX;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Oyama Y., Kurabayashi M., Nagai R., Shimomura Y., Sekiguchi K.;
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF182950; AA12833.1; -; Genomic_DNA.
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1125 MW; 2644D7FBE686761F7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 11;

Best Local Similarity 44.4%; Pred. No. 9.6e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 YEYPSRLG 10
DB 3 YPHPEPAG 11

RESULT 74

012074 CAEV

ID 012074 CAEV PRELIMINARY; PRT; 12 AA.

AC 012074;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Tat protein (Fragment).

GN Name-tat;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus;

OC Ovine/caprine lentivirus.

OX NCBI_Taxid=11660;

RN

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81428; AAB60810.1; -; Genomic RNA.

DR GO; GO:0016563; F:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

FT NON_TER 1

SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 75

012076 CAEV

ID 012076 CAEV PRELIMINARY; PRT; 12 AA.

AC 012076;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Tat protein (Fragment).

GN Name-tat;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus;

OC Ovine/caprine lentivirus.

OX NCBI_Taxid=11660;

RN

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81429; AAB60812.1; -; Genomic RNA.

DR GO; GO:0016563; F:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

FT NON_TER 1

SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

DB 2 GCRLCNP 8

RESULT 76

012078 CAEV

ID 012078 CAEV PRELIMINARY; PRT; 12 AA.

AC 012078;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Tat protein (Fragment).

GN Name-tat;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus;

OC Ovine/caprine lentivirus.

OX NCBI_Taxid=11660;

RN

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81430; AAB60814.1; -; Genomic RNA.

DR GO; GO:0016563; F:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

FT NON_TER 1

SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 77

012080 CAEV

ID 012080 CAEV PRELIMINARY; PRT; 12 AA.

AC 012080;

DT 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Tat protein (Fragment).

GN Name-tat;

OS Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retroid viruses; Retroviridae; Lentivirus;

OC Ovine/caprine lentivirus.

OX NCBI_Taxid=11660;

RN

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81431; AAB60816.1; -; Genomic RNA.

DR GO; GO:0016563; F:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

FT NON_TER 1

SQ SEQUENCE 12 AA; 1266 MW; 5A60BBB1B644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 78

012082 CAEV

ID 012082_CAEV PRELIMINARY; PRT; 12 AA.
 AC 012082;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tac;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DCC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81432; AAB60818.1; -, Genomic RNA.
 DR GO; GO:0016563; P:transcriptional activator activity; IEA.
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.
 DR InterPro; IPR004247; Lentiviral Tat.
 DR Pfam; PF02998; Lentiviral_Tat; I.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;
 QY
 Db 6 GSRICNP 12
 2 GCRLCNP 8

Query Match 21.1%; Score 24; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 79
 ID 012084_CAEV PRELIMINARY; PRT; 12 AA.
 AC 012084;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tac;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DCC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81433; AAB60820.1; -, Genomic RNA.
 DR GO; GO:0016563; P:transcriptional activator activity; IEA.
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.
 DR InterPro; IPR004247; Lentiviral Tat.
 DR Pfam; PF02998; Lentiviral_Tat; I.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;
 QY
 Db 6 GSRICNP 12
 2 GCRLCNP 8

Query Match 21.1%; Score 24; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 80
 ID 012086_CAEV PRELIMINARY; PRT; 12 AA.
 AC 012086;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DE 01-JUN-2003 (TReMBLrel. 24, Last annotation update)

DE Tat protein (Fragment).
 GN Name=tac;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DCC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81434; AAB60822.1; -, Genomic RNA.
 DR GO; GO:0016563; P:transcriptional activator activity; IEA.
 DR GO; GO:0045941; P:positive regulation of transcription; IEA.
 DR InterPro; IPR004247; Lentiviral Tat.
 DR Pfam; PF02998; Lentiviral_Tat; I.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;
 QY
 Db 6 GSRICNP 12
 2 GCRLCNP 8

Query Match 21.1%; Score 24; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 81
 ID 012088_CAEV PRELIMINARY; PRT; 12 AA.
 AC 012088;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tac;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DCC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U81435; AAB60824.1; -, Genomic RNA.
 FT NON TER 1
 SQ SEQUENCE 12 AA; 1279 MW; 4B90BB1B8644EB7 CRC64;
 QY
 Db 6 GSRICNP 12
 2 GCRLCNP 8

Query Match 21.1%; Score 24; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

RESULT 82
 ID 012090_CAEV PRELIMINARY; PRT; 12 AA.
 AC 012090;
 DT 01-JUL-1997 (TReMBLrel. 04, Created)
 DT 01-JUL-1997 (TReMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tac;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OX NCBI_TaxID=11660;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

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RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; U81436; AAB60826.1; -; Genomic RNA.
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02398; Lentiviral_Tat; 1.
FT NON_TER
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 83
ID 012092_CAEV PRELIMINARY; PRT; 12 AA.
AC 012092;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN NUCLEOTIDE SEQUENCE.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U81437; AAB60828.1; -; Genomic RNA.
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02398; Lentiviral_Tat; 1.
FT NON_TER
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 84
ID 012094_CAEV PRELIMINARY; PRT; 12 AA.
AC 012094;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN NUCLEOTIDE SEQUENCE.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U81438; AAB60830.1; -; Genomic RNA.
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.

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DR Pfam; PF02398; Lentiviral_Tat; 1.
FT NON_TER
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 85
ID 012106_CAEV PRELIMINARY; PRT; 12 AA.
AC 012106;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN NUCLEOTIDE SEQUENCE.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U81444; AAB60842.1; -; Genomic RNA.
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02398; Lentiviral_Tat; 1.
FT NON_TER
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 12;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 86
ID 012108_CAEV PRELIMINARY; PRT; 12 AA.
AC 012108;
DT 01-JUL-1997 (TRENBLrel. 04, Created)
DT 01-JUL-1997 (TRENBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TRENBLrel. 24, Last annotation update)
DE Tat protein (Fragment).
GN Name=tat;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
OC Ovine/caprine lentivirus.
OX NCBI_TaxId=11660;
RN NUCLEOTIDE SEQUENCE.
RP Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
RA Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RL EMBL; U81445; AAB60844.1; -; Genomic RNA.
DR GO; GO:0015563; P:transcriptional activator activity; IEA.
DR GO; GO:0045941; P:positive regulation of transcription; IEA.
DR InterPro; IPR004247; Lentiviral_Tat.
DR Pfam; PF02398; Lentiviral_Tat; 1.
FT NON_TER
SQ SEQUENCE 12 AA; 1266 MW; 5A60BB1B8644EB7 CRC64;

Query Match
Best Local Similarity 21.1%; Score 24; DB 2; Length 12;

```

Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 87

012110_CAEV
ID 012110_CAEV PRELIMINARY; PRT; 12 AA.

AC 012110; 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OC Tact protein (Fragment).

OS Name=cat;

OC Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Lentivirus;

OC Ovine/caprine lentivirus.

OC NCBI_TaxID=11660;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81446; AAB60846.1; -; Genomic RNA.

DR GO; GO:0016563; P:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

PT NON_TER 1 1

SO SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 88

012112_CAEV
ID 012112_CAEV PRELIMINARY; PRT; 12 AA.

AC 012112; 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OC Tact protein (Fragment).

OS Name=cat;

OC Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Lentivirus;

OC Ovine/caprine lentivirus.

OC NCBI_TaxID=11660;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81447; AAB60848.1; -; Genomic RNA.

DR GO; GO:0016563; P:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

PT NON_TER 1 1

SO SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

DB 2 GCRLCNP 8

RESULT 89

012114_CAEV
ID 012114_CAEV PRELIMINARY; PRT; 12 AA.

AC 012114; 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OC Tact protein (Fragment).

OS Name=cat;

OC Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Lentivirus;

OC Ovine/caprine lentivirus.

OC NCBI_TaxID=11660;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81448; AAB60850.1; -; Genomic RNA.

DR GO; GO:0016563; P:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

PT NON_TER 1 1

SO SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 90

012116_CAEV
ID 012116_CAEV PRELIMINARY; PRT; 12 AA.

AC 012116; 01-JUL-1997 (TREMBlrel. 04, Created)

DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)

DE 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

OC Tact protein (Fragment).

OS Name=cat;

OC Caprine arthritis encephalitis virus (CAEV).

OC Viruses; Retrovirdae; Lentivirus;

OC Ovine/caprine lentivirus.

OC NCBI_TaxID=11660;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;

RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.

DR EMBL; U81449; AAB60852.1; -; Genomic RNA.

DR GO; GO:0016563; P:transcriptional activator activity; IEA.

DR GO; GO:0045941; P:positive regulation of transcription; IEA.

DR InterPro; IPR004247; LentiViral_Tat.

DR Pfam; PF02998; LentiViral_Tat; I.

PT NON_TER 1 1

SO SEQUENCE 12 AA; 1266 MW; 5A60BBB1B8644EB7 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 12;
Best Local Similarity 71.4%; Pred. No. 1.1e+04;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
DB 2 GCRLCNP 8

RESULT 91

012118_CAEV

ID 012118 CAEV PRELIMINARY; PRT; 12 AA.
 AC 012118;
 DT 01-JUL-1997 (T-EMBLrel. 04, Created)
 DT 01-JUL-1997 (T-EMBLrel. 04, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Tat protein (Fragment).
 GN Name=tat;
 OS Caprine arthritis encephalitis virus (CAEV).
 OC Viruses; Retroid viruses; Retroviridae; Lentivirus;
 OC Ovine/caprine lentivirus.
 OC NCBI_TaxID=11660;
 RX [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Turelli P., Guiguen F., Mornex J.-F., Vigne R., Querat G.;
 RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL: U01450; AAB60854.1; -, Genomic RNA.
 DR GO: GO:0016563; F:transcriptional activator activity; IEA.
 DR GO: GO:0045941; P:positive regulation of transcription; IEA.
 DR InterPro: IPR004247; Lentiviral Tat.
 DR Pfam: PF02998; Lentiviral_Tat; 1.
 FT NON TER 1 1
 SQ SEQUENCE 12 AA; 1260 MW; 5A60BBB1B8644EB7 CRC64;
 Query Match 21.1%; Score 24; DB 2; Length 12;
 Best Local Similarity 71.4%; Pred. No. 1.1e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 GSRLGNP 12
 DB 2 GCRLCNP 8

RESULT 92
 Q9UDC6 HUMAN PRELIMINARY; PRT; 13 AA.
 ID Q9UDC6;
 AC Q9UDC6;
 DT 01-MAY-2000 (T-EMBLrel. 13, Created)
 DT 01-MAY-2000 (T-EMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (T-EMBLrel. 21, Last annotation update)
 DE ENDOTHELIN-derived RELATING factor, nitric oxide synthase
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP MEDLINE=93054573; PubMed=1385404;
 RA Janssens S.P., Simouchi A., Quertemous T., Bloch D.B., Bloch K.D.;
 RT "Cloning and expression of a cDNA encoding human endothelium-derived
 RT relating factor/nitric oxide synthase.";
 RL J. Biol. Chem. 267:22694-22694(1992).
 FT NON TER 1 1
 SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;
 Query Match 21.1%; Score 24; DB 2; Length 13;
 Best Local Similarity 36.4%; Pred. No. 1.1e+04;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 YRYGSLGNP 12
 DB 3 FDEPGSDTNSP 13

RESULT 93
 O6LAI1 DROME PRELIMINARY; PRT; 15 AA.
 ID O6LAI1;
 AC O6LAI1;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)

DE Andropin (Fragment).
 GN Name=And;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP STRAIN=Montemayor.
 RC MEDLINE=98393576; PubMed=9725836;
 RX Ramos-Onsins S., Aguade M.;
 RA "Molecular evolution of the Ceeroplin multigene family in Drosophila;
 RT functional genes vs pseudogenes.";
 RL Genetics 150:157-171(1998).
 DR EMBL: Y16853; CAA76430.1; -, Genomic DNA.
 DR EMBL: Y16854; CAA76436.1; -, Genomic DNA.
 DR EMBL: Y16855; CAA76442.1; -, Genomic DNA.
 DR EMBL: Y16856; CAA76448.1; -, Genomic DNA.
 DR EMBL: Y16857; CAA76454.1; -, Genomic DNA.
 DR EMBL: Y16858; CAA76460.1; -, Genomic DNA.
 DR EMBL: Y16859; CAA76466.1; -, Genomic DNA.
 DR EMBL: Y16861; CAA76476.1; -, Genomic DNA.
 DR EMBL: Y16852; CAA76424.1; -, Genomic DNA.
 FT NON TER 1 1
 SQ SEQUENCE 15 AA; 1659 MW; C86F9313DEE24182 CRC64;
 Query Match 21.1%; Score 24; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PGSRLGNPK 13
 DB 7 PPKSLINPK 15

RESULT 94
 Q9NP07 HUMAN PRELIMINARY; PRT; 16 AA.
 ID Q9NP07;
 AC Q9NP07;
 DT 01-OCT-2000 (T-EMBLrel. 15, Created)
 DT 01-OCT-2000 (T-EMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RN NUCLEOTIDE SEQUENCE.
 RP Aulfray C., Ansoyge W., Ballabio A., Estvill X., Gibson K.,
 RA Lehnach H., Pousetka A., Lundeberg J.;
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RN NUCLEOTIDE SEQUENCE.
 RP Puvion R., Estvill X., Escarceller M., Sumoy L.;
 RA Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL389982; CAB97537.1; -, mRNA.
 KW Hypothetical protein.
 FT NON TER 1 1
 SQ SEQUENCE 16 AA; 1484 MW; 97C92837C881A371 CRC64;

QY 10 GNPXAP 15
 DB 2 GQPSAP 7

RESULT 95
 Query Match 21.1%; Score 24; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 1.4e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

Q4TZV7_PAPHA
ID Q4TZV7_PAPHA PRELIMINARY; PRT; 18 AA.
AC Q4TZV7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Ubiqlucous TPR-motif protein Y isoform (Fragment).
GN Name=UTP;
OS Papio hamadryas (Hamadryas baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Cercopithecinae; Papio.
NCBI_TaxID=9557;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Lawson Handley L.J., Hammond R.L., Emareest G., Reber A., Perrin N.;
RT "Low Y chromosome polymorphism in Saudi-Arabian hamadryas baboons
(Papio hamadryas hamadryas)".
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; DQ023315; AAY58227.1; -; Genomic_DNA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 18 AA; 1861 MW; BAE484439EB6986 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.6e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 NPXAPL 16
Db 1 NPKNPV 6

RESULT 96
Q507E3_RAT
ID Q507E3_RAT PRELIMINARY; PRT; 18 AA.
AC Q507E3;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Proto-oncogene c-fos (Fragment).
GN Name=c-Fos;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=Mistar; TISSUE=Liver;
RA Weller E.;
RT "cFos expression in visual cortex".
RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY786174; AAY41063.1; -; Genomic_DNA.
FT NON_TER 18
FT NON_TER 18
SQ SEQUENCE 18 AA; 1990 MW; A378217C052C6052 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.6e+04;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DVEYPSR 8
Db 9 DYEASSR 16

RESULT 97
HBH2_UROHA
ID HBH2_UROHA STANDARD; PRT; 19 AA.
AC P18952;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)

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DE Hemoglobin beta-2 chain (Fragment).
OS Uromastix hardwickii (Indian spiny-tailed lizard).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Lepidodonta; Squamata; Iguania; Acrodonta; Agamidae; Uromastycinae;
OC Uromastix.
NCBI_TaxID=40250;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=84029159; Pubmed=6628672; DOI=10.1016/0014-5793(83)80774-1;
RA Naqvi S., Zaidi Z.H., von Bahr-Lindstroem H., Carlquist M.,
RT Joernvall H.;
RT "Characterization of hemoglobin from the lizard Uromastix
hardwickii".
RL FEBS Lett. 162:290-295(1983).
CC -1- FUNCTION: Involved in oxygen transport from the lung to the
various peripheral tissues.
CC -1- SUBUNIT: Heterotrimer of two alpha chains and two beta chains.
CC -1- TISSUE SPECIFICITY: Red blood cells.
CC -1- SIMILARITY: Belongs to the globin family.
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CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
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CC PIR; A05305; A05305.
DR InterPro; IPR000971; Globin.
DR PROSITE; PS01033; GLOBIN; PARTIAL.
KW Direct protein sequencing; Erythrocyte; Heme; Iron; Metal-binding;
KW Oxygen transport; Transport.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 1914 MW; C40AD8EA30019057 CRC64;

Query Match 21.1%; Score 24; DB 1; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 GNPX 13
Db 16 GNPX 19

RESULT 98
Q8WTX6_HUMAN
ID Q8WTX6_HUMAN PRELIMINARY; PRT; 19 AA.
AC Q8WTX6;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA TISSUE=Eye;
RX MEDLINE=22386257; Pubmed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA Diachenko L., Murnusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ueda T.B., Yoshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Millar S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

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RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green B.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield V.S.N., Krzywiński M.I., Skalska U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maira M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAUSBERG R.;
 RA Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC021928; AA021928.1; -; mRNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2251 MW; AE463E57E7A8702 CRC64;
 Query Match 21.1%; Score 24; DB 2; Length 19;
 Best Local Similarity 60.0%; Pred. No. 1.7e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 1 DYKFP 5
 DB 7 DYKFP 11

RESULT 99
 Q51K80 MAGGR PRELIMINARY; PRT; 20 AA.
 ID Q51K80 MAGGR PRELIMINARY;
 AC Q51K80;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Predicted protein.
 GN ORFNames=MG09625.4;
 OS Magnaporthe oryzae 70-15.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetes; Incertae sedis; Magnaporthaceae; Magnaporthe.
 OX NCBI_TaxID=242507;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Birren B., Nussbaum C., Abebe A., Aboueleil A., Adekoya E.,
 RA Altshuler M., Allen N., Allen T., An P., Anderson M., Anderson S.,
 RA Arachchi H., Ambrose J., Bachantang P., Baldwin J., Barry A.,
 RA Bayat T., Bittencourt B., Bloom T., Bye J., Boguslavsky L.,
 RA Borowsky M., Boukhalter B., Brunache A., Butler J., Calixte N.,
 RA Calvo S., Camarata J., Campo K., Chang J., Chesnais Y., Clifton M.,
 RA Collymore A., Considine T., Cook A., Cooke P., Corum B., Cuomo C.,
 RA David R., Dawoe T., Degray S., Dodge S., Dooley K., Dorje P.,
 RA Dorjee K., Dorris L., Duffey N., Dupes A., Elkins T., Engels R.,
 RA Erickson J., Farina K., Fato S., Ferreira P., Fischer H.,
 RA Fitzgerald M., Foley K., Gage D., Galagan J., Garin G., Gnerre S.,
 RA Ghitke A., Goyette A., Graham J., Grandbois E., Gyaltsen K., Hafez N.,
 RA Hagopian D., Hages B., Hall J., Hatcher B., Heller A., Higgins H.,
 RA Honan T., Horn A., Houde N., Hughes L., Hulme W., Husby E., Iliev I.,
 RA Jaffe D., Jones C., Kamal M., Kamat A., Kamyssele M., Karlsson B.,
 RA Kelle C., Klein A., Kiser P., Kodira C., Kulbokas E., Labucci K.,
 RA Lama D., Landers T., Leger J., Levine S., Lewis T., Lewis T.,
 RA Lindblad-Toh K., Liu X., Lorkytang T., Lorkytang Y., Lucien O.,
 RA Lui A., Ma L.J., Mabbitt R., MacDonald J., Maclean C., Major J.,
 RA Manning J., Maraballa R., Maru K., Matthews C., Mancelli B.,
 RA McCarthy M., McDonough S., Mcghee T., Meldrum J., Menes L.,
 RA Mesirov J., Milnelev A., Mihova T., Mikkelsen T., Mieng V., Moru K.,
 RA Mozer J., Mulrain L., Munson G., Mykiet J., News C., Nguyen C.,
 RA Nguyen N., Nguyen T., Nicol R., Nielsen C., Nizzari M., Norbu C.,
 RA Norbu N., O'donnell P., Okoawo O., O'leary S., Omotosho B.,
 RA O'Neill K., Oman S., Parker S., Perrin D., Phunkhang P., Pigani B.,
 RA Purcell S., Rachupka T., Ramasamy U., Rameau R., Ray V., Raymond C.,
 RA Recta R., Richardson S., Rice C., Rodriguez J., Rogers J., Rogov P.,
 RA Rutman M., Schupbach R., Seaman C., Settipalli S., Sharpe T.,
 RA Sheridan J., Sherpa N., Shi J., Smirnov S., Smith C., Sougen C.,

RA Spencer B., Stalker J., Stange-thomann N., Stavropoulos S.,
 RA Stenson K., Stone S., Stone S., Scrubs M., Talmas J., Tohinga P.,
 RA Tensing P., Tsfige S., Theodore J., Thoulisang Y., Toham K.,
 RA Towey S., Tsamila T., Tsomo N., Vallee D., Vassiliev H.,
 RA Venkataraman V., Vinson J., Vo A., Wade C., Wang S., Wangchuk T.,
 RA Wangdi T., Whitaker C., Wilkinson J., Wu Y., Wyman D., Yadav S.,
 RA Yang S., Yang X., Yeager S., Yee E., Young G., Zainoun J., Zembeck L.,
 RA Zimmer A., Zody M., Zander E.;
 RT "The genome sequence of Magnaporthe oryzae.";
 RT Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Dean R., Mitchell T., Brown D., Pan H., Thon M.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=70-15;
 RA Zhu H., Blackmon B.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AACT01001666; EAA48088.1; -; Genomic DNA.
 SQ SEQUENCE 20 AA; 2251 MW; CFS58A2F6FB2226C4 CRC64;
 Query Match 21.1%; Score 24; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 13 KAPLYKP 20
 DB 8 QAGIKNP 15

RESULT 100
 Q9T209 SOLTU PRELIMINARY; PRT; 20 AA.
 ID Q9T209 SOLTU PRELIMINARY;
 AC Q9T209;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE Cytochrome-C reductase 14 kDa subunit (EC 1.10.2.2) (Fragment).
 OS Solanum tuberosum (potato).
 OC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC asterids; lamiales; Solanales; Solanaceae; Solanum.
 OX NCBI_TaxID=4113;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94198758; PubMed=7764624; DOI=10.1007/BF00191612;
 RA Braun H.-P., Kruit V., Schmitz U.K.;
 RT "Molecular identification of the ten subunits of cytochrome-c
 RT reductase from potato mitochondria.";
 RT Planta 193:99-106(1994).
 DR GO: GO:0008121; P:ubiquinol-cytochrome-c reductase activity; IEA.
 SQ SEQUENCE 20 AA; 2302 MW; 356532D111F826 CRC64;

Query Match 21.1%; Score 24; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.8e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 15 PLYKR 19
 DB 14 PLYKR 18

Search completed: January 20, 2006, 19:11:04
 Job time : 69.5385 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 75.5769 Seconds

(without alignments)
116.273 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115
Sequence: 1 DIPHPNIMKYLVCESVNGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 680474

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21:*

- 1: geneseq219808:*
- 2: geneseq219908:*
- 3: geneseq220008:*
- 4: geneseq220108:*
- 5: geneseq220208:*
- 6: geneseq220308:*
- 7: geneseq220408:*
- 8: geneseq220508:*
- 9: geneseq220608:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	20	3	AAV52512
2	115	100.0	20	5	AAU96316
3	109	94.8	19	5	AAU96316
4	109	94.8	19	5	AAU96316
5	37.5	32.6	20	4	AAU96316
6	37.5	32.6	20	4	AAU96316
7	37.5	32.6	20	4	AAU96316
8	37.5	32.6	20	4	AAU96316
9	37.5	32.6	20	4	AAU96316
10	37.5	32.6	20	4	AAU96316
11	37.5	32.6	20	4	AAU96316
12	37.5	32.6	20	4	AAU96316
13	37.5	32.6	20	4	AAU96316
14	37.5	32.6	20	4	AAU96316
15	37.5	32.6	20	4	AAU96316
16	37.5	32.6	20	4	AAU96316
17	37.5	32.6	20	4	AAU96316
18	37.5	32.6	20	4	AAU96316
19	37.5	32.6	20	4	AAU96316
20	37.5	32.6	20	4	AAU96316
21	37.5	32.6	20	4	AAU96316
22	37.5	32.6	20	4	AAU96316
23	37.5	32.6	20	4	AAU96316
24	37.5	32.6	20	4	AAU96316

25	35	30.4	19	2	AAW30783	Prostate
26	35	30.4	20	2	AAW31168	Human PSA
27	35	30.4	20	4	AAW31939	Ubiquitin
28	34.5	30.0	15	7	ADP70892	Human 161
29	34.5	30.0	15	7	ADP70440	Human 161
30	34.5	30.0	12	8	ADN08675	Cotton w1
31	33	28.7	10	6	ABR47248	Staphyloc
32	33	28.7	10	9	ADY92058	Human tum
33	33	28.7	20	9	ADY70566	Vaccinia
34	32	27.8	10	2	AAW38258	HIV-deriv
35	32	27.8	10	2	AAW45830	Immunogen
36	32	27.8	10	5	ABP14809	HIV A03 s
37	32	27.8	10	5	ABJ15141	Immunogen
38	32	27.8	10	5	ABJ15176	Immunogen
39	32	27.8	10	6	ABU70353	Human imm
40	32	27.8	10	6	ABU69777	Human imm
41	32	27.8	10	6	ABU69799	Human imm
42	32	27.8	10	6	ABU69801	Human imm
43	32	27.8	10	6	ABU69729	Human imm
44	32	27.8	10	7	ADD96334	HIV-1 cro
45	32	27.8	10	7	ADD96886	HIV-1 cro
46	32	27.8	10	7	ADD96262	HIV-1 cro
47	32	27.8	10	7	ADD96332	HIV-1 cro
48	32	27.8	10	7	ADD96310	HIV-1 cro
49	32	27.8	14	6	ABG75542	Human spe
50	32	27.8	14	7	ADP53446	KCRC 603
51	32	27.8	14	8	ADT41277	hSARS vir
52	32	27.8	14	8	ADT38807	hSARS vir
53	32	27.8	15	2	AAW5207	hSARS vir
54	32	27.8	15	4	ABP24655	HIV DR bu
55	32	27.8	15	7	ADN14050	HIV helpe
56	32	27.8	15	7	ADW36336	HIV-1 pol
57	32	27.8	15	9	ADV22436	HIV-1 pol
58	32	27.8	15	9	ADV22435	HIV-1 pol
59	32	27.8	15	9	ADT24615	HIV-1 HLA
60	32	27.8	20	7	ADG9725	Cotton fl
61	32	27.8	8	2	AAW79123	Peptide o
62	31	27.0	12	1	AAW79123	Peptide o
63	31	27.0	12	8	ADQ15533	Targeting
64	31	27.0	13	1	AAW40114	Sequence
65	31	27.0	15	5	ABG61667	Human HGP
66	31	27.0	15	9	ADY21780	SIV pol p
67	31	27.0	15	9	ADY21781	SIV pol p
68	31	27.0	16	3	AAW90148	Ligand ep
69	31	27.0	17	2	AAW65652	UPAR-bind
70	31	27.0	17	2	AAW65650	Antagonis
71	31	27.0	17	2	AAW65658	Clone 20
72	31	27.0	17	2	AAW76564	Clone 20
73	31	27.0	17	3	AAW79011	Drokinase
74	31	27.0	17	3	AAW79011	Ukr antag
75	31	27.0	17	3	AAW79011	Ligand ep
76	31	27.0	17	3	AAW90149	Ligand ep
77	31	27.0	17	4	AAW74578	Context-d
78	31	27.0	17	5	ABR73284	Ukr antag
79	31	27.0	17	7	ADG25933	INPIONCHO
80	31	27.0	17	7	ADY73438	Somatocsta
81	31	27.0	17	8	ADY53072	CHI delet
82	31	27.0	17	8	ADY52033	CHI delet
83	31	27.0	18	4	ABR39967	Peptide #
84	31	27.0	18	4	AAW33587	Peptide #
85	31	27.0	18	4	AAW73385	Human bon
86	31	27.0	18	4	AAW60712	Human bon
87	31	27.0	18	4	ABG55102	Human 11v
88	31	27.0	18	5	ABG43339	Human pep
89	31	27.0	19	9	ADY53056	Hedgehog
90	31	27.0	19	9	ADY52657	Hedgehog
91	31	27.0	20	2	AAW85293	Helper 1-
92	31	27.0	20	3	AAW90154	UPAR targ
93	30.5	26.5	14	2	AAW88603	Secreted
94	30.5	26.5	15	7	ADG70889	Human 161
95	30.5	26.5	15	7	ADG70889	Human 161
96	30.5	26.5	15	7	ADG70889	Human 161
97	30	26.1	8	8	ADT92805	Consensus

98	30	26.1	9	4	AAM22945	Aam22945 HIV pep1
99	30	26.1	9	4	AAM22902	Aam22902 HIV pep1
100	30	26.1	9	9	ADY92047	Ady92047 Human tum

ALIGNMENTS

RESULT 1

ID AAY52512 standard; peptide, 20 AA.

AC AAY52512;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(2).

KW Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

KW canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

PN WO954349-A2.

XX 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animals' hypersensitivity to mite allergens.

PS Claim 3; Page 69; 154pp; English.

XX Sequences AAY52510-Y52522 represent proteolytic fragments of

CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW

CC -map) composition. The HMW-map composition was isolated from a D. farinae

CC homogenate by gel filtration, with each fraction being analysed for the

CC presence of proteins that bound to Ige present in mite-allergic dog

CC antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and

CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

CC encoding them, may be used in therapeutic compositions to modify an

CC animal's hypersensitivity reaction to mite allergens. Animals that may be

CC treated include mammals and birds, especially felines, canines, equines,

CC humans, other pets, and work or domestic animals. The proteins or

CC fragments may also be used to diagnose allergies via a skin test. The

CC proteins and peptides can also be used to raise antibodies, which have a

CC variety of potential uses. For example, they can be used as vaccines to

CC passively immunise animals against dust mite hypersensitivity, as

CC positive controls in test kits and as tools to recover desired dust mite

CC allergens from a mixture of proteins

XX Sequence 20 AA;

SQ

Query Match 100.0%; Score 115; DB 3; Length 20;

Best Local Similarity 100.0%; Pred. No. 1,1e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIPHPTNIHKYLVCSVNGG 20

DB 1 DIPHPTNIHKYLVCSVNGG 20

RESULT 2

ID AAU96316 standard; peptide, 20 AA.

AC AAU96316;

DT 15-JUL-2002 (first entry)

DE Der HMW-map polypeptide #3.

KW Der HMW-map; American house dust mite; anti-allergic; mite; IGE;

KW mite allergenic protein; immunoglobulin E; hypersensitivity;

KW immunocomplex formation.

OS Dermatophagoides farinae.

PN WO200222807-A2.

XX 21-MAR-2002.

PF 14-SEP-2001; 2001WO-US028730.

PR 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

PT New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic

CC acid. The Der HMW-map protein is useful for eliciting an immune response

CC against Der HMW-map protein. The protein or a reagent comprising a non-

CC proteinaceous epitope is useful for identifying an animal (e.g., dog,

CC cat) susceptible to or having an allergic response to a mite. A

CC therapeutic composition is useful for desensitising a host animal to an

CC allergic response to a mite. The DNA and protein can be used in the

CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting

CC binding of proteins to IGE, to prevent immunocomplex formation, thus

CC reducing hypersensitivity responses to mite allergens, and as vaccines

CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

CC represent Der HMW-map polypeptides of the invention

XX Sequence 20 AA;

SQ

Query Match 100.0%; Score 115; DB 5; Length 20;

Best Local Similarity 100.0%; Pred. No. 1,1e-11;

Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DIPHPTNIHKYLVCSVNGG 20

DB 1 DIPHPTNIHKYLVCSVNGG 20

RESULT 3

ID AAY52520 standard; peptide, 19 AA.

AC AAY52520;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(10).

```

XX KM Mite allergen protein; map; high molecular weight; HMW-map; allergy;
XX KM house dust mite; IgE; immunoglobulin E; allergen; mapA; mapB;
XX KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;
XX KM canine; veterinary; antibody; vaccine; immunisation.
XX OS Dermatophagoides farinae.
XX PN MO9954349-A2.
XX PD 28-OCT-1999.
XX PF 16-APR-1999; 99WO-US0808524.
XX PR 17-APR-1998; 98US-00062013.
XX PR 13-MAY-1998; 98US-0085295P.
XX PR 02-SEP-1998; 98US-0098909P.
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX DR WPI; 2000-052700/04.
XX PT Novel high molecular weight Dermatophagoides nucleic acid polypeptides
XX PT used to modify an animals' hypersensitivity to mite allergens.
XX PS Claim 3; Page 70; 154pp; English.
XX CC Sequences AA52510-Y52522 represent proteolytic fragments of
XX CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW
XX CC -map) composition. The HMW-map composition was isolated from a D. farinae
XX CC homogenate by gel filtration, with each fraction being analysed for the
XX CC presence of proteins that bound to IgE present in mite-allergic dog
XX CC antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and
XX CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids
XX CC encoding them, may be used in therapeutic compositions to modify an
XX CC animal's hypersensitivity reaction to mite allergens. Animals that may be
XX CC treated include mammals and birds, especially felines, canines, equines,
XX CC humans, other pets, and work or domestic animals. The proteins or
XX CC fragments may also be used to diagnose allergies via a skin test. The
XX CC proteins and peptides can also be used to raise antibodies, which have a
XX CC variety of potential uses. For example, they can be used as vaccines to
XX CC passively immunise animals against dust mite hypersensitivity, as
XX CC positive controls in test kits and as tools to recover desired dust mite
XX CC allergens from a mixture of proteins
XX SQ Sequence 19 AA;
XX
XX Query Match 94.8%; Score 109; DB 3; Length 19;
XX Best Local Similarity 100.0%; Pred. No. 1e-10;
XX Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 1 DIPHPTNIHKYLVCSVNG 19
XX |||||||||||||||
XX 1 DIPHPTNIHKYLVCSVNG 19
XX Db
XX
XX RESULT 4
XX AAU96324
XX ID AAU96324 standard; peptide; 19 AA.
XX AC AAU96324;
XX XX
XX DT 15-JUL-2002 (first entry)
XX XX
XX DB Der HMW-map polypeptide #11.
XX KM Der HMW-map; American house dust mite; antiallergic; mite; IgE;
XX KM mite allergenic protein; immunoglobulin E; hypersensitivity;
XX KM immunocomplex formation.
XX OS Dermatophagoides farinae.

```

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XX XX
XX PN WO200222807-A2.
XX XX
XX PD 21-MAR-2002.
XX XX
XX PF 14-SEP-2001; 2001WO-US028730.
XX XX
XX PR 14-SEP-2000; 2000US-00662293.
XX XX
XX PA (HESK-) HESKA CORP.
XX PI McCall CA, Hunter SW, Weber ER;
XX XX
XX DR WPI; 2002-351888/38.
XX PT New mite allergenic protein isolated from Dermatophagoides, designated
XX PT Der HMW-map protein, useful as a vaccine for treating mite allergy.
XX XX
XX PS Claim 12; Page 71; 161pp; English.
XX CC The invention relates to an isolated mite allergenic protein of
XX CC Dermatophagoides, designated Der HMW-map protein, and its related nucleic
XX CC acid. The Der HMW-map protein is useful for eliciting an immune response
XX CC against Der HMW-map protein. The protein or a reagent comprising a non-
XX CC proteinaceous epitope is useful for identifying an animal (e.g., dog,
XX CC cat) susceptible to or having an allergic response to a mite. A
XX CC therapeutic composition is useful for desensitising a host animal to an
XX CC allergic response to a mite. The DNA and protein can be used in the
XX CC detection of anti-Der HMW-map antibodies in animal fluids, and inhibition
XX CC of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a
XX CC disease. Antibodies that bind to Der HMW-map are useful for inhibiting
XX CC binding of proteins to IgE, to prevent immunocomplex formation, thus
XX CC reducing hypersensitivity responses to mite allergens, and as vaccines
XX CC against mite allergen hypersensitivity. Sequences AAU96314-AAU96342
XX SQ represent Der HMW-map polypeptides of the invention
XX
XX QY 1 DIPHPTNIHKYLVCSVNG 19
XX |||||||||||||||
XX 1 DIPHPTNIHKYLVCSVNG 19
XX Db
XX
XX RESULT 5
XX AAM18898
XX ID AAM18898 standard; protein; 20 AA.
XX AC AAM18898;
XX XX
XX DT 12-OCT-2001 (first entry)
XX XX
XX DB Peptide #5332 encoded by probe for measuring cervical gene expression.
XX KM Probe; human; microarray; gene expression; cervical epithelial cell;
XX KM cervical cancer.
XX XX
XX OS Homo sapiens.
XX PN WO200157278-A2.
XX PD 09-AUG-2001.
XX PF 30-JAN-2001; 2001WO-US000670.
XX PR 04-FEB-2000; 2000US-0180312P.
XX PR 26-MAY-2000; 2000US-0207456P.
XX PR 30-JUN-2000; 2000US-00608408.
XX PR 03-AUG-2000; 2000US-00632366.
XX PR 21-SEP-2000; 2000US-0234687P.

```

PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488901/53.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human cervical epithelial cells.
XX
XX Claim 27; SEQ ID NO 23724; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
XX (SENP: see AAI10068-AA128459). The present sequence is a peptide encoded
XX by one such probe. The SENPs are derived from human HeLa cells. The SENPs
XX can be used to produce a single exon microarray, which can be used for
XX measuring human gene expression in a sample derived from human cervical
XX epithelial cells. By measuring gene expression, the probes are therefore
XX useful in grading and/or staging of diseases of the cervix, notably
XX cervical cancer. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
Qy 2 IPHPTNHHKYLVC E 15
:||||:|:|:|:
Db 8 LPHP-HSHTHLDCQ 20

RESULT 6
ABB38020
ID ABB38020 standard; peptide; 20 AA.
XX
XX ABB38020;
AC
XX 04-FEB-2002 (first entry)
XX
XX Peptide #5526 encoded by human foetal liver single exon probe.
XX DE
XX Human; foetal liver; gene expression; single exon nucleic acid probe.
XX KM
XX Homo sapiens.
XX OS
XX WO200157277-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX
XX 30-JAN-2001; 2001WO-US000669.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX PR
XX 26-MAY-2000; 2000US-0207456P.
XX PR
XX 30-JUN-2000; 2000US-00608408.
XX PR
XX 03-AUG-2000; 2000US-00632366.
XX PR
XX 21-SEP-2000; 2000US-0234687P.
XX PR
XX 27-SEP-2000; 2000US-0236359P.
XX PR
XX 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-483447/52.
XX DR
XX Human genome-derived single exon nucleic acid probes useful for analyzing
XX PT gene expression in human fetal liver.
XX

PS Claim 27; SEQ ID NO 30655; 639pp + Sequence Listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for measuring
XX human gene expression in a sample derived from human foetal liver. The
XX single exon nucleic acid probes may be used for predicting, measuring and
XX displaying gene expression in samples derived from human fetal liver. The
XX present sequence is a peptide encoded by a single exon nucleic acid probe
XX of the invention. Note: The sequence data for this patent did not form
XX part of the printed specification, but was obtained in electronic format
XX directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
Qy 2 IPHPTNHHKYLVC E 15
:||||:|:|:|:
Db 8 LPHP-HSHTHLDCQ 20

RESULT 7
AAM31434
ID AAM31434 standard; protein; 20 AA.
XX
XX AAM31434;
AC
XX 17-OCT-2001 (first entry)
XX DT
XX Peptide #5471 encoded by probe for measuring placental gene expression.
XX DE
XX Probe; microarray; human; placenta; antenatal diagnosis;
XX KM genetic disorder.
XX KW
XX Homo sapiens.
XX OS
XX WO200157272-A2.
XX PN
XX 09-AUG-2001.
XX PD
XX
XX 30-JAN-2001; 2001WO-US000663.
XX PF
XX 04-FEB-2000; 2000US-0180312P.
XX PR
XX 26-MAY-2000; 2000US-0207456P.
XX PR
XX 30-JUN-2000; 2000US-00608408.
XX PR
XX 03-AUG-2000; 2000US-00632366.
XX PR
XX 21-SEP-2000; 2000US-0234687P.
XX PR
XX 27-SEP-2000; 2000US-0236359P.
XX PR
XX 04-OCT-2000; 2000GB-00024263.
XX

XX (MOLE-) MOLECULAR DYNAMICS INC.
XX PA Penn SG, Hanzel DK, Chen W, Rank DR;
XX PI WPI; 2001-488897/53.
XX DR
XX WPI; 2001-488897/53.
XX PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human placenta.
XX PS
XX Claim 27; SEQ ID NO 31703; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP:
XX see AAI31315-AA157546). The present sequence is a peptide encoded by one
XX such probe. The probes are useful for producing a microarray for
XX predicting, measuring and displaying gene expression in samples derived
XX from human placenta. The probes are useful for antenatal diagnosis of
XX human genetic disorders
XX
SQ Sequence 20 AA;
Query Match 32.6%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 80;

Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
 QY 2 IHPPTNHHKLVCE 15
 :|||:|:|:|:
 Db 8 LPHP-HSHTHLCCQ 20

RESULT 8
 ABB23254
 ID ABB23254 standard; protein; 20 AA.
 AC ABB23254;
 XX
 XX

DT 23-JAN-2002 (first entry)
 XX

DE Protein #5253 encoded by probe for measuring heart cell gene expression.

KW Human; gene expression; heart; microarray; vascular system;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;
 KW congenital heart disease.
 XX

OS Homo sapiens.
 XX

PN WO200157274-A2.
 XX

PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US000666.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 XX

PR 26-MAY-2000; 2000US-0207456P.
 XX

PR 30-JUN-2000; 2000US-00608408.
 XX

PR 03-AUG-2000; 2000US-00632366.
 XX

PR 21-SEP-2000; 2000US-0234687P.
 XX

PR 27-SEP-2000; 2000US-0236359P.
 XX

PR 04-OCT-2000; 2000GB-00024263.
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI; 2001-488990/53.
 XX

PT Single exon nucleic acid probes for analyzing gene expression in human
 XX hearts.
 XX

PS Claim 15; SEQ ID NO 25024; 530bp; English.
 XX

CC The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart (see
 CC ABA21535-ADA41105). The present sequence is a protein encoded by one such
 CC probe. The probes may be used for predicting, measuring and displaying
 CC gene expression in samples derived from the human heart via microarrays.
 CC By measuring gene expression, the probes are useful for predicting,
 CC diagnosing, grading, staging, monitoring and prognosing diseases of the
 CC human heart and vascular system e.g. cardiovascular disease,
 CC hypertension, cardiac arrhythmias and congenital heart disease. Note: The
 CC sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences
 XX

SO Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;
 Best Local Similarity 42.9%; Pred. No. 80;
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IHPPTNHHKLVCE 15
 :|||:|:|:|:
 Db 8 LPHP-HSHTHLCCQ 20

RESULT 9

AAM71153
 ID AAM71153 standard; protein; 20 AA.
 XX

AC AAM71153;
 XX

DT 06-NOV-2001 (first entry)
 XX

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 31459.

KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX

OS Homo sapiens.
 XX

PN WO200157276-A2.
 XX

PD 09-AUG-2001.
 XX

PF 30-JAN-2001; 2001WO-US000666.
 XX

PR 04-FEB-2000; 2000US-0180312P.
 XX

PR 26-MAY-2000; 2000US-0207456P.
 XX

PR 30-JUN-2000; 2000US-00608408.
 XX

PR 03-AUG-2000; 2000US-00632366.
 XX

PR 21-SEP-2000; 2000US-0234687P.
 XX

PR 27-SEP-2000; 2000US-0236359P.
 XX

PR 04-OCT-2000; 2000GB-00024263.
 XX

PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX

PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX

DR WPI; 2001-488990/53.
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 XX gene expression in human bone marrow.
 XX

PS Example 4; SEQ ID NO 31459; 658bp + Sequence Listing; English.
 XX

CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 XX

SO Sequence 20 AA;

Query Match 32.6%; Score 37.5; DB 4; Length 20;
 Best Local Similarity 42.9%; Pred. No. 80;
 Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

QY 2 IHPPTNHHKLVCE 15
 :|||:|:|:|:
 Db 8 LPHP-HSHTHLCCQ 20

RESULT 10
 AAM58647
 ID AAM58647 standard; protein; 20 AA.
 XX

AC AAM58647;
 XX

DT 05-NOV-2001 (first entry)
 XX

DE Human brain expressed single exon probe encoded protein SEQ ID NO: 30752.

KW Human; brain expressed exon; gene expression analysis; probe; microarray;
 KW Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX

OS Homo sapiens.
 XX

PN WO200157275-A2.
 XX

```
XX 09-AUG-2001.
PD
XX
PF 30-JAN-2001; 2001WO-US000667.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483446/52.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX brains.
XX
PS Example 4; SEQ ID NO 30752; 650bp + Sequence Listing; English.
XX
CC The present invention provides a number of single exon nucleic acid
CC probes which are derived from genomic sequences expressed in the human
CC brain. They can be used to measure gene expression in brain cell samples,
CC which may enable the diagnosis and improved treatment of nervous system
CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC epilepsy and cancers. The present sequence is a protein encoded by one of
CC the probes of the invention
XX
SQ Sequence 20 AA;
XX
Query Match 32.6%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
XX
QY 2 IPHPTNHHKYLVCE 15
DB 8 LPHP-HSHTHLQCQ 20
XX
RESULT 11
ABG52865
ID ABG52865 standard; peptide; 20 AA.
XX
AC ABG52865;
XX
DT 25-FEB-2003 (first entry)
XX
DE Human liver peptide, SEQ ID No 31513.
XX
KW Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
KW hypercholesterolaemia; coronary heart disease.
XX
OS Homo sapiens.
XX
PN WO200157273-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US000664.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
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XX Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX WPI; 2001-488898/53.
XX
DR
XX
PT Human genome-derived single exon nucleic acid probes useful for analyzing
XX gene expression in human adult liver.
XX
PS Claim 27; SEQ ID NO 31513; 650bp; English.
XX
CC The invention relates to a single exon nucleic acid probe (SENP) (i) for
CC measuring human gene expression in a sample derived from human adult
CC liver, comprising one of 13109 defined nucleotide sequences given in the
CC specification (or complements/ fragments). The probe hybridises at high
CC stringency to a nucleic acid molecule expressed in the human adult liver.
CC (i) may be used for predicting, measuring and displaying gene expression
CC in samples derived from human adult liver. The genes identified may be
CC involved in genetic liver diseases such as cirrhosis,
CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is
CC associated with coronary heart disease. ABG47348-ABG59930 represent human
CC liver single exon encoded peptides of the invention. Note: The sequence
CC information for this patent does not appear in the printed specification
CC but was obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 20 AA;
XX
Query Match 32.6%; Score 37.5; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 80;
Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;
XX
QY 2 IPHPTNHHKYLVCE 15
DB 8 LPHP-HSHTHLQCQ 20
XX
RESULT 12
ABG40950
ID ABG40950 standard; peptide; 20 AA.
XX
AC ABG40950;
XX
DT 19-AUG-2002 (first entry)
XX
DE Human peptide encoded by genome-derived single exon probe SEQ ID 30615.
XX
KW Human; single exon probe; asthma; lung cancer; COPD; ILD;
KW chronic obstructive pulmonary disease; interstitial lung disease;
KW familial idiopathic pulmonary fibrosis; neurofibromatosis;
KW tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;
KW Heremansky-Pudlak syndrome; sarcoidosis; pulmonary haemorrhoidosis;
KW pulmonary histiocytosis; lymphangioleiomyomatosis; Karsenger syndrome;
KW pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;
KW primary ciliary dyskinesia; pulmonary hypertension;
KW hyaline membrane disease.
XX
OS Homo sapiens.
XX
PN WO200186003-A2.
XX
PD 15-NOV-2001.
XX
PF 30-JAN-2001; 2001WO-US000665.
XX
PR 04-FEB-2000; 2000US-0180312P.
PR 26-MAY-2000; 2000US-0207456P.
PR 30-JUN-2000; 2000US-00608408.
PR 03-AUG-2000; 2000US-00632366.
PR 21-SEP-2000; 2000US-0234687P.
PR 27-SEP-2000; 2000US-0236359P.
PR 04-OCT-2000; 2000GB-00024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
```


PA (WOLF/) WOLFGANG A.
PA (BALD/) BALDWIN T M.
PA (VGAS/) VAN GASTEL F J C.
PA (JANS/) JANSSEN G G.
PA (MURR/) MURRAY C J.
PA (WANG/) WANG H.
PA (WINE/) WINETZKY D S.
XX
PI Wolfgang A. Baldwin TM, Van Gastel FJC, Janssen GG, Murray CJ;
PI Wang H, Winetzky DS;
XX
DR WPI; 2005-222220/23.
XX
PT New peptides that bind to carotenoid compounds, useful as detergents for
PT targeting or removing stains on textiles or fabrics, in personal care or
PT food industry applications, or in various diagnostic applications.
XX
PS claim 1; SEQ ID NO 54; 107pp; English.
XX
CC The invention relates to 432 cyclic or linear carotenoid-binding phage
CC display peptides (ADY56178-ADY56609); to carotenoid-binding peptides
CC which comprise a repeatable motif selected from PPP, SSP, SSK, SPT, PLP,
CC SLH, SPT, TTT, NTS, APS, TPV or a motif shown in ADY5623-ADY5651; and
CC to a complex comprising a phenol-oxidizing enzyme (especially a
CC stachybotrya laccase such as ADY56177 or variants thereof) covalently
CC attached to one of the 432 carotenoid-binding peptides. The invention
CC also relates to polynucleotides encoding a carotenoid-binding peptide,
CC and expression vectors and host cells comprising a polynucleotide
CC encoding a phenol-oxidizing enzyme/carotenoid-binding peptide complex.
CC The carotenoid-binding peptides are useful in complexes with a phenol-
CC oxidizing enzyme for enhancing the selectivity of the enzyme to a target
CC carotenoid stain on a textile or other surface, where the enzyme can then
CC act to bleach the stain. Such enzyme/peptide complexes can be used in
CC detergent or cleaning compositions for targeting or removing food stains
CC (e.g., tomato or paprika) on fabrics, and can also be used in the textile
CC industry in the treatment, processing, finishing, polishing or production
CC of fibers. The enzyme/peptide complexes are additionally useful in
CC personal care applications (e.g., in skin cosmetics as skin tanners), in
CC food industry applications (e.g., as fruit ripening agents) or in
CC diagnostic uses, such as in pharmaceutical applications e.g., to localize
CC the presence of carotenoids in tissues. The present sequence represents a
CC specifically claimed carotenoid-binding cyclic peptide isolated from a
CC phage display library.
XX
SQ Sequence 7 AA;
XX
Query Match 30.4%; Score 35; DB 9; Length 7;
Best Local Similarity 83.3%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 3 PHPTNI 8
| | | | |
| | | | |
Db 1 PHPTNL 6
XX
RESULT 15
ABCO6055
ID ABCO6055 standard; peptide; 10 AA.
XX
AC AEC06055;
XX
DT 20-OCT-2005 (first entry)
XX
DE H3 or D3-acetylated tumor-associated peptide.
XX
KW cytostatic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;
XX cancer; neoplasm.
XX
OS Unidentified.
XX
PN WO2005076009-A2.
XX
PD 18-AUG-2005.
XX

XX
PF 28-JAN-2005; 2005WO-EP000873.
XX
PR 28-JAN-2004; 2004DE-10005273.
PR 06-MAR-2004; 2004DE-10011503.
XX
PA (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.
XX
PI Lemmel C, Rammensee H;
XX
DR WPI; 2005-618379/63.
XX
PT Identifying and quantifying tumor-associated peptides by chemically
PT identifying modifying peptides to generate different physical
PT characteristics, useful for treating tumorous and/or adenomatous
PT diseases.
XX
PS Disclosure; Page 12; 43pp; English.
XX
CC The invention describes a method of identifying and quantifying tumor-
CC associated peptides comprising chemically identifying modifying peptides
CC from samples in order to generate different physical characteristics in
CC the peptides from the different samples. The peptides are useful for
CC producing a medicament for the treatment of tumorous diseases and/or
CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,
CC breast, prostate, ovarian and/or skin cancer. The peptide is used
CC together with an adjuvant. A peptide bound to an antigen-presenting cell
CC is used. The peptides are also useful for the labeling of leukocytes, in
CC particular of T-lymphocytes, for evaluating the progress of therapy in a
CC tumorous disease, and for producing an antibody. The nucleic acid and/or
CC vector and/or cell are useful in producing a medicament for the treatment
CC of tumorous and/or adenomatous diseases. This is the amino acid sequence
CC of a tumor-associated peptide that binds human MHC class I.
XX
SQ Sequence 10 AA;
XX
Query Match 30.4%; Score 35; DB 9; Length 10;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 1 DIPHTNIHK 10
| | | | | :
| | | | | :
Db 1 DAHPHTNVR 10
XX
RESULT 16
ABCO6029
ID ABCO6029 standard; peptide; 10 AA.
XX
AC AEC06029;
XX
DT 20-OCT-2005 (first entry)
XX
DE Tumor-associated peptide SEQ ID NO 12.
XX
KW cytostatic; vaccine; gene therapy; pharmaceutical; immunotherapy; tumor;
XX cancer; neoplasm.
XX
OS Homo sapiens.
XX
PN WO2005076009-A2.
XX
PD 18-AUG-2005.
XX
PF 28-JAN-2005; 2005WO-EP000873.
XX
PR 28-JAN-2004; 2004DE-10005273.
PR 06-MAR-2004; 2004DE-10011503.
XX
PA (IMMA-) IMMATICS BIOTECHNOLOGIES GMBH.
XX
PI Lemmel C, Rammensee H;
XX

DR WPI, 2005-618379/63.
 XX Identifying and quantifying tumor-associated peptides by chemically
 PT identically modifying peptides to generate different physical
 PT characteristics, useful for treating tumorous and/or adenomatous
 PT diseases.
 XX Claim 19, SEQ ID NO 12, 43pp; English.
 XX
 CC The invention describes a method of identifying and quantifying tumor-
 CC associated peptides comprising chemically identically modifying peptides
 CC from samples in order to generate different physical characteristics in
 CC the peptides from the different samples. The peptides are useful for
 CC producing a medication for the treatment of tumorous diseases and/or
 CC adenomatous diseases, such as renal, lung, colon, stomach, pancreatic,
 CC breast, prostate, ovarian and/or skin cancer. The peptide is used
 CC together with an adjuvant. A peptide bound to an antigen-presenting cell
 CC is used. The peptides are also useful for the labeling of leukocytes, in
 CC particular of T-lymphocytes, for evaluating the progress of therapy in a
 CC tumorous disease, and for producing an antibody. The nucleic acid and/or
 CC vector and/or cell are useful in producing a medication for the treatment
 CC of tumorous and/or adenomatous diseases. This is the amino acid sequence
 CC of a tumor-associated peptide that binds human MHC class I.
 CC
 SQ Sequence 10 AA;
 XX
 Query Match 30.4%; Score 35; DB 9; Length 10;
 Best Local Similarity 50.0%; Pred. No. 92;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 1 DIPHTNTHK 10
 | | | | | : |
 1 DAHPNTNVR 10
 DB
 RESULT 17
 AAW30771
 ID AAW30771 standard; peptide; 15 AA.
 XX
 AC AAW30771;
 XX
 DT 27-FEB-1998 (first entry)
 XX
 DE Prostate Specific Antigen (PSA) derived peptide ABT3.
 XX
 DE Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;
 XX
 KM hK2; antigen; antibody; detection; diagnosis; prostate cancer.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9729199-A2.
 XX
 PD 14-AUG-1997.
 XX
 PF 06-FEB-1997, 97WO-US001911.
 XX
 PR 06-FEB-1996; 96US-00595945.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dowell BL, Bridon DP, Qiu X, Lillja H, Pihlmen T, Vihinen M,
 XX
 PI Pettersson IK;
 XX
 DR WPI, 1997-415352/38.
 XX
 PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate
 PT cancer.
 XX
 PS Claim 2, Page 10, 42pp; English.
 XX
 CC AAW30769-84 are synthetic peptides derived from the prostate specific
 CC antigen (PSA) sequence. These peptides are identical to a highly

CC immunogenic region of PSA, and also comprise one or more amino acids
 CC identical or non-identical to the amino acid sequence of human glandular
 CC kallikrein (hK2). The peptides are used as antigens for the production of
 CC antibodies (hK2). The peptides are used to detect PSA in a test sample (claimed). This
 CC is useful for diagnosis of prostate cancer. The peptides enable the
 CC production of antisera necessary to determine the amount of total PSA,
 CC free PSA and PSA-ACT complex present in a sample and thus improve the
 CC ability of the clinician to distinguish, e.g., between BPH (benign
 CC prostatic hyperplasia) and prostatic cancer in a patient
 CC
 SQ Sequence 15 AA;
 XX
 Query Match 30.4%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 4 HPTNTHKYLVC 14
 | | | | | : | | | | |
 5 HPQKVTKFMVC 15
 DB
 RESULT 18
 AAW58054
 ID AAW58054 standard; peptide; 15 AA.
 XX
 AC AAW58054;
 XX
 DT 11-AUG-1998 (first entry)
 XX
 DE Human prostate specific antigen SEQ ID NO:72.
 XX
 DE Human; prostate specific antigen; PSA; epitope; monoclonal antibody;
 XX
 KM detection; cancer; serine protease.
 XX
 OS Synthetic.
 OS Homo sapiens.
 XX
 PN WO9810292-A1.
 XX
 PD 12-MAR-1998.
 XX
 PF 25-AUG-1997, 97WO-US014909.
 XX
 PR 06-SRP-1996; 96US-0025404P.
 XX
 PA (CENZ) CENTOCOR INC.
 XX
 PI Heavner GA;
 XX
 DR WPI, 1998-193789/17.
 XX
 PT Monoclonal antibodies specific for prostate specific antigen - useful,
 PT e.g. in screening for prostate or breast cancer and especially to
 PT distinguish between benign prostatic hyperplasia and prostate cancer.
 XX
 PS Example, Page 59, 84pp; English.
 XX
 CC The present sequence represents a prostate specific antigen (PSA)
 CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing
 CC them have been developed. The antibodies: (a) bind to free PSA; (b) are
 CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LQRRFL)
 CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and
 CC 15.2, 156 or 225 binding to amino acids 139-144 (BSLFLTP) and 55-60
 CC (SLRFPB) respectively of free and bound PSA, or fragments. The antibodies
 CC are useful to detect PSA. For detecting free PSA only, an immunoassay
 CC comprising a solid support with attached labelled monoclonal antibody
 CC specific for free PSA (especially (b)) and a PSA standard can be used. To
 CC detect both free and bound PSA, a second solid support with attached
 CC (differently labelled) monoclonal antibody binding free and bound PSA
 CC (especially selected from (c)) can be used either with, or in place of,
 CC the first solid support. The antibodies are useful in cancer screening,
 CC especially prostate and breast cancer. By obtaining total and free PSA
 CC values, their ratio can be used to separate prostatic cancer (PCA) from

CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also
 CC useful after radical prostatectomy, to predict disease persistence. The
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously
 CC possible by total PSA testing, avoiding biopsies
 XX
 SQ Sequence 15 AA;

Query Match 30.4%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHKYLVC 14
 || : ||::||
 Db 5 HPQKVTKFMLC 15

RESULT 19
 AAMS8055
 ID AAMS8055 standard; peptide; 15 AA.
 XX
 AC AAMS8055;

DT 11-AUG-1998 (first entry)

DE Human prostate specific antigen peptide SEQ ID NO:73.

KM Human; prostate specific antigen; PSA; epitope; monoclonal antibody;
 KW detection; cancer; serine protease.

OS Synthetic.

OS Homo sapiens.

PN WO9810292-A1.

PD 12-MAR-1998.

PF 25-AUG-1997; 97WO-US014909.

PR 06-SEP-1996; 96US-0025404P.

PA (CENZ) CENTOCOR INC.

PI Heavner GA;

DR WPI; 1998-193789/17.

PT Monoclonal antibodies specific for prostate specific antigen - useful,
 PT e.g. in screening for prostate or breast cancer and especially to
 PT distinguish between benign prostatic hyperplasia and prostate cancer.

PS Example; Page 60; 84pp; English.

CC The present sequence represents a prostate specific antigen (PSA)
 CC peptide. Monoclonal antibodies specific for PSA and hybridomas producing
 CC them have been developed. The antibodies: (a) bind to free PSA; (b) are
 CC monoclonal antibody 365 binding to amino acids 82-87 of free PSA (LKNRFL)
 CC or fragment, and (c) are monoclonal antibodies 10, 11, 16 or 22.2 and
 CC 15.2, 156 or 225 binding to amino acids 139-144 (ESLFLTP) and 55-60
 CC (SLRFPB) respectively of free and bound PSA, or fragments. The antibodies
 CC are useful to detect PSA. For detecting free PSA only, an immunoassay
 CC comprising a solid support with attached labeled monoclonal antibody
 CC specific for free PSA (especially (b)) and a PSA standard can be used. To
 CC detect both free and bound PSA, a second solid support with attached
 CC (differently labelled) monoclonal antibody binding free and bound PSA
 CC (especially selected from (c)) can be used either with, or in place of,
 CC the first solid support. The antibodies are useful in cancer screening,
 CC especially prostate and breast cancer. By obtaining total and free PSA
 CC values, their ratio can be used to separate prostatic cancer (PCA) from
 CC benign prostatic hyperplasia (BHP) patients. Measurement of PSA is also
 CC useful after radical prostatectomy, to predict disease persistence. The
 CC antibodies allow evaluation of PSA free/total ratio, enabling separation
 CC of BPH and PCA patients with PSA values 4-10 ng/ml not previously

CC possible by total PSA testing, avoiding biopsies
 XX
 SQ Sequence 15 AA;

Query Match 30.4%; Score 35; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHKYLVC 14
 || : ||::||
 Db 2 HPQKVTKFMLC 12

RESULT 20
 ADW37502
 ID ADW37502 standard; peptide; 15 AA.
 XX
 AC ADW37502;

DT 10-MAR-2005 (first entry)

DE HLA binding epitope #8252.

KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;

KW viral disease; cancer.

OS Unidentified.

PN WO2003040165-A2.

PD 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

PA (EPIM-) EPIMONB INC.

PI Sette A, Sidney J, Southwood S;

DR WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

PS Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.

SQ Sequence 15 AA;

Query Match 30.4%; Score 35; DB 7; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14
 || : ||: ||
 Db 5 HPQKVTKEFMLC 15

RESULT 21
 ID ADM35209
 ADM35209 standard; peptide; 15 AA.

XX ADM35209;

DT 10-MAR-2005 (first entry)

XX HLA binding epitope #5959.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.

XX Unidentified.

XX WO2003040165-A2.

XX 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific
 binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Qy Query Match 30.4%; Score 35; DB 7; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14
 || : ||: ||
 Db 5 HPQKVTKEFMLC 15

RESULT 22

ADM33268
 ID ADM33268 standard; peptide; 15 AA.

XX ADM33268;

DT 10-MAR-2005 (first entry)

XX HLA binding epitope #4018.

XX Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.

XX Unidentified.

XX WO2003040165-A2.

XX 15-MAY-2003.

PF 18-OCT-2001; 2001WO-US051650.

PR 19-OCT-2000; 2000US-0242350P.

PR 20-APR-2001; 2001US-0285624P.

XX (EPIM-) EPIMMUNE INC.

PI Sette A, Sidney J, Southwood S;

XX WPI; 2003-441519/41.

PT New composition comprising at least one peptide having allele-specific
 binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.

XX Claim 1; Page 52-379; 382pp; English.

CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.

XX Sequence 15 AA;

Qy Query Match 30.4%; Score 35; DB 7; Length 15;
 Best Local Similarity 36.4%; Pred. No. 1.5e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14
 || : ||: ||
 Db 5 HPQKVTKEFMLC 15

RESULT 23

ID ADM33976
 ADM33976 standard; peptide; 15 AA.

XX ADM33976;

DT 10-MAR-2005 (first entry)

KW	prostate cancer; AIDS; renal carcinoma; cervical carcinoma; lymphoma;
XX	chondyroma acuminatum.
XX	
OS	unidentified.
PN	WO2004031211-A2.
XX	
PD	15-Apr-2004.
XX	
PF	03-OCT-2003; 2003WO-US031308.
XX	
PR	03-OCT-2002; 2002US-0416207P.
PR	08-OCT-2002; 2002US-0417269P.
XX	
PA	(EPIM-) EPIMMUNE INC.
XX	
PI	Sidney J., Southwood S., Sette A;
DR	WPI, 2004-347953/32.
XX	
PT	New composition of peptides and nucleic acids capable of binding Major
PT	Histocompatibility Complex molecules, useful for diagnosing, preventing
PT	or treating viral infections or cancer, such as prostate cancer,
PT	hepatitis B or AIDS.
XX	
PS	Claim 1, SEQ ID NO 2035; 186pp; English.
XX	
CC	The invention relates to a novel composition comprising one or more
CC	peptides or nucleic acids encoding an HIV binding peptide. The
CC	composition further comprises an HTL epitope. It also comprises a spacer
CC	molecule, a carrier, an MHC targeting sequence or a lipid. The peptides
CC	are incorporated as part of a liposome. The peptide is from an antigen
CC	selected from prostate specific antigen (PSA), prostate specific membrane
CC	antigen (PSM), hepatitis B virus (HBV) antigen, hepatitis C virus (HCV)
CC	antigen, malignant melanoma antigen (MAGE), Epstein Barr virus, human
CC	immunodeficiency type-1 (HIV-1), human immunodeficiency type-2 (HIV-2),
CC	Papilloma virus, Lassa virus, Mycobacterium tuberculosis (MT), p53,
CC	murine p53 (mp53), CEA, HER2/neu, and tyrosine kinase related protein
CC	(TRP). The composition is useful for preventing or treating viral
CC	infections or cancer, such as prostate cancer, hepatitis B, hepatitis C,
CC	AIDS, renal carcinoma, cervical carcinoma, lymphoma, CMV or chondyroma
CC	acuminatum. The composition is also be used for diagnosing such diseases.
CC	This sequence represents a peptide of the invention.
XX	
SQ	Sequence 15 AA;
	Query Match 30.4%; Score 35; DB 8; Length 15;
	Best Local Similarity 36.4%; Pred. NO. 1.5e+02;
	Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY	4 HPTNHRKYLVC 14 : :: Db 5 HPQVKTKFMC 15
RESULT 25	
AAW30783	
ID	AAW30783 standard; peptide; 19 AA.
XX	
AC	AAW30783;
XX	
DT	27-FEB-1998 (first entry)
XX	
DE	Prostate Specific Antigen (PSA) derived peptide ABT15.
XX	
KW	Prostate specific antigen; PSA; immunogenic; human glandular kallikrein;
KX	hk2; antigen; antibody; detection; diagnosis; prostate cancer.
XX	
OS	Synthetic.
OS	Homo sapiens.
XX	
FN	WO9729199-A2.
XX	

PD 14-AUG-1997.
 XX
 PF 06-FEB-1997; 97MO-US001911.
 XX
 PR 06-FEB-1996; 96US-00595945.
 XX
 PA (ABBO) ABBOTT LAB.
 XX
 PI Dowell BL, Bridon DP, Qiu X, LiJia H, Pihonen T, Vihtinen M,
 PI Pectersson IK,
 XX WPI, 1997-415352/38.
 DR
 PT Prostate Specific Antigen peptide(s) - useful for diagnosis of prostate
 PT cancer.
 XX
 XX Claim 2; Page 10; 42pp; English.
 XX
 CC AAM0769-84 are synthetic peptides derived from the prostate specific
 CC antigen (PSA) sequence. These peptides are identical to a highly
 CC immunogenic region of PSA, and also comprise one or more amino acids
 CC identical or non-identical to the amino acid sequence of human glandular
 CC kallikrein (hK2). The peptides are used as antigens for the production of
 CC antibodies which are used to detect PSA in a test sample (claimed). This
 CC is useful for diagnosis of prostate cancer. The peptides enable the
 CC production of antisera necessary to determine the amount of total PSA,
 CC free PSA and PSA-AC complex present in a sample and thus improve the
 CC ability of the clinician to distinguish, e.g., between BPH (benign
 CC prostatic hyperplasia) and prostatic cancer in a patient
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 30.4%; Score 35; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 2e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 4 HPTNHHKYLVC 14
 ||:|::|
 Db 9 HPOKVKFPLC 19
 XX
 RESULT 26
 AAY31168
 ID AAY31168 standard; peptide; 20 AA.
 XX
 AC AAY31168;
 XX
 DT 28-OCT-1999 (first entry)
 XX
 DE Human PSA loop peptide PUS 7.
 XX
 KW Ubiquitin; immunocastration; fusion protein; heat shock protein; epitope;
 KW immune response stimulation; vaccine; T cell; viral; infection; cancer;
 KW bacterial; parasitic; treatment; gastrointestinal disease; HIV infection;
 KW pulmonary infection; respiratory infection; scaffold; anti-self; p1g;
 KW steriodogenesis; gamete maturation; prostate; breast; castration; TNF;
 KW tumour necrosis factor; septic shock; arthritis; Crohn's disease;
 KW inflammatory bowel disease; ulcerative colitis; chorioidic gonadotropin;
 KW fertility; sperm protein; growth rate; antibody; detection; PSA; human;
 KW prostate specific antigen; loop peptide.
 XX
 OS Homo sapiens.
 XX
 PN WO9942472-A1.
 XX
 PD 26-AUG-1999.
 XX
 PF 26-JAN-1999; 99MO-US001588.
 XX
 PR 19-FEB-1998; 98US-00026276.
 XX
 PA (IGEN-) IGEN INT INC.
 XX

PI Kenten JH, Tramontano A, Pilon AL, Lohas GL, Roberts SF;
 XX WPI, 1999-518582/43.
 DR
 XX
 PT Epitope-containing fusion proteins used to generate a highly specific
 PT immune responses.
 XX
 XX Example 2; Page 38; 67pp; English.
 XX
 CC This invention describes a novel fusion protein, comprising a heat shock
 CC protein (e.g. ubiquitin), fused to an epitope(s) in a defined manner
 CC which is useful for the stimulation of a highly specific immune response
 CC when administered to an animal. The protein of the invention may be post-
 CC translationally modified (e.g. by the addition of fatty acids to enhance
 CC immunogenicity). The fusion proteins of the invention can be used as
 CC vaccines to induce an immune response. When a T cell epitope is attached,
 CC they can be used for control of viral infections, bacterial infections,
 CC parasitic infection and cancer. The fusion proteins can be used in
 CC pharmaceutical compositions for the treatment of gastrointestinal
 CC diseases, pulmonary infections, respiratory infections, and HIV
 CC infections. The use of ubiquitin as a scaffold is also useful for the
 CC presentation and stimulation of anti-self immune responses, e.g.
 CC generation of anti-gonadotropin releasing hormone antibodies which result
 CC in the suppression of luteinizing hormone and follicle stimulating
 CC hormone. This indirectly suppresses steroidogenesis and gamete maturation
 CC in males and females. This type of anti-self response in humans is useful
 CC in the treatment of prostate cancer and breast cancer. In livestock, the
 CC ability to stimulate an anti-self response provides a simple alternative
 CC to physical castration. Immunocastration of pigs is a better alternative
 CC to physical castration, as it does not result in any of the detrimental
 CC side effects associated with physical castration. Other examples of
 CC diseases and conditions treated with self proteins fused with ubiquitin
 CC are TNF and its epitopes to modulate septic shock, arthritis,
 CC inflammatory bowel disease, Crohn's disease, and ulcerative colitis; Ig
 CC epsilon heavy chain for the control of allergic reactions; chorioidic
 CC gonadotropin for fertility control; and sperm proteins for fertility
 CC control. A further use of the fusion proteins is as part of a vaccine to
 CC enhance growth rate and thereby the final weight of the livestock prior
 CC to shipment to market. In addition, the fusion proteins of the invention
 CC can be used to detect and identify antibodies from experimental samples.
 CC This sequence represents a human prostate specific antigen (PSA) peptide
 CC loop used in the method of the invention
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 30.4%; Score 35; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 2.1e+02;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
 QY 4 HPTNHHKYLVC 14
 ||:|::|
 Db 7 HPOKVKFPLC 17
 XX
 RESULT 27
 AAB71939
 ID AAB71939 standard; peptide; 20 AA.
 XX
 AC AAB71939;
 XX
 DT 10-MAY-2001 (first entry)
 XX
 DE Ubiquitin fusion protein epitope insertion PUS 7.
 XX
 KW Human; immunostimulant; antiallergic; growth promoting; vaccine;
 KW heat shock fusion protein; ubiquitin; self-epitope; immunogen;
 KW male-specific peptide hormone; female-specific peptide hormone;
 KW prostate specific antigen; PSA.
 XX
 OS Homo sapiens.
 XX
 PN WO200112216-A1.
 XX

CC that modulates the status of a novel human protein (161P2F10B) and its
 CC variants having a sequence of 875 amino acids provided in the
 CC specification. The protein of the invention is over-expressed in certain
 CC cancers. The compounds of the invention may have cytostatic activity and
 CC be useful for gene therapy or the development of a vaccine. The
 CC sequence of the 161P2F10B protein, and the gene which encodes it, may
 CC competition and methods of the invention are useful in diagnosing,
 CC preventing and treating cancer. The present sequence is the amino acid
 CC sequence of a peptide which is derived from the sequence of the human
 CC 161P2F10B protein and which may be used in the development of the
 CC compounds of the invention.

XX Sequence 15 AA;

Query Match 30.0%; Score 34.5; DB 7; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.8e+02;
 Matches 10; Conservative 1; Mismatches 2; Indels 7; Gaps 2;

Qy 2 IPR-PTNHHKYLVCESVNGG 20
 :|||:|:
 Db 1 IPRHPTNV-----ESCPCG 14

RESULT 30

ID ADN08675 standard; peptide; 12 AA.

AC ADN08675;

DT 15-JUL-2004 (first entry)

XX Cotton wine stain binding peptide, SEQ ID No 240.

KW tannin; polyphenolic; anthocyanin; tea; wine; stain; fabric; surface;
 KM enzymatic; ceramic; hair; skin; detergent; cleaning; wine ageing;
 KM fermentation; reducing; eliminating; astringency; conjugate; bleaching;
 KM personal care product; cream; lotion; ointment.

XX Unidentified.

PN WO2004033482-A2.

PD 22-APR-2004.

PF 06-OCT-2003; 2003WO-US031776.

PR 08-OCT-2002; 2002US-0417210P.

XX (GENV) GENENCOR INT INC.

PA Murray CJ, Tijerina P, Van Gaestel FJC;

PI WPI; 2004-340885/31.

DR Novel binding peptide binding to tannin, anthocyanin and phenolic
 PT compounds, useful for delivering agent to target, and for modifying tea
 PT or wine stain on fabric or surface chosen from ceramic, glasses, wood,
 PT paper, skin, hair and plastic.

XX Claim 1; SEQ ID NO 240; 38pp; English.

CC The invention relates to a novel peptide which binds to tannin,
 CC polyphenolic or anthocyanin compounds. The binding peptide consists
 CC essentially of any one of 316 amino acid sequences of 5-13 amino acids in
 CC length or has at least 70% identity to one of the 316 amino acid
 CC sequences. The binding peptide is useful for delivering an agent to a
 CC target, which involves conjugating the binding peptide to an agent to
 CC form a binding peptide conjugate and exposing a target to the binding
 CC peptide conjugate, where the binding peptide conjugate binds to the
 CC target. An enzymatic composition comprising the binding peptide is useful
 CC for modifying a tea or wine stain on a fabric or a surface, which
 CC involves contacting the surface having tea or wine stain with the
 CC enzymatic composition. The surface is preferably a ceramic surface, hair

CC or skin. The binding peptide is useful for producing enzymatic
 CC compositions for use in detergent or cleaning compositions such as for
 CC removing food stains on fabrics or removing food stains on surfaces such
 CC as ceramic and teeth. The binding peptide is useful in the wine ageing
 CC process, where a tannin compound is targeted at the early stage of wine
 CC fermentation process for reducing or eliminating astringency of tannins
 CC in the wine. The binding conjugate, combined with a bleaching agent is
 CC useful for delivering a bleaching agent to stained teeth for bleaching.
 CC The binding peptide and binding conjugate are useful in personal care
 CC products such as creams, lotions and ointments. The binding peptide is
 CC useful for modifying astringency in skin. This sequence represents a
 CC binding peptide which specifically binds to wine stains on cotton for use
 CC in the stain removal process of the invention.

XX Sequence 12 AA;

Query Match 29.6%; Score 34; DB 8; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.7e+02;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPRPTNHH 9
 :|||:|:
 Db 2 MPHATVH 9

RESULT 31

ID ABR47248 standard; peptide; 10 AA.

AC ABR47248;

DT 10-JUN-2003 (first entry)

XX Staphylococcus aureus CHIPS-related peptide #2437.

KW CHIPS; Chemotaxis Inhibitory Protein; C5a-receptor; C5AR;
 KM formulated peptide receptor; FPR; neutrophil; monocyte; endothelial cell;
 KM inflammation; cardiovascular disease; central nervous system disease;
 KM gastrointestinal disease; skin disease; genitourinary disease;
 KM joint disease; respiratory disease; HIV infection; antiinflammatory;
 KM cardiant; cerebroprotective; neuroprotective; nootropic; dermatological;
 KM gynecological; immunosuppressive; anti-HIV.

XX Staphylococcus aureus.

OS Synthetic.

XX WO2003006048-A1.

PD 23-JAN-2003.

PF 11-JUL-2001; 2001WO-BP008004.

PR 11-JUL-2001; 2001WO-BP008004.

XX (JARI-) JARI PHARM BV.

PA Van Kessel CPM, Gosselaar-De Haas CTC, Kruijtz JAW;

PI Van Strijp JAG;

XX WPI; 2003-256333/25.

DR Combination of peptides derived from chemotaxis inhibiting protein from
 XX Staphylococcus aureus (CHIPS) having CHIPS activity, useful in
 PT prophylaxis and treatment of inflammation, cardiovascular, skin and
 PT kidney diseases.

PS Example 1; Page 56; 89pp; English.

XX The present invention relates to peptides (ABR44811-ABR47162 and ABR47164
 CC -ABR47365) derived from the Chemotaxis Inhibitory Protein (CHIPS) from
 CC Staphylococcus aureus. The peptide fragments are useful in the
 CC prophylaxis or treatment of diseases or disorders involving the C5a-
 CC receptor (C5AR) and/or formulated peptide receptor (FPR) or neutrophils,

CC monocytes and endothelial cells or involving acute or chronic
 CC inflammation reactions. The diseases or disorders include cardiovascular
 CC disease, disease of the central nervous system, gastrointestinal
 CC diseases, skin diseases, genitourinary diseases, joint diseases,
 CC respiratory diseases and HIV infection

CC Sequence 10 AA;

Query Match 28.7%; Score 33; DB 6; Length 10;
 Best Local Similarity 100.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 5; Conservative 0; Mismatches 0;

QY 3 PPTN 7
 |||||
 DB 5 PPTN 9

RESULT 32
 ADY92058
 ID ADY92058 standard; peptide; 10 AA.

XX ADY92058;

DT 02-JUN-2005 (first entry)

DE Human tumor-associated antigen LDHC MHC I epitope peptide - SEQ ID 378.

XX tumor-associated antigen, LDHC; lactate dehydrogenase C; gene expression;
 KM cell death; cell growth; tumor; cancer; neoplasm; cytostatic.

OS Homo sapiens.

PN WO2005026205-A2.

XX 24-MAR-2005.

PF 10-SEP-2004; 2004WO-EP010164.

XX 10-SEP-2003; 2003DE-01041812.

PA (GANY-) GANYMED PHARM AG.

PI Therescl O, Sahlin U, Koslowski M;

DR WPI; 2005-242374/25.

PT Pharmaceutical composition, with an agent to restrict the expression or
 PT activity of an antigen associated with a tumor, incorporates structured
 PT nucleic acids.

PS Disclosure; SEQ ID NO 378; 353pp; German.

XX The invention relates to a novel pharmaceutical composition, whereby the
 CC composition contains an agent which restricts the expression or activity
 CC of an antigen associated with a tumor and the antigen has a sequence,
 CC coded by a nucleic acid, where the nucleic acid is selected from SEQ ID
 CC NOS: 19-21, 54-57, 1-5, 29, 31-33, 37, 39, 40, 62, 63, 70, 74 or 85-88.
 CC The composition of the invention induces cell death and a reduction of
 CC cell growth, cell membrane damage or secretion of cytokines. The
 CC composition may be useful for the identification of differentially
 CC expressed genes in tumors with combined in silico and wet bench studies.
 CC The current sequence is that of a human tumor-associated antigen lactate
 CC dehydrogenase C (LDHC) MHC class I HLA-B*0702 epitope peptide of the
 CC invention which stimulates cytotoxic T-lymphocytes in vivo.

XX Sequence 10 AA;

Query Match 28.7%; Score 33; DB 9; Length 10;
 Best Local Similarity 40.0%; Pred. No. 2e+02; Indels 0; Gaps 0;
 Matches 4; Conservative 4; Mismatches 2;

QY 4 HPTNKLVLV 13
 |||||

DB 1 HPTSGWII 10

RESULT 33
 ADX70566
 ID ADX70566 standard; peptide; 20 AA.

XX ADX70566;

DT 05-MAY-2005 (first entry)

DE Vaccinia BSR ectodomain peptide, BSR pep#10.

XX vaccine; pox virus infection; virucide; infection;
 KM variola virus infection; BSR.

OS Vaccinia virus.

PN WO2005013918-A2.

XX 17-FEB-2005.

PF 27-FEB-2004; 2004WO-US005903.

PR 28-FEB-2003; 2003US-0451337P.

PA (UNIV-) UNIV PENNSYLVANIA.

PA (NAME-) NAT INST OF HEALTH JAPAN.

PA (COIN-) COHEN G.

PA (EISE-) EISENBERG R J.

PA (WHIT-) WHITEBECK J C.

PA (ALDA-) ALDAR C L.

PA (MOSS-) MOSS B.

PA (LUST-) LUSTIG S.

PA (FOGG-) FOGG C.

XX WPI; 2005-152502/16.

XX New vaccine having a soluble truncated mammalian poxvirus envelope

PT protein or an isolated nucleic acid encoding the protein, useful for

PT preventing and treating a poxvirus infection, in particular a smallpox

PT infection.

PS Example 4; SEQ ID NO 16; 168pp; English.

XX The invention relates to a vaccine comprising a soluble truncated

CC mammalian poxvirus envelope protein or an isolated nucleic acid encoding

CC the protein, and a carrier, where the protein is at least one protein

CC selected from A33Rc, B5Rc, and L1R(185c), or its homolog. The methods and

CC compositions of the present invention are useful for preventing and

CC treating a poxvirus infection, in particular a smallpox infection. The

CC present sequence represents a vaccinia BSR ectodomain peptide.

XX Sequence 20 AA;

Query Match 28.7%; Score 33; DB 9; Length 20;
 Best Local Similarity 60.0%; Pred. No. 4.5e+02; Indels 0; Gaps 0;
 Matches 6; Conservative 0; Mismatches 4;

QY 10 KYLVCESVNG 19
 |||||
 DB 6 KYFRCBCKNG 15

RESULT 34

AA38258
 ID AA38258 standard; peptide; 10 AA.

XX AA38258;

DT 29-SEP-1999 (first entry)

XX HIV-derived HLA-binding peptide.


```

XX Immunogen; HLA; human leukocyte antigen; binding motif; antiviral; MHC;
KM major histocompatibility complex; viral infection; anticancer;
KM prostate cancer; lymphoma; hepatitis; AIDS; diagnostic; diagnosis.
XX Human immunodeficiency virus.
XX MO9403205-A1.
XX PD 17-FEB-1994.
XX PF 06-AUG-1993; 93MO-US007421.
XX PR 07-MAR-1992; 92US-00926666.
XX PR 05-MAR-1993; 93US-00027746.
XX (CYTE-) CYTEL CORP.
XX PA Kubo RT, Grey HM, Sette A, Cells E;
XX PI WPI, 1994-065403/08.
XX DR Peptide which specifically binds selected MHC allele - used to induce an
XX PT immune response for treatment or prevention of viral infection or cancer,
XX or for diagnosis.
XX PS Disclosure, Page 110, 150pp; English.
XX CC The sequence is a specific example of a group of new immunogenic peptides
XX CC having an HLA-A3.2, HLA-A1, HLA-A11 or HLA-A24.1 binding motif. For
XX CC example, the peptides having an HLA-A3.2 binding motif each have 9-10
XX CC residues and contain, from the N-terminus to the C-terminus, (a) a first
XX CC conserved residue selected from L, M, I, V, S, A, T, F, C, G, D and E and
XX CC (b) a second conserved residue of K, R, Y, H or F, where the first and
XX CC second conserved residues are separated by 6-7 residues. The peptides are
XX CC capable of binding selected MHC molecules and inducing an immune
XX CC response. They can be used to treat and/or prevent viral infection and
XX CC cancer, e.g. prostate cancer, lymphoma, hepatitis or AIDS. They can also
XX CC be used to produce antibodies for use as diagnostic or therapeutic
XX CC agents. The peptides can also be used as diagnostic agents
XX SQ
XX Sequence 10 AA;
XX
XX Query Match 27.8%; Score 32; DB 2; Length 10;
XX Best Local Similarity 55.6%; Pred. No. 2.9e+02;
XX Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 IPHPTNIHK 10
XX ||||| : |
XX Db 2 IPHPAGLKK 10
XX
XX RESULT 35
XX ID AAY45830
XX AAY45830 standard; peptide; 10 AA.
XX AC AAY45830;
XX DT 01-DEC-1999 (first entry)
XX DE Immunogenic peptide having a human leukocyte antigen binding motif #441.
XX XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
XX KM immune response; T cell activation; major histocompatibility complex;
XX KM cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
XX KM prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
XX KM vaccine; immunisation.
XX OS Synthetic.
XX OS Homo sapiens.
XX PF MO945954-A1.
XX PN
XX

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PD 16-SEP-1999.
XX PF 13-MAR-1998; 98MO-US005039.
XX PR 13-MAR-1998; 98MO-US005039.
XX PA (BPIW-) BPIWUNE INC.
XX PI Sette A, Kubo RT, Sidney J, Cells E, Grey HM, Southwood S;
XX DR WPI, 1999-551214/46.
XX PT New immunogenic peptides with HLA binding motif, useful in treatment and
XX PT diagnosis of cancers and viral diseases.
XX PS Claim 1; Page 44; 150pp; English.
XX CC AAY45390 to AAY48214 represent specifically claimed immunogenic peptides
XX CC having a human major histocompatibility complex (MHC) Class I (also known
XX CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
XX CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
XX CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
XX CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
XX CC (CTLs) which destroy antigen-bearing cells are normally induced by an
XX CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
XX CC than the intact foreign antigen itself, and are particularly important in
XX CC tumour rejection and in fighting viral infections. The peptides are
XX CC therefore useful therapeutically to treat or prevent viral infections and
XX CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
XX CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
XX CC elicit an immune response in individuals susceptible or otherwise at risk
XX CC of viral infection or cancer, or used to treat chronic or acute
XX CC conditions. They are also useful diagnostically, and can be used to
XX CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
XX CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
XX CC patient. The polypeptides encoding the immunogenic peptides are also
XX CC useful therapeutically and for immunisation as above
XX SQ
XX Sequence 10 AA;
XX
XX Query Match 27.8%; Score 32; DB 2; Length 10;
XX Best Local Similarity 55.6%; Pred. No. 2.9e+02;
XX Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX QY 2 IPHPTNIHK 10
XX ||||| : |
XX Db 2 IPHPAGLKK 10
XX
XX RESULT 36
XX ID ABP14809
XX ABP14809 standard; peptide; 10 AA.
XX AC ABP14809;
XX DT 11-SEP-2003 (revised)
XX DT 15-JUL-2002 (first entry)
XX DE HIV A03 super motif pol peptide #183.
XX XX HIV; HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
XX KM vif; tat; cytotoxic T lymphocyte; CTL; immune response; epitope; antigen;
XX KM vaccine; HIV infection; immunisation; virucide.
XX OS Human immunodeficiency virus 1.
XX PN MO200124810-A1.
XX XX
XX PD 12-APR-2001.
XX PF 05-OCT-2000; 2000MO-US027766.
XX PR 05-OCT-1999; 99US-00412863.
XX

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XX (EPIM-) EPIMUNE INC.
XX
XX
PI Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
PI Baker DM, Celis E, Kubo RT, Grey HM;
XX
XX WPI; 2001-354887/37.
XX
PT Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
PT peptide groups, useful for vaccinating against HIV-1.
XX
XX
PS Claim 32; Page 171; 448pp; English.
XX
XX
CC The present invention describes a composition (I) comprising a prepared
CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
CC sequence selected from 51 defined amino acid sequences (ABL25347 to
CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
CC be used for immunising subjects against HIV-1 infections. The use of
CC group-based vaccines has several advantages over traditional vaccines,
CC particularly when compared to the use of whole antigens in vaccine
CC compositions. There is evidence that the immune response to whole
CC antigens is directed largely toward variable regions of the antigen,
CC allowing for immune escape due to mutations. The groups for inclusion in
CC an group-based vaccine may be selected from conserved regions of viral or
CC tumour-associated antigens, which therefore reduces the likelihood of
CC escape mutants. Furthermore, immunosuppressive groups that may be present
CC in whole antigens can be avoided with the use of group-based vaccines. An
CC additional advantage of an group-based vaccine approach is the ability to
CC combine selected groups (CTL and HTL), and further, to modify the
CC composition of the groups, achieving, for example, enhanced
CC immunogenicity. Accordingly, the immune response can be modulated, as
CC appropriate, for the target disease. Similar engineering of the response
CC is not possible with traditional approaches. ABP1501 to ABP25412
CC represent peptide sequences used in the exemplification of the present
CC invention. (Updated on 11-SEP-2003 to standardise OS field)
XX
SQ Sequence 10 AA;
XX
Query Match 27.8%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IPHPTNIHK 10
DB 2 IPHPAGLKK 10
XX
RESULT 37
ABJ15141
ID ABJ15141 standard; peptide; 10 AA.
XX
AC ABJ15141;
XX
DT 02-JAN-2003 (first entry)
XX
DB Immunogenic HIV peptide #1.
XX
XX HIV; gene therapy; vaccine; immunogenic HIV peptide;
XX cytotoxic T lymphocyte; HIV infection.
XX
OS Human immunodeficiency virus.
XX
PN WO200269691-A2.
XX
PD 12-SEP-2002.
XX
PP 01-MAR-2002; 2002WO-US006314.
XX
XX
PR 01-MAR-2001; 2001US-0272565P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (UYBR-) UNIV BROWN RES FOUND.
XX

PI Menicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;
XX
XX WPI; 2002-750429/81.
XX
PT New immunogenic HIV peptide having one or more epitopes immunoreactive
PT with cytotoxic T lymphocytes, useful for diagnosing, treating and
PT monitoring HIV infection in humans.
XX
XX
PS Claim 6; Page 42; 65pp; English.
XX
XX
CC The invention comprises immunogenic HIV peptides which contain one or
CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from
CC an HIV-positive individual. The immunogenic HIV peptides of the invention
CC are useful for diagnosing, treating and monitoring HIV infection. The
CC present amino acid sequence represents an immunogenic HIV peptide of the
CC invention
XX
SQ Sequence 10 AA;
XX
Query Match 27.8%; Score 32; DB 5; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 2 IPHPTNIHK 10
DB 2 IPHPAGLKK 10
XX
RESULT 38
ABJ15176
ID ABJ15176 standard; peptide; 10 AA.
XX
AC ABJ15176;
XX
DT 02-JAN-2003 (first entry)
XX
DE Immunogenic HIV peptide #36.
XX
XX HIV; gene therapy; vaccine; immunogenic HIV peptide;
XX cytotoxic T lymphocyte; HIV infection.
XX
OS Human immunodeficiency virus.
XX
PN WO200269691-A2.
XX
PD 12-SEP-2002.
XX
PP 01-MAR-2002; 2002WO-US006314.
XX
XX
PR 01-MAR-2001; 2001US-0272565P.
XX
XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
XX (UYBR-) UNIV BROWN RES FOUND.
XX
PI Menicholl JM, Bond K, Sriwanthana B, Pau C, Degroot A;
XX
XX WPI; 2002-750429/81.
XX
PT New immunogenic HIV peptide having one or more epitopes immunoreactive
PT with cytotoxic T lymphocytes, useful for diagnosing, treating and
PT monitoring HIV infection in humans.
XX
XX
PS Claim 6; Page 43; 65pp; English.
XX
XX
CC The invention comprises immunogenic HIV peptides which contain one or
CC more epitopes that are immunoreactive with cytotoxic T lymphocytes from
CC an HIV-positive individual. The immunogenic HIV peptides of the invention
CC are useful for diagnosing, treating and monitoring HIV infection. The
CC present amino acid sequence represents an immunogenic HIV peptide of the
CC invention
XX
SQ Sequence 10 AA;
XX

Query Match 27.8%; Score 32; DB 5; Length 10;
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
 |||||
 :
 1 IPHPAGLKK 9

RESULT 39

ABU070353
 ID ABU070353 standard; peptide; 10 AA.

XX ABU070353;

DT 23-OCT-2003 (revised)
 DT 05-JUN-2003 (first entry)

XX Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #671.

XX Human immunodeficiency virus; HIV; vaccine; immunological excipient;
 KM anti-HIV immune response; T cell response;
 KW viral multiplication inhibitor; chronic viraemia; AIDS.

XX Human immunodeficiency virus 1.

XX US2002182222-A1.

XX 05-DEC-2002.

XX 26-OCT-2001; 2001US-00055524.

XX 10-JUL-1998; 98US-0092346P.

XX 08-JAN-1999; 99US-0115145P.

XX 23-APR-1999; 99US-0130677P.

XX 09-JUL-1999; 99US-00351036.

XX (GROO/) GROOT A D.

XX Groot AD;

XX WPI; 2003-352642/33.

XX New vaccine comprising human immunodeficiency virus (HIV) vaccine
 PT candidate peptides, useful as antigens for raising anti-HIV immune
 PT responses, such as T cell responses, and for inducing antibodies and
 PT impairing viral multiplication.

XX Claim 1; Fig 9; 32pp; English.

XX The invention describes a vaccine comprising a human immunodeficiency
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence
 CC selected from 669 amino acid sequences given in the specification, in an
 CC immunological excipient. The HIV vaccine peptides are useful as antigens
 CC for raising anti-HIV immune responses, such as T cell responses, and for
 CC inducing antibodies that react with HIV-1 and impairing viral
 CC multiplication in vivo. These antibodies reduce viral multiplication
 CC during any initial acute infection with HIV-1 and minimise chronic
 CC viraemia or progression leading to AIDS. This is the amino acid sequence
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.
 CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 10 AA;

XX Query Match 27.8%; Score 32; DB 6; Length 10;

XX Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
 |||||
 :
 2 IPHPAGLKK 10

RESULT 40
 ABU69777
 ID ABU69777 standard; peptide; 10 AA.

XX ABU69777;

DT 23-OCT-2003 (revised)
 DT 05-JUN-2003 (first entry)

XX Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #95.

XX Human immunodeficiency virus; HIV; vaccine; immunological excipient;
 KM anti-HIV immune response; T cell response;
 KW viral multiplication inhibitor; chronic viraemia; AIDS.

XX Human immunodeficiency virus 1.

XX US2002182222-A1.

XX 05-DEC-2002.

XX 26-OCT-2001; 2001US-00055524.

XX 10-JUL-1998; 98US-0092346P.

XX 08-JAN-1999; 99US-0115145P.

XX 23-APR-1999; 99US-0130677P.

XX 09-JUL-1999; 99US-00351036.

XX (GROO/) GROOT A D.

XX Groot AD;

XX WPI; 2003-352642/33.

XX New vaccine comprising human immunodeficiency virus (HIV) vaccine
 PT candidate peptides, useful as antigens for raising anti-HIV immune
 PT responses, such as T cell response, and for inducing antibodies and
 PT impairing viral multiplication.

XX Claim 1; Page 13; 32pp; English.

XX The invention describes a vaccine comprising a human immunodeficiency
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence
 CC selected from 669 amino acid sequences given in the specification, in an
 CC immunological excipient. The HIV vaccine peptides are useful as antigens
 CC for raising anti-HIV immune responses, such as T cell responses, and for
 CC inducing antibodies that react with HIV-1 and impairing viral
 CC multiplication in vivo. These antibodies reduce viral multiplication
 CC during any initial acute infection with HIV-1 and minimise chronic
 CC viraemia or progression leading to AIDS. This is the amino acid sequence
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.
 CC (Updated on 23-OCT-2003 to standardise OS field)

XX Sequence 10 AA;

XX Query Match 27.8%; Score 32; DB 6; Length 10;

XX Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
 |||||
 :
 2 IPHPAGLKK 10

RESULT 41

ABU69799
 ID ABU69799 standard; peptide; 10 AA.

XX ABU69799;

DT 23-OCT-2003 (revised)
 DT 05-JUN-2003 (first entry)

XX

DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #117.
 XX
 XX Human immunodeficiency virus; HIV; vaccine; immunological excipient;
 KM anti-HIV immune response; T cell response;
 KM viral multiplication inhibitor; chronic viraemia; AIDS.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2002182222-A1.
 PD
 PD 05-DEC-2002.
 XX
 PF 26-OCT-2001; 2001US-00055524.
 XX
 PR 10-JUL-1998; 98US-0092346P.
 PR 08-JAN-1999; 99US-0115145P.
 PR 23-APR-1999; 99US-0130677P.
 PR 09-JUL-1999; 99US-00351036.
 XX
 PA (GROO/) GROOT A D.
 XX
 PI Groot AD;
 XX
 DR WPI; 2003-352642/33.
 XX
 PT New vaccine comprising human immunodeficiency virus (HIV) vaccine
 PT candidate peptides, useful as antigens for raising anti-HIV immune
 PT responses, such as T cell responses, and for inducing antibodies and
 PT impairing viral multiplication.
 XX
 PS Claim 1; Page 14; 32pp; English.
 XX
 CC The invention describes a vaccine comprising a human immunodeficiency
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence
 CC selected from 669 amino acid sequences given in the specification, in an
 CC immunological excipient. The HIV vaccine peptides are useful as antigens
 CC for raising anti-HIV immune responses, such as T cell responses, and for
 CC inducing antibodies that react with HIV-1 and impairing viral
 CC multiplication in vivo. These antibodies reduce viral multiplication
 CC during any initial acute infection with HIV-1 and minimise chronic
 CC viraemia or progression leading to AIDS. This is the amino acid sequence
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.
 CC (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 27.8%; Score 32; DB 6; Length 10;
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPTNIHK 10
 ||||| : |
 Db 2 IPHPAGLKK 10
 XX
 RESULT 42
 ABU69801
 ID ABU69801 standard; peptide; 10 AA.
 XX
 AC ABU69801;
 XX
 DT 23-OCT-2003 (revised)
 DT 05-JUN-2003 (first entry)
 XX
 DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #119.
 XX
 KM Human immunodeficiency virus; HIV; vaccine; immunological excipient;
 KM anti-HIV immune response; T cell response;
 KM viral multiplication inhibitor; chronic viraemia; AIDS.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2002182222-A1.

XX
 PD 05-DEC-2002.
 XX
 PF 26-OCT-2001; 2001US-00055524.
 XX
 PR 10-JUL-1998; 98US-0092346P.
 PR 08-JAN-1999; 99US-0115145P.
 PR 23-APR-1999; 99US-0130677P.
 PR 09-JUL-1999; 99US-00351036.
 XX
 PA (GROO/) GROOT A D.
 XX
 PI Groot AD;
 XX
 DR WPI; 2003-352642/33.
 XX
 PT New vaccine comprising human immunodeficiency virus (HIV) vaccine
 PT candidate peptides, useful as antigens for raising anti-HIV immune
 PT responses, such as T cell responses, and for inducing antibodies and
 PT impairing viral multiplication.
 XX
 PS Claim 1; Page 14; 32pp; English.
 XX
 CC The invention describes a vaccine comprising a human immunodeficiency
 CC virus (HIV) vaccine candidate peptide containing an amino acid sequence
 CC selected from 669 amino acid sequences given in the specification, in an
 CC immunological excipient. The HIV vaccine peptides are useful as antigens
 CC for raising anti-HIV immune responses, such as T cell responses, and for
 CC inducing antibodies that react with HIV-1 and impairing viral
 CC multiplication in vivo. These antibodies reduce viral multiplication
 CC during any initial acute infection with HIV-1 and minimise chronic
 CC viraemia or progression leading to AIDS. This is the amino acid sequence
 CC of a human immunodeficiency virus 1 (HIV1) vaccine candidate peptide.
 CC (Updated on 23-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 10 AA;
 XX
 Query Match 27.8%; Score 32; DB 6; Length 10;
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPTNIHK 10
 ||||| : |
 Db 1 IPHPAGLKK 9
 XX
 RESULT 43
 ABU69729
 ID ABU69729 standard; peptide; 10 AA.
 XX
 AC ABU69729;
 XX
 DT 23-OCT-2003 (revised)
 DT 05-JUN-2003 (first entry)
 XX
 DE Human immunodeficiency virus 1 (HIV1) vaccine candidate peptide #47.
 XX
 KM Human immunodeficiency virus; HIV; vaccine; immunological excipient;
 KM anti-HIV immune response; T cell response;
 KM viral multiplication inhibitor; chronic viraemia; AIDS.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2002182222-A1.
 PD
 PD 05-DEC-2002.
 XX
 PF 26-OCT-2001; 2001US-00055524.
 XX
 PR 10-JUL-1998; 98US-0092346P.
 PR 08-JAN-1999; 99US-0115145P.
 PR 23-APR-1999; 99US-0130677P.
 PR 09-JUL-1999; 99US-00351036.

Query Match	27.8%	Score 32;	DB 6;	Length 10;
Best Local Similarity	55.6%	Pred. No. 2.9e+02;		
Matches	5;	Conservative	1;	Mismatches 3;
			Indels	0;
			Gaps	0;

RESULT 44
ADD96334
ID ADD96334 standard; peptide; 10 AA

KM HIV-1, cross-clade candidate peptide; HIV clade;
KM major histocompatibility complex; MHC, human leukocyte antigen; HLA
KM T-cell activation; HIV positive patient; HIV infection; anti-HIV.

PN US2003180314-A1.

PD 25-SEP-2003

PF 22-JUL-2002; 2002US-00200708.

PR 10-JUL-1998; 98US-0092346P

PR 23-APR-1999 99US-0130677P

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45	46	47	48	49	50	51	52	53	54	55	56	57	58	59	60	61	62	63	64	65	66	67	68	69	70	71	72	73	74	75	76	77	78	79	80	81	82	83	84	85	86	87	88	89	90	91	92	93	94	95	96	97	98	99	100
---	---	---	---	---	---	---	---	---	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	----	-----

(DEGR / DEGR001 A.

XX

Değişim A
F1
XX

DR WPI, 2003-852210/79

PT New cross-clade HIV candidate peptide that binds a human major histocompatibility complex binding matrix motif or activates T-cells from HIV positive patients, useful for preventing or treating HIV infection.

CC The present invention relates to HIV-1 cross-clade candidate peptides comprising a sequence of about 8-50 amino acids, the sequence having CC complete, sequential sequence identity with a partial HIV-1 amino acid CC sequence that is absolutely conserved across at least 2 clades of HIV-1

The HIV cross-clade candidate peptides possess at least one of the biological properties selected from (i) the ability to bind a human major histocompatibility complex (MHC) binding matrix motif for a human MHC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the T2 in vitro peptide binding assay, and (iii) the ability to activate T-cells from HIV positive patients in at least one in vitro assay. The invention also discloses a pharmaceutical composition comprising the above peptide, and methods for the production and use of the cross-clade peptides. The composition and methods are useful in preventing or treating HIV infection. The present sequence represents a HIV-1 cross-clade candidate peptide.

SQ Sequence 10 AA;

Query Match	27.8%	Score 32;	DB 7;	Length 10;
Best Local Similarity	55.6%	Pred. NO.	2.9e+02;	
Matches	5;	Conservative	1;	Mismatches 3;
				Indels 0;
				Gaps 0;

Qy	2	I P H P T N I H K	10
			:
Db	1	I P H P A G L K K	9

RESULT 45
ADD96886
ID ADD96886 standard; peptide; 10 AA

AC	ADD96886;
XX	
DT	29-JAN-2004 (first entry)

DE HIV-1 cross-clade candidate peptide #671

KW HIV-1; cross-clade candidate peptide; HIV clade;

KW T-cell activation; HIV positive patient; HIV infection; anti-HIV.

OS Human immunodeficiency virus 1.

PN US2003180314-A1

PD 25-SEP-2003

PF 22-JUL-2002; 2002US-00200708

10-JUL-1998; 98US-0092346P

PR 23-APR-1999: 99US-0130677P

03-000-1333; 3303-00331036

FA	DEGR/	DEGR001 A.
XX		

Degroot A,
P1
YY

DR WP1; 2003-852210/79
VY

PT New cross-clade HIV candidate peptide that binds a human major histocompatibility complex binding motif or activates T-cells from HIV positive patients, useful for preventing or treating HIV infection.

PS Example 2; SEQ ID NO 671; 146pp; English.

CC The present invention relates to HIV-1 cross-clade candidate peptides comprising a sequence of about 8-50 amino acids, the sequence having complete, sequential sequence identity with a partial HIV-1 amino acid sequence that is absolutely conserved across at least 2 clades of HIV-1

CC The HIV-1 cross-clade candidate peptides possess at least one of the
CC biological properties selected from (i) the ability to bind a human major
CC histocompatibility complex (MHC) binding matrix motif for a human MHC
CC allele, (iii) the ability to bind MHC human leukocyte antigen (HLA) in the
CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-
CC cells from HIV positive patients in at least one in vitro assay. The
CC invention also discloses a pharmaceutical composition comprising the
CC above peptide, and methods for the production and use of the cross-clade
CC peptides. The composition and methods are useful in preventing or
CC treating HIV infection. The present sequence represents a HIV-1 cross-
CC clade candidate peptide.

XX
XX Sequence 10 AA;

QY 27.8%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 2 IPHPTNIHK 10
2 IPHPAGLKK 10

RESULT 46
ADD96262
ID ADD96262 strand; peptide; 10 AA.
XX
XX ADD96262;
XX
XX 29-JAN-2004 (first entry)
XX
XX HIV-1 cross-clade candidate peptide #47.
XX
XX
XX HIV-1, cross-clade candidate peptide; HIV clade;
XX major histocompatibility complex; MHC; human leukocyte antigen; HLA;
XX T-cell activation; HIV positive patient; HIV infection; anti-HIV.
XX
XX Human immunodeficiency virus 1.
XX
XX US2003180314-A1.
XX
XX
XX 25-SEP-2003.
XX
XX
XX 22-JUL-2002; 2002US-00200708.
XX
XX
XX 10-JUL-1998; 98US-0092346P.
XX 08-JAN-1999; 99US-0115145P.
XX 23-APR-1999; 99US-0130677P.
XX 09-JUL-1999; 99US-00351036.
XX
XX (DEGR/) DEGROOT A.
XX
XX Degroot A;
XX
XX
XX WPI; 2003-852210/79.
XX
XX
XX New cross-clade HIV candidate peptide that binds a human major
XX histocompatibility complex binding matrix motif or activates T-cells from
XX HIV positive patients, useful for preventing or treating HIV infection.
XX
XX
XX Example 3; SEQ ID NO 47; 146pp; English.

CC The present invention relates to HIV-1 cross-clade candidate peptides
CC comprising a sequence of about 8-50 amino acids, the sequence having
CC complete, sequential sequence identity with a partial HIV-1 amino acid
CC sequence that is absolutely conserved across at least 2 clades of HIV.
CC The HIV-1 cross-clade candidate peptides possess at least one of the
CC biological properties selected from (i) the ability to bind a human major
CC histocompatibility complex (MHC) binding matrix motif for a human MHC
CC allele, (iii) the ability to bind MHC human leukocyte antigen (HLA) in the
CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-
CC cells from HIV positive patients in at least one in vitro assay. The
CC invention also discloses a pharmaceutical composition comprising the

CC above peptide, and methods for the production and use of the cross-clade
CC peptides. The composition and methods are useful in preventing or
CC treating HIV infection. The present sequence represents a HIV-1 cross-
CC clade candidate peptide.

XX
XX Sequence 10 AA;

QY 27.8%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

DB 2 IPHPTNIHK 10
1 IPHPAGLKK 9

RESULT 47
ADD96332
ID ADD96332 strand; peptide; 10 AA.
XX
XX ADD96332;
XX
XX 29-JAN-2004 (first entry)
XX
XX HIV-1 cross-clade candidate peptide #117.
XX
XX
XX HIV-1, cross-clade candidate peptide; HIV clade;
XX major histocompatibility complex; MHC; human leukocyte antigen; HLA;
XX T-cell activation; HIV positive patient; HIV infection; anti-HIV.
XX
XX Human immunodeficiency virus 1.
XX
XX US2003180314-A1.
XX
XX
XX 25-SEP-2003.
XX
XX
XX 22-JUL-2002; 2002US-00200708.
XX
XX
XX 10-JUL-1998; 98US-0092346P.
XX 08-JAN-1999; 99US-0115145P.
XX 23-APR-1999; 99US-0130677P.
XX 09-JUL-1999; 99US-00351036.
XX
XX (DEGR/) DEGROOT A.
XX
XX Degroot A;
XX
XX
XX WPI; 2003-852210/79.
XX
XX
XX New cross-clade HIV candidate peptide that binds a human major
XX histocompatibility complex binding matrix motif or activates T-cells from
XX HIV positive patients, useful for preventing or treating HIV infection.
XX
XX
XX Example 3; SEQ ID NO 117; 146pp; English.

CC The present invention relates to HIV-1 cross-clade candidate peptides
CC comprising a sequence of about 8-50 amino acids, the sequence having
CC complete, sequential sequence identity with a partial HIV-1 amino acid
CC sequence that is absolutely conserved across at least 2 clades of HIV.
CC The HIV-1 cross-clade candidate peptides possess at least one of the
CC biological properties selected from (i) the ability to bind a human major
CC histocompatibility complex (MHC) binding matrix motif for a human MHC
CC allele, (iii) the ability to bind MHC human leukocyte antigen (HLA) in the
CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-
CC cells from HIV positive patients in at least one in vitro assay. The
CC invention also discloses a pharmaceutical composition comprising the
CC above peptide, and methods for the production and use of the cross-clade
CC peptides. The composition and methods are useful in preventing or
CC treating HIV infection. The present sequence represents a HIV-1 cross-
CC clade candidate peptide.

XX
XX Sequence 10 AA;

Query Match 27.8%; Score 32; DB 7; Length 10;
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIRK 10
 |||||
 Db 2 IHPHAGLKK 10

RESULT 48

ADD96310
 ID ADD96310 standard; peptide; 10 AA.

XX ADD96310;

DT 29-JAN-2004 (first entry)

DE HIV-1 cross-clade candidate peptide #95.

XX HIV-1, cross-clade candidate peptide; HIV clade;

KM major histocompatibility complex; MHC; human leukocyte antigen; HLA;
 T-cell activation; HIV positive patient; HIV infection; anti-HIV.

OS Human immunodeficiency virus 1.

PN US2003180314-A1.

PD 25-SEP-2003.

PF 22-JUL-2002; 2002US-00200708.

PR 10-JUL-1998; 98US-0092346P.

PR 08-JAN-1999; 98US-0115145P.

PR 23-APR-1999; 99US-0130677P.

PR 09-JUL-1999; 99US-00351036.

PA (DEGR/) DEGR00T A.

PI Degroot A;

XX WPI; 2003-852210/79.

XX New cross-clade HIV candidate peptide that binds a human major

PT histocompatibility complex binding matrix motif or activates T-cells from

PT HIV positive patients; useful for preventing or treating HIV infection.

XX Example 3; SEQ ID NO 95; 146pp; English.

XX The present invention relates to HIV-1 cross-clade candidate peptides

CC comprising a sequence of about 8-50 amino acids, the sequence having

CC complete, sequential sequence identity with a partial HIV-1 amino acid

CC sequence that is absolutely conserved across at least 2 clades of HIV.

CC The HIV-1 cross-clade candidate peptides possess at least one of the

CC biological properties selected from (i) the ability to bind a human major

CC histocompatibility complex (MHC) binding matrix motif for a human MHC

CC allele, (ii) the ability to bind MHC human leukocyte antigen (HLA) in the

CC T2 in vitro peptide binding assay, and (iii) the ability to activate T-

CC cells from HIV positive patients in at least one in vitro assay. The

CC invention also discloses a pharmaceutical composition comprising the

CC above peptide, and methods for the production and use of the cross-clade

CC peptide. The composition and methods are useful in preventing or

CC treating HIV infection. The present sequence represents a HIV-1 cross-

CC clade candidate peptide.

XX Sequence 10 AA;

SO

Query Match 27.8%; Score 32; DB 7; Length 10;
 Best Local Similarity 55.6%; Pred. No. 2.9e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIRK 10
 |||||
 Db 2 IHPHAGLKK 10

RESULT 49

ABG75542
 ID ABG75542 standard; peptide; 14 AA.

XX ABG75542;

DT 17-APR-2003 (first entry)

DE Human sperm acrosomal protein (ACRP) dinucleotide repeat translation #2.

XX Polymorphic repeat; tandem repeat; sperm acrosomal protein; ACRP;

KM polymorphic marker prediction of ubiquitous simple sequences; POMPOUS;

KM Rep-X; human; genetic disease; drug-treatment; Machado-Joseph;

KM Haw River syndrome; Huntington's disease; fragile-X syndrome;

KM Friedrich's ataxia; myotonic dystrophy; hyperandrogenaemia;

XX spinal atrophy; bulbar atrophy; spinocerebellar ataxia.

OS Homo sapiens.

PN US6472154-B1.

PD 29-OCT-2002.

PF 31-DEC-1999; 99US-00475947.

PR 31-DEC-1999; 99US-00475947.

PR (TEXA) UNIV TEXAS SYSTEM.

PA Garner HR, Wren JD, Minna JD, Fondon JW;

PI WPI; 2003-208818/20.

XX Identifying a candidate polymorphic repeat within a coding sequence, for

PT understanding or creating genetic disease, comprises detecting tandem

PT repeats in a target coding sequence and scoring the repeats for

XX polymorphic probability.

XX Example; Col 12; 588pp; English.

XX The invention discloses a method for identifying a candidate polymorphic

CC repeat within a coding sequence (expressed sequence tag, EST), which

CC comprises detecting tandem repeats in a target coding sequence, scoring

CC the repeats for polymorphic probability and generating a dataset

CC correlating the repeats with polymorphic probability to identify a

CC candidate polymorphic repeat. The computational method (polymorphic

CC marker prediction of ubiquitous simple sequences, POMPOUS, and Rep-X) are

CC useful for identifying and detecting candidate polymorphic repeats in

CC human genes, which can be used to understand, treat or eliminate genetic

CC diseases, predispositions or adverse drug-treatment reactions. Examples

CC of diseases linked to nucleotide repeats are Machado-Joseph, Haw River

CC syndrome, Huntington's disease, fragile-X syndrome, Friedrich's ataxia,

CC myotonic dystrophy, hyperandrogenaemia, spinal and bulbar atrophy and

CC spinocerebellar ataxia. The sequence presented is the translated product

CC of one reading frame of a polymorphic dinucleotide repeat within the 3'

CC terminus of the human sperm acrosomal protein (ACRP) coding sequence

XX Sequence 14 AA;

SO

Query Match 27.8%; Score 32; DB 6; Length 14;
 Best Local Similarity 100.0%; Pred. No. 4.3e+02;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 VCESVN 18
 |||||
 Db 4 VCESVN 9

RESULT 50
 ADP53446
 ID ADP53446 standard; peptide; 14 AA.

XX ADF53446;
 XX 12-FEB-2004 (first entry)
 DT MCPC 603 antibody CDR2 mutant peptide amino acid sequence 7.
 XX
 DE walk-through mutagenesis; prototype amino acid; prototype nucleotide;
 KM mutant polypeptide production; MCPC 603;
 KM complementarity determining region; CDR; heavy chain; CDR2; mutant;
 KM nuclein.
 XX
 OS unidentified.
 OS Synthetic.
 XX
 PN WO2003089671-A1.
 XX
 PD 30-OCT-2003.
 XX
 PF 16-APR-2003; 2003WO-US011935.
 XX
 PR 17-APR-2002; 2002US-0373686P.
 XX
 PA (CREA/) CREA R.
 PA (CAPE/) CAPPUCCILLI G.
 PI Crea R, Cappuccilli G;
 PI
 DR WPI, 2003-854132/79.
 XX
 XX Walk-through mutagenesis of a nucleic acid encoding a polypeptide, useful
 PT for producing mutant polypeptides comprising synthesizing oligonucleotides
 PT comprising a nucleotide sequence for each target region of a prototype
 PT amino acid.
 XX
 PS Example; Fig 6; 40pp; English.
 XX
 CC This invention relates to a novel method of walk-through mutagenesis of a
 CC nucleic acid encoding a polypeptide which comprises synthesizing a
 CC mixture of oligonucleotides comprising a nucleotide sequence for each
 CC target region of a prototype amino acid, where each oligonucleotide
 CC contains, at each sequence position in the target region, a prototype
 CC nucleotide for synthesis of the prototype amino acid, or a predetermined
 CC nucleotide that is required for synthesis of the predetermined amino
 CC acid. The method is useful in producing mutant polypeptides in which the
 CC overall presence of the predetermined amino acid is limited to one or two
 CC positions per mutated polypeptide, leaving the remaining amino acids in
 CC the targeted region intact or as close as possible to the prototype
 CC sequence. The invention was exemplified using the three complementarity
 CC determining regions (CDRs) of the heavy chain of the monoclonal antibody
 CC MCPC 603.
 CC
 XX Sequence 14 AA;
 SQ

Query Match 27.8%; Score 32; DB 7; Length 14;
 Best Local Similarity 55.6%; Pred. No. 4.3e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHYKL 12
 DB 4 HPTQHHYV 12

RESULT 51
 ADT41277
 ID ADT41277 standard; peptide; 14 AA.
 XX
 AC ADT41277;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE hSARS virus peptide, SEQ ID 2265.
 XX

KM Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
 XX
 OS SARS coronavirus.
 XX
 PN WO2004085650-A1.
 XX
 PD 07-OCT-2004.
 XX
 PF 24-MAR-2004; 2004WO-CN000246.
 XX
 PR 24-MAR-2003; 2003US-0457031P.
 PR 26-MAR-2003; 2003US-0457730P.
 PR 02-APR-2003; 2003US-0455931P.
 PR 03-APR-2003; 2003US-0460357P.
 PR 08-APR-2003; 2003US-0461265P.
 PR 14-APR-2003; 2003US-0462805P.
 PR 23-APR-2003; 2003US-0464886P.
 PR 25-APR-2003; 2003US-0465738P.
 PR 14-MAY-2003; 2003US-0470935P.
 XX
 PA (UYHK-) UNIV HONG KONG.
 XX
 PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
 PI Leung FC;
 PI
 DR WPI, 2004-737326/72.
 XX
 XX New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of
 PT a human Severe Acute Respiratory Syndrome (SARS) virus, useful for
 PT diagnosing and treating SARS.
 PT
 PS Example; SEQ ID NO 2265; 200pp; English.
 XX
 CC The present invention relates to novel human Severe Acute Respiratory
 CC Syndrome (SARS) viral nucleic acid and protein sequences derived from a
 CC hSARS virus having China Center for Type Culture Collection Deposit
 CC Accession No. CCTCC-V200303. The present invention also relates to novel
 CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-
 CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are
 CC methods for detecting the presence of a N- or S-gene of the hSARS virus
 CC or of the protein in a biological sample and identifying a subject
 CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein
 CC sequences are useful as vaccines for diagnosing or treating SARS. They
 CC are also useful in clinical and scientific research applications. The
 CC hSARS virus genome (ADT39027) was obtained and the amino acid sequences
 CC of all three reading frames were deduced from the complementary strand.
 CC ADT40120 is the full-length protein encoded by the first reading frame of
 CC the complementary strand and ADT40121-ADT40601 are the peptides from the
 CC first reading frame protein. ADT40602 is the full-length protein encoded
 CC by the second reading frame of the complementary strand and ADT40603-
 CC ADT40976 are the peptides from the second reading frame protein. ADT40977
 CC is the full-length protein encoded by the third reading frame of the
 CC complementary strand and ADT40978-ADT41482 are the peptides from the
 CC third reading frame protein.
 CC
 XX Sequence 14 AA;
 SQ

Query Match 27.8%; Score 32; DB 8; Length 14;
 Best Local Similarity 83.3%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNTH 9
 DB 9 HPTTTH 14

RESULT 52
 ADS80692
 ID ADS80692 standard; protein; 14 AA.
 XX
 AC ADS80692;
 XX
 DT 30-DEC-2004 (first entry)
 XX

XX SARS virus complementary DNA strand reading frame 3 protein #300.
 DE
 XX
 KM virulence; vaccine; detection; severe acute respiratory syndrome;
 KM real-time quantitative polymerase chain reaction; SARS.
 XX
 OS SARS coronavirus.
 XX
 PN MO2004085455-A1.
 XX
 PD 07-OCT-2004.
 XX
 PF 24-MAR-2004; 2004MO-CN000247.
 XX
 PR 24-MAR-2003; 2003US-0457031P.
 PR 26-MAR-2003; 2003US-0457730P.
 PR 02-APR-2003; 2003US-0459931P.
 PR 03-APR-2003; 2003US-0460357P.
 PR 08-APR-2003; 2003US-0461265P.
 PR 14-APR-2003; 2003US-0462805P.
 PR 23-APR-2003; 2003US-0464886P.
 PR 05-MAY-2003; 2003US-0468139P.
 PR 16-MAY-2003; 2003US-0471200P.
 XX
 PA (UYHK-) UNIV HONG KONG.
 XX
 PI Chan K, Guan Y, Nicholls JM, Petris JSM, Poon L, Yuen K;
 XX
 DR WPI, 2004-737292/72.
 XX
 PT New isolated nucleic acid molecule useful for detecting, treating,
 PT ameliorating, or preventing the virus causing severe acute respiratory
 PT syndrome in humans using a real-time quantitative polymerase chain
 reaction assay.
 XX
 XX Example; SEQ ID NO 2265; 183bp; English.
 XX
 CC The invention relates to an isolated nucleic acid molecule consisting
 CC essentially of, and/or hybridizes under stringent conditions to a fully
 CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-
 CC 2476), or its complement. The methods and compositions of the present
 CC invention are useful for the detection of the virus causing Severe Acute
 CC Respiratory Syndrome (SARS) in humans using a real-time quantitative
 CC polymerase chain reaction (PCR) assay. They can also be used in treating,
 CC ameliorating, managing or preventing SARS. This sequence corresponds to a
 CC partial SARS protein sequence from the complementary reading frame 3.
 CC
 XX
 SQ Sequence 14 AA;
 XX
 QY Query Match 27.8%; Score 32; DB 8; Length 14;
 DB Best Local Similarity 83.3%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 HPTNIIH 9
 DB 9 HPTTIIH 14
 XX
 AC AADT38807 standard; peptide; 14 AA.
 XX
 AC AADT38807;
 XX
 DT 30-DEC-2004 (first entry)
 XX
 DE hSARS virus peptide, SEQ ID 2265.
 XX
 KM virulence; Severe Acute Respiratory Syndrome; SARS; vaccine.
 OS SARS coronavirus.
 XX
 PN MO2004085633-A1.

XX 07-OCT-2004.
 PD
 XX
 XX 24-MAR-2004; 2004MO-CN000248.
 XX
 PR 24-MAR-2003; 2003US-0457031P.
 PR 26-MAR-2003; 2003US-0457730P.
 PR 02-APR-2003; 2003US-0459931P.
 PR 03-APR-2003; 2003US-0460357P.
 PR 08-APR-2003; 2003US-0461265P.
 PR 14-APR-2003; 2003US-0462805P.
 PR 23-APR-2003; 2003US-0464886P.
 XX
 PA (UYHK-) UNIV HONG KONG.
 XX
 PI Chan K, Guan Y, Nicholls JM, Petris JSM, Poon L, Yuen K;
 PI Leung FC;
 XX
 DR WPI, 2004-728736/71.
 XX
 PT New isolated human severe acute respiratory syndrome (hSARS) virus,
 PT useful as vaccine for diagnosing or treating SARS or in clinical and
 PT scientific research applications.
 XX
 XX Example; SEQ ID NO 2265; 176bp; English.
 XX
 CC The present invention relates to novel human Severe Acute Respiratory
 CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a
 CC hSARS virus having China Center for Type Culture Collection Deposit
 CC Accession No. CCTCC-V200303. The hSARS virus, nucleic acid and protein
 CC sequences are useful as vaccines for diagnosing or treating SARS. They
 CC are also useful in clinical and scientific research applications. The
 CC hSARS virus genome (ADT36557) was obtained and the amino acid sequences
 CC of all three reading frames were deduced from the complementary strand.
 CC ADT37650 is the full-length protein encoded by the first reading frame of
 CC the complementary strand and ADT37651-ADT38131 are the peptides from the
 CC first reading frame protein. ADT38132 is the full-length protein encoded
 CC by the second reading frame of the complementary strand and ADT38133-
 CC ADT38506 are the peptides from the second reading frame protein. ADT38507
 CC is the full-length protein encoded by the third reading frame of the
 CC complementary strand and ADT38508-ADT39012 are the peptides from the
 CC third reading frame protein.
 CC
 XX
 SQ Sequence 14 AA;
 XX
 QY Query Match 27.8%; Score 32; DB 8; Length 14;
 DB Best Local Similarity 83.3%; Pred. No. 4.3e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 4 HPTNIIH 9
 DB 9 HPTTIIH 14
 XX
 AC AAM85207 standard; peptide; 15 AA.
 XX
 AC AAM85207;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Helper T-cell peptide derived from a POL protein.
 XX
 KM Helper T-cell peptide; human leucocyte antigen; HLA; DR4*4; DR1; DR7;
 KM cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;
 KM acquired immune deficiency syndrome; malaria; cancer;
 KM allograft rejection; allergy; Lyme disease; hepatitis;
 KM post-streptococcal endocarditis; glomerulonephritis;
 KM food hypersensitivity.
 XX
 OS Synthetic.
 OS Human immunodeficiency virus 1.

XX WO9832456-A1.
 PN 30-JUL-1998.
 PD 23-JAN-1998; 98WO-US001373.
 XX 23-JAN-1997; 97US-0036713P.
 PR 07-FEB-1997; 97US-0037432P.
 XX (EPTM-) EPTIMUNE INC.
 PA Sette A, Sidney J, Southwood S;
 PI MPI; 1998-427679/36.
 DR Composition containing peptide that induces cytotoxic T lymphocyte
 PT response, and helper peptide - can bind to human leucocyte antigen
 PT alleles, used to treat or prevent cancers, parasitic infections and
 PT autoimmune disease.
 XX Claim 11; Page 38; 51pp; English.
 PS AAW85138-283 represent helper T-cell peptides, which can bind to the
 CC human leucocyte antigens (HLA) DR4W4, DR1 and DR7. The peptides are used
 CC in the course of the invention. The specification describes peptides that
 CC that induce a cytotoxic T lymphocyte (CTL) response, and T-helper
 CC peptides, that are used together to generate a CTL response for the
 CC treatment or prevention of viral, fungal, bacterial or parasitic
 CC infections (e.g. hepatitis, acquired immune deficiency syndrome or
 CC malaria) or cancer (e.g. renal or cervical carcinoma, lymphoma, prostate
 CC cancer or condyloma acuminatum). Helper T-cell peptides may be used alone
 CC to induce a helper T cell response, e.g. in cases of autoimmune disease,
 CC allograft rejection, allergy, Lyme disease, hepatitis, post-streptococcal
 CC endocarditis, glomerulonephritis and food hypersensitivity
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 32; DB 2; Length 15;
 Best Local Similarity 55.6%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPTNIHK 10
 ||||| :
 Db 6 IPHPAGLKK 14
 RESULT 55
 ABP24655
 ID ABP24655 standard; peptide; 15 AA.
 XX
 AC ABP24655;
 XX
 DT 11-SEP-2003 (revised)
 DT 15-JUL-2002 (first entry)
 XX
 DE HIV DR super motif pol peptide #22.
 KW HIV, HIV-1; human immunodeficiency virus; env; pol; gag; nef; vpr; vpu;
 KW vif; tat; cytoxic T lymphocyte; CTL; immune response; epitope; antigen;
 KW vaccine; HIV infection; immunisation; virucide.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO200124810-A1.
 PD 12-APR-2001.
 XX
 PF 05-OCT-2000; 2000WO-US027766.
 XX
 PR 05-OCT-1999; 99US-00412863.
 XX
 PA (EPTM-) EPTIMUNE INC.

XX Sette A, Sidney J, Southwood S, Livingston BD, Chesnut R;
 PI Baker DM, Celis E, Kudo RT, Grey HM;
 XX MPI; 2001-354887/37.
 DR Vaccine compositions comprising human immunodeficiency virus-1 (HIV-1)
 PT peptide groups, useful for vaccinating against HIV-1.
 XX
 PS Claim 32; Page 374; 448pp; English.
 CC The present invention describes a composition (I) comprising a prepared
 CC human immunodeficiency virus-1 (HIV-1) group comprising an amino acid
 CC sequence selected from 51 defined amino acid sequences (ABL25347 to
 CC ABP25397). (I) has virucide activity and can be used in vaccines. (I) may
 CC be used for immunising subjects against HIV-1 infections. The use of
 CC group-based vaccines has several advantages over traditional vaccines,
 CC particularly when compared to the use of whole antigens in vaccine
 CC compositions. There is evidence that the immune response to whole
 CC antigens is directed largely toward variable regions of the antigen,
 CC allowing for immune escape due to mutations. The groups for inclusion in
 CC an group-based vaccine may be selected from conserved regions of viral or
 CC tumour-associated antigens, which therefore reduces the likelihood of
 CC escape mutants. Furthermore, immunosuppressive groups that may be present
 CC in whole antigens can be avoided with the use of group-based vaccines. An
 CC additional advantage of an group-based vaccine approach is the ability to
 CC combine selected groups (CTL and HTL), and further, to modify the
 CC composition of the groups, achieving, for example, enhanced
 CC immunogenicity. Accordingly, the immune response can be modulated, as
 CC appropriate, for the target disease. Similar engineering of the response
 CC is not possible with traditional approaches. ABP1501 to ABP25412
 CC represent peptide sequences used in the exemplification of the present
 CC invention. (Updated on 11-SEP-2003 to standardise OS field)
 XX
 SQ Sequence 15 AA;
 Query Match 27.8%; Score 32; DB 4; Length 15;
 Best Local Similarity 55.6%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPTNIHK 10
 ||||| :
 Db 6 IPHPAGLKK 14
 RESULT 56
 ADN14050
 ID ADN14050 standard; peptide; 15 AA.
 XX
 AC ADN14050;
 XX
 DT 17-JUN-2004 (first entry)
 XX
 DE HIV helper T cell epitope #17.
 KW CTL; cytotoxic T lymphocyte; HIV infection; cancer; tuberculosis; tumour;
 KW hepatitis; melanoma; breast cancer; Hodgkin lymphoma;
 KW nasopharyngeal carcinoma; vaccine; immune response; hyaluronic acid; HA;
 KW CD8+ T cell; CD4+ T cell; viral infection; bacterial infection;
 KW fungal infection; parasitic infection.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN US2003049253-A1.
 PD 13-MAR-2003.
 XX
 PF 05-FEB-2002; 2002US-00062710.
 XX
 PR 08-AUG-2001; 2001US-0310498P.
 XX
 PA (LIFO/) LI F Q.

PA (CHUV/) CHU Y.
 PA (QIUC/) QIU J.
 XX
 PI L1 FQ, Chu Y, Qiu J,
 XX
 DR WPI, 2003-540464/51.
 XX
 PT Modulating an immune system response to an antigen in a mammal, comprises
 PT administering a particle-free therapeutic comprising a hyaluronic acid
 PT polymer analogue covalently linked to a peptide that comprises a T cell
 PT epitope.
 XX
 PS Disclosure, Page 12, 23pp, English.
 XX
 CC The invention relates to modulating an immune system response to an
 CC antigen in a mammal comprising administering to the mammal a particle-
 CC free therapeutic comprising a hyaluronic acid (HA) polymer analogue
 CC covalently linked to at least one peptide that comprises a T cell epitope
 CC recognised by a major histocompatibility complex molecule of the mammal.
 CC The T cell epitope comprises a sequence of at least about eight amino
 CC acids of the antigen. Also included are a method of improving major
 CC histocompatibility complex (MHC) presentation of a T cell epitope of an
 CC antigen in a mammal (comprising administration of a T cell epitope of an
 CC histocompatibility complex (MHC) Class I molecule and by a CD8+ T cell of
 CC the mammal, or an MHC Class II molecule and a CD4+ T cell of the mammal.
 CC The immune system response comprises a cytotoxic T lymphocyte, a CD4+T
 CC cell, or an antibody that recognises the antigen. The immune system
 CC response to the antigen is increased after administration of the
 CC conjugate, where the antigen is an antigen of a pathogenic agent or a
 CC tumour cell. The immune system response to the antigen is decreased after
 CC administration of the conjugate, where the antigen is an antigen of a
 CC tissue or organ transplanted to the mammal. The composition and methods
 CC are useful for modulating, i.e. enhancing or diminishing, an immune
 CC system response to an antigen in a mammal. The composition is also useful
 CC for improving major histocompatibility complex presentation of a T cell
 CC epitope of an antigen in a mammal. The polymeric hyaluronic acid
 CC conjugates are useful as peptide vaccines against an antigen, a
 CC pathogenic agent such as viral, bacterial, fungal or parasitic protein,
 CC or a tumour cell) in a mammal. The peptide vaccine compositions are
 CC useful for treating or preventing diseases associated with any of the
 CC antigens above e.g. HIV infection, cancer, tuberculosis, hepatitis,
 CC melanoma, breast cancer, Hodgkin's lymphoma and nasopharyngeal carcinoma.
 CC The peptide vaccine compositions of the present invention do not require
 CC additional adjuvants, but still induce a stronger cell-mediated response
 CC than peptide vaccines of the prior art. The present sequence is an HIV-1
 CC derived epitope suitable for the vaccine of the invention.
 XX
 SQ Sequence 15 AA:
 Query Match 27.8%; Score 32; DB 7; Length 15;
 Best Local Similarity 55.6%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPNIIHK 10
 Db 7 IPHPAGLKK 15
 XX
 RESULT 57
 ADW36336
 ID ADW36336 standard; peptide, 15 AA.
 XX
 AC ADW36336;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #7086.
 XX
 KW Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KW MHC class I; CTL; HTLV; A2-restricted cytotoxic lymphocyte; HLA;
 KW viral disease; cancer.
 XX

OS Unidentified.
 XX
 FN WO2003040165-A2.
 XX
 PD 15-MAY-2003.
 XX
 PF 18-OCT-2001; 2001WO-US051650.
 XX
 PR 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 PA (EPIM-) EPIMUNE INC.
 XX
 PI Sette A, Sidney J, Southwood S;
 XX
 DR WPI, 2003-441519/41.
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 XX
 PS Claim 1; Page 52-379; 382pp, English.
 XX
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADW29251-
 CC ADW37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 SQ Sequence 15 AA:
 Query Match 27.8%; Score 32; DB 7; Length 15;
 Best Local Similarity 55.6%; Pred. No. 4.7e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPNIIHK 10
 Db 6 IPHPAGLKK 14
 XX
 RESULT 58
 ADV22436
 ID ADV22436 standard; peptide, 15 AA.
 XX
 AC ADV22436;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HIV-1 Pol protein, immunogenic peptide #63.
 XX
 KW Vaccine; virucide; antigen; autoimmune disease; infection;
 KW immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KW breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KW pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KW Hodgkin's lymphoma.
 XX
 OS Human immunodeficiency virus 1.
 XX
 PN WO2004108753-A1.
 XX
 PD 16-DEC-2004.
 XX

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XX 10-JUN-2004; 2004WO-AU000775.
PF
XX
XX 10-JUN-2003; 2003AU-00902875.
PR
XX 25-MAR-2004; 2004AU-00901589.
PR
XX (UYME ) UNIV MELBOURNE.
PA
XX
XX Kent SJ;
PI
XX WPI; 2005-031657/03.
XX
XX Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
XX Disclosure; SEQ ID NO 856; 645bp; English.
XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for administering an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease
CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC of aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from an HIV-1
CC protein.
XX
XX Sequence 15 AA;
SQ
XX
XX Query Match 27.8%; Score 32; DB 9; Length 15;
XX Best Local Similarity 55.6%; Pred. No. 4.7e+02;
XX Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
XX
XX 2 IPHPTIHK 10
XX | | | | : |
XX 1 IPHPLGLK 9
XX
XX RESULT 59
XX ADV22435
XX ID ADV22435 standard; peptide; 15 AA.
XX AC ADV22435;
XX XX
XX DT 10-MAR-2005 (first entry)

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```

XX
XX DE HIV-1 Pol protein, immunogenic peptide #62.
XX
XX Vaccine; virucide; antigen; autoimmune disease; infection;
XX immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
XX breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
XX pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
XX hodgkin's lymphoma.
XX
XX Human immunodeficiency virus 1.
XX
XX WO2004108753-A1.
XX
XX 16-DEC-2004.
XX
XX 10-JUN-2004; 2004WO-AU000775.
XX
XX 10-JUN-2003; 2003AU-00902875.
XX
XX 25-MAR-2004; 2004AU-00901589.
XX
XX (UYME ) UNIV MELBOURNE.
XX
XX Kent SJ;
XX
XX WPI; 2005-031657/03.
XX
XX Use of at least one set of peptides in the preparation of a medicament
PT for modulating an immune response, and for treating cancer or yeast,
PT viral, bacterial, protozoal and mycoplasma infections.
XX
XX Disclosure; SEQ ID NO 855; 645bp; English.
XX
XX The invention relates to the use of at least one set of peptides in the
CC preparation of a medicament for modulating an immune response, where
CC individual peptides of a respective set comprise different portions of an
CC amino acid sequence corresponding to a single polypeptide of interest and
CC display partial sequence identity or similarity to at least one other
CC peptide of the same set of peptides (i.e. they are overlapping). Also
CC included are an antigen-presenting cell which has been contacted with the
CC peptides above and thus presents the peptides, a population of such
CC antigen-presenting cells, a process for producing antigen-presenting
CC cells for modulating an immune response to a polypeptide of interest, a
CC method for producing antigen-specific lymphocytes, a composition
CC comprising at least one set of the peptides (and a carrier and/or
CC diluent), a method for administering an immune response to a polypeptide of
CC interest comprising administering to a patient in need at least one set
CC of the peptides, a method for treatment and/or prophylaxis of a disease
CC or condition associated with the presence of a polypeptide of interest
CC and a composition of matter for modulating an immune response in a
CC subject to a target antigen. The polypeptide of interest is also a
CC disease- or condition-associated polypeptide that is a polypeptide
CC produced by a pathogenic organism or a cancer, and produced by a
CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
CC protozoans and mycoplasmas. The disease- or condition-associated
CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncultured
CC antigen-presenting cells or their precursors are useful in the
CC preparation of a medicament for the treatment of a disease or condition
CC in a subject, which disease or condition is associated with the presence
CC of aberrant expression of a target antigen, where the antigen-presenting
CC cells or their precursors have not been subjected to activating
CC conditions but have been contacted with an antigen that corresponds to
CC the target antigen to express a processed or modified form of the antigen
CC for presentation to the subject's immune system. The present sequence is
CC one of a set of overlapping immunogenic peptides derived from an HIV-1
CC protein.
XX
XX Sequence 15 AA;
SQ
XX
XX Query Match 27.8%; Score 32; DB 9; Length 15;
XX Best Local Similarity 55.6%; Pred. No. 4.7e+02;
XX

```

Matches	5;	Conservative	1;	Mismatches	3;	Indels	0;	Gaps	0;
Qy	2	IPHPNTIHK	10		:				
Db	5	IPHPAGLKK	13						

RESULT 60
ADI24615
ID ADI24615 standard; peptide; 17 AA

AC ADI24615,

DT 22-APR-2004 (First entry)

HIV-1 HLA class I restricted CTL peptide epitope SeqID 32.

KW Immunogenic; epitope; HIV-1 infection; Human Leukocyte Antigen; HLA, cytotoxic T lymphocyte; CTL; vaccine; immunostimulant; virucidal.

OS Human immunodeficiency virus 1.

PN US2004001845-A1.

01-JAN-2004 .

PF 20-MAY-2003; 2003US-00442909.

PR 20-MAY-2002; 2002US-0382120P.

PA (ALTP/) ALTFELD M.

PA (WALK/) WALKER B D.
PA (WALK/) WALKER B D.

PI Altfeld M, Yu X, Walker BD, Addo M, ...

DR WPI, 2004-098245/10.

PT New immunogenic composition, useful in eliciting an immune response and
PT in treating human immunodeficiency virus, comprises an HLA class I
PT restricted HIV-1 polypeptide, .

PS Disclosure; SEQ ID NO 32; 18pp; English.

CC This invention relates to novel immunogenic compositions that contain HIV
CC -1 epitopes and represent early targets in a naturally occurring response
CC against HIV-1 infection. Specifically, these epitopes contain a human
CC leukocyte Antigen (HLA) class I restricted HIV-1 peptide that is
CC recognised by cytotoxic T lymphocytes (CTLs). The present invention
CC describes a method of using these peptides to stimulate an HIV-specific
CC immune response, such that these peptide compositions can be used to as
CC highly immunogenic HIV-1 vaccine. Accordingly, these compositions that
CC exhibit immunostimulant and virucidal activities can also be used to
CC treat an HIV-1 infection. This peptide sequence is an HIV-1 peptide
CC epitope of the invention.

Sequence 17 AA,

Query Match	27.8%	Score 32	DB 8	Length 17
Best Local Similarity	55.6%	Pred. No. 5.4e+02		
Matches 5, Conservative	1	Mismatches 3	Indels 0	Gaps 0

```
Qy      2 I P H P T I N I H K 10
          ||||| : |
Db      8 I P H P A G L K K 16
```

RESULT 61	
ADC89725	
ID	ADC89725 standard, peptide, 20 AA
XX	
AC	ADC89725,

XX 01-JAN-2004 (first entry)
DT

DE Cotton fibre transcription factor 4-4 probable peptide #1.

KM Cotton; fibre; transcription factor; 4-4; rac13; plant; fibre phenotype;
KW pigment biosynthesis pathway.

OS *Gosypium hirsutum*.

PN US2003106089-A1

PD 05-JUN-2003.

PF 31-OCT-2002; 2002US-00285649.

PR 07-JUN-1995; 95US-00480178.

PR 03-DEC-1997; 97US-00984099.

PA (MCBR/) MCBRIDE K.

PA (PEAR/) PEAR J R.

2000

DR WPI; 2003-801255/75.

XX

PT New DNA sequence comprising a cotton fiber transcriptional factor and an
PT open reading frame of a protein of interest, for modifying fiber
PT phenotype in a cotton plant.

PS Disclosure; SEQ ID NO 9; 63pp; English.

The invention relates to a DNA sequence comprising a cotton fibre transcriptional factor and an open reading frame (orf) encoding a protein of interest, operably joined in the direction of transcription, where the transcription factor is selected from the 4-4 and rac1s promoter sequences. Also included are a DNA construct comprising a promoter for transcribing in a plant cell the construct above, a plant cell comprising the construct, a plant comprising the cell, modifying fibre phenotype in a cotton plant (comprising: transforming a plant cell with a DNA comprising a construct for expression of a protein in a pigment biosynthesis pathway, where the construct expresses operably joined components: a transcriptional initiation region functional in cells of the plant tissue; and an open reading frame encoding a protein of interest, and a transcriptional termination region functional in cells of the plant tissue, where the plant tissue comprises a substrate of the protein and growing the plant cell to produce a plant comprising the tissue, where the protein reacts with the substrate to produce the pigment), a recombinant DNA construct comprising a cotton tissue transcriptional sequence appearing as ADC89735 or ADC89731 and an isolated DNA encoding sequence appearing as ADC89737 and ADC89728, being the 4-4 and Rac1s cDNAs. The construct is used in a method for modifying fibre phenotype in a cotton plant. The construct is also used as a molecular probe. The present sequence is probably a transcription factor 4-4 promoter cassette peptide, although the authors do not refer to the sequence explicitly in the specification.

SQ Sequence 20 AA;

Query Match	27.8%	Score 32	DB 7	Length 20
Best Local Similarity	42.9%	Pred. No.	6.5e+02	
Matches	6	Conservative	2	Mismatches 6
				Indels 0
				Gaps 0

```
QY      2 I P H P T N I H K Y L V C E 15
          : | | | | | :
Db      6 L P P P T F T H K C L T S D 19
```

RESULT 62

```

AAW79123
ID AAW79123 standard; peptide; 8 AA.
XX
XX AAW79123;
AC
XX
XX
DT 27-AUG-2003 (revised)
DT 18-NOV-1998 (first entry)
XX
XX
DE Peptide obtained by oligomerisation of a minimal motif.
XX
XX
XX Fusion protein; stabilising polypeptide; proteolytic degradation;
XX resistance; half-life; autoimmune disease; inflammation; nitro drug;
XX Ikappab regulator protein; inflammatory bowel disease; in vivo imaging;
XX nitroreductase protein; enzyme therapy; prodrug therapy; protease;
XX cancer; pathological condition.
XX
XX Human herpesvirus 4.
XX
XX WO9822577-A1.
XX
XX 28-MAY-1998.
XX
XX 17-NOV-1997; 97WO-IB001508.
XX
XX 15-NOV-1996; 96US-0030986P.
XX
XX 25-JUN-1997; 97US-0048945P.
XX
XX (MASU/) MASUCCI M G.
XX
XX Masucci MG;
XX
XX WPI; 1998-312463/27.
XX
XX New fusion proteins resistant to proteolytic degradation - comprising a
XX core protein with a stabilising polypeptide comprising a peptide sequence
XX containing glycine repeats.
XX
XX Disclosure; Page 73; 120pp; English.
XX
XX Sequences shown in AAW79110 to AAW79125 are obtained by oligomerisation
XX of a selected minimal motif by complementary oligonucleotides. The
XX invention provides a method for increasing the resistance of a core
XX protein to proteolytic degradation that comprises linking or inserting
XX onto or into the core protein a stabilising polypeptide of formula
XX [(Gly $\alpha$ )X(Gly $\beta$ )Y(Gly $\gamma$ )Z] $n$  where Gly $\alpha$ , Gly $\beta$ , Gly $\gamma$  are 1-6 sequential Gly
XX residues and X, Y, Z are Ala, Ser, Val, Ile, Leu, Met, Phe, Pro or Thr
XX and n can be anything between 1-66. X, Y and Z need not be identical from
XX n repeat to n repeat. Alternatively a nucleic acid encoding a stabilising
XX polypeptide can be linked onto or inserted into a nucleic acid encoding a
XX core protein. The fusion proteins of the invention are more resistant to
XX degradation by proteases and, thus, have a longer half-life than the
XX unfused core protein. The products can be used for treating autoimmune
XX diseases, cancer and inflammation. In particular, the core protein may be
XX an Ikappab regulator protein for the treatment of inflammatory bowel
XX disease, or a nitroreductase protein which can activate nitro drugs in
XX enzyme/prodrug therapy to treat cancer or other pathological conditions.
XX The fusion proteins can also be used in diagnostic methods such as in
XX vivo imaging. (Updated on 27-AUG-2003 to correct OS field.)
XX
XX
SQ Sequence 8 AA;

Query Match          27.0%; Score 31; DB 2; Length 8;
Best Local Similarity 71.4%; Pred. No. 2e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 IHKYLVC 14
      ||:|:|
      1 IHRYLRC 7

Db

RESULT 63
AAP50408
ID AAP50408 standard; protein; 12 AA.

```

```

XX
XX AAP50408;
AC
XX
XX 25-MAR-2003 (revised)
DT 20-JAN-1992 (first entry)
XX
XX
XX Human leukaemic virus antigen.
XX
XX
XX Adult T-cell leukaemia virus; ATL; diagnosis.
XX
XX
XX Synthetic.
XX
XX JP60067432-A.
XX
XX 17-APR-1985.
XX
XX 22-SEP-1983; 83JP-00176079.
XX
XX 22-SEP-1983; 83JP-00176079.
XX
XX 22-SEP-1983; 83JP-00176079.
XX
XX (SAKA-) OTSUKA PHARM CO LTD.
XX (GANK-) GAN KANKU-KAI ZH.
XX
XX WPI; 1985-130934/22.
XX
XX
XX Human leukaemic virus antibody prodn. - by dosing mammal with immune
XX antigen comprising complex of carrier and peptide.
XX
XX Claim 1; Page 171; 20pp; Japanese.
XX
XX
XX Antigenic peptides may be used to form peptide-carrier complex, allowing
XX Abs to be raised, useful in the diagnosis of infection by the adult T-
XX cell leukaemia virus. (Updated on 25-MAR-2003 to correct PA field.)
XX
XX
SQ Sequence 12 AA;

Query Match          27.0%; Score 31; DB 1; Length 12;
Best Local Similarity 83.3%; Pred. No. 5.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      2 IHPPTN 7
      |||||
      1 IHPPTN 6

Db

RESULT 64
ADQ15533
ID ADQ15533 standard; peptide; 12 AA.
XX
XX
XX ADQ15533;
AC
XX
XX 07-OCT-2004 (first entry)
DT
XX
XX
XX Targeting peptide for Pseudomonas #6.
XX
XX
XX Antimicrobial peptide; targeting peptide; microbial infection;
XX mucosal surface; mouth; vagina; gastrointestinal tract;
XX oesophageal tract; Staphylococcus mutans infection;
XX Candida albicans infection; Helicobacter pylori infection;
XX Campylobacter jejuni infection; Vibrio cholerae infection;
XX Salmonella infection; Shigella infection; Escherichia coli infection.
XX
XX Synthetic.
XX
XX US2004137482-A1.
XX
XX 15-JUL-2004.
XX
XX 12-NOV-2003; 2003US-00706391.
XX
XX 20-AUG-1999; 99US-00378577.
XX 19-JUL-2001; 2001US-00910358.
XX 14-FEB-2002; 2002US-00077624.

```

XX (ECKE/) ECKERT R.
 PA (OIF/) OI F.
 PA (SHW/) SHI W.
 PA (ANDE/) ANDERSON M H.
 XX
 PI Eckert R, OI F, Shi W, Anderson MH;
 DR WPI, 2004-542706/52.
 XX
 PT Composition used for treating microbial infections on mucosal surface
 PT e.g. mouth, vagina, gastrointestinal tract or esophageal tract comprises
 PT targeting group and antimicrobial peptide group.
 XX
 PS Claim 37, SEQ ID NO 29; 44pp; English.
 XX
 CC The invention relates to a composition comprising a targeting group and
 CC an antimicrobial peptide group. The targeting group is coupled to the
 CC antimicrobial peptide group and recognises a target microbial organism.
 CC The composition has an antimicrobial effect on the target microbial
 CC organism. Also included are a method of treating a target microbial
 CC organism infection (by administering the composition), and the targeting
 CC peptide that specifically binds to the microorganism). The targeting
 CC group is coupled to the C-terminus of the antimicrobial peptide moiety,
 CC preferably of novipirin G10. The targeting group and the antimicrobial
 CC peptide group are fused via a peptide linker to form a fusion peptide.
 CC The composition is useful for treating a microbial infection e.g. on the
 CC mucosal surface of the mouth, vagina, gastrointestinal tract or
 CC oesophagel tract, such as S. mutans infection in a mouth, a Candida
 CC albicans infection in the vagina and a gastrointestinal infection
 CC selected from Helicobacter pylori infection, Campylobacter jejuni
 CC infection, Vibrio cholerae infection, Salmonella infection, Shigella
 CC infection and Escherichia coli infection. The present sequence is
 CC bacterial targeting peptide suitable for use in the composition of the
 CC invention.
 XX
 SQ Sequence 12 AA;
 XX
 Query Match 27.0%; Score 31; DB 8; Length 12;
 Best Local Similarity 57.1%; Pred. No. 5.3e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 PHPTNTH 9
 ||| |
 Db 2 PHPHKVN 8
 RESULT 65
 AAP40114
 ID AAP40114 standard; protein; 13 AA.
 AC AAP40114;
 XX
 DT 27-AUG-2003 (revised)
 DT 25-MAR-2003 (revised)
 DT 01-FEB-1992 (first entry)
 XX
 DE Sequence of human leukaemia virus-related peptide number 3.
 XX
 XX Human leukaemia virus; adult T-cell leukaemia virus; lymphoma;
 KM cutaneous T-cell lymphoma; immunos assay; diagnosis.
 XX
 OS Human T-cell leukemia virus.
 XX
 XX Key Location/Qualifiers
 FH Modified-site 1
 FT /label= OTHER
 FT /note= "Hydrogen atom or a group of the formula, H-Tyr-
 FT in which Tyr moiety may be labelled with radioactive
 FT iodine"
 FT Modified-site 13
 FT /label= Val-OH
 XX

PN BP107053-A.
 XX
 PD 02-MAY-1984.
 XX
 XX 23-SEP-1983; 83EP-00109481.
 XX
 PR 30-SEP-1982; 83JP-00171313.
 PR 07-JAN-1983; 83JP-00001495.
 PR 16-FEB-1983; 83JP-00025233.
 PR 23-FEB-1983; 83JP-00030096.
 XX
 PA (SAKA) OTSUKA PHARM CO LTD.
 PA (NICA-) JAPAN FOUND CANCER RES.
 PA (GANK-) GAN KENKIU-KAI ZH.
 XX
 XX Yoshida M, Sugano H, Shimizu F, Tachikawa T, Ikei N, Noda A;
 PI Hashimura E, Imagawa K;
 DR WPI, 1984-115670/19.
 XX
 PT Antibody of human leukaemia virus related peptide - useful in diagnosis
 PT of leukaemia and lymphoma and in affinity chromatography.
 XX
 PS Claim 6(3); Page 75; 86pp; English.
 XX
 CC The inventors claim HTLV-related peptides and antibodies obtd. after
 CC admin. of an antigen consisting of one of the peptides as happen, bound
 CC to a carrier. The specific antibodies are useful for purification of
 CC virus-associated proteins, and in immunological measurements related to
 CC the proteins. (Updated on 25-MAR-2003 to correct PA field.) (Updated on
 CC 27-AUG-2003 to correct OS field.)
 XX
 SQ Sequence 13 AA;
 XX
 Query Match 27.0%; Score 31; DB 1; Length 13;
 Best Local Similarity 83.3%; Pred. No. 5.8e+02;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 2 IPHPTN 7
 ||| |
 Db 2 IPHPKN 7
 RESULT 66
 ABG61667
 ID ABG61667 standard; peptide; 15 AA.
 AC ABG61667;
 XX
 DT 13-AUG-2002 (first entry)
 XX
 DE Human HGPBMY7 peptide modulator #5.
 XX
 XX G protein-coupled receptor; HGPBMY7; spinal chord; ligand library;
 KM spinal chord-related disorder; breast cancer; neoplastic disease;
 KM brain disorder; leukaemia; myeloma; immunological disorder;
 KM cholecyctitis; Grave's disease; osteoarthritis; asthma;
 KM neurological disorder; dementia; depression; Alzheimer's disease;
 KM Down's syndrome; epilepsy; intracellular calcium level; NFAT;
 KM nuclear factor activator of transcription element.
 XX
 OS Synthetic.
 XX
 XX WO200226823-A2.
 PN
 PD 04-APR-2002.
 XX
 XX 26-SEP-2001; 2001WO-US030351.
 PF
 XX 27-SEP-2000; 2000US-0235731P.
 PR 14-FEB-2001; 2001US-0268580P.
 PR 28-AUG-2001; 2001US-0315423P.
 XX

Query	Match	Best Local Similarity	Score	DB	Length	Indels	Gaps
Matches	4/	Conservative	3/	Mismatches	3/	Indels	0/
DB	11	YLVCESVNGG	20	3	YVECDINGG	12	
RESULT 67	ID	ADV21780	ADV21780	standard; peptide; 15 AA.			
XX	XX	ADV21780;					
XX	XX	10-MAR-2005	(first entry)				
XX	XX	SIV pol protein, immunogenic peptide #75.					
XX	XX	Vaccine; virinide; antigen; autoimmune disease; infection;					
XX	XX	immune modulation; cancer; neoplasia; cytostatic; melanoma; lung tumor;					
XX	XX	breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;					
XX	XX	pancreas tumor; stomach tumor; bladder tumor; kidney tumor;					
XX	XX	hodgkin's lymphoma.					
XX	XX	Simian immunodeficiency virus SIVmac; isolate 236.					
XX	XX	WO2004108753-A1.					
XX	XX	16-DEC-2004.					
XX	XX	10-JUN-2004; 2004WO-AU000775.					
XX	XX	10-JUN-2003; 2003AU-00902875.					

[illegible]

KM Immune modulation; cancer; neoplasm; cytostatic; melanoma; lung tumor;
 KM breast tumor; uterine cervix tumor; prostatic cancer; colon tumor;
 KM pancreas tumor; stomach tumor; bladder tumor; kidney tumor;
 KM Hodgkin's lymphoma.
 XX
 XX
 OS Bimlan immunodeficiency virus STWmac; isolate 236.
 XX
 XX MO2004108753-A1.
 XX
 PD 16-DEC-2004.
 XX
 XX 10-JUN-2004; 2004MO-AU000775.
 XX
 XX 10-JUN-2003; 2003AU-00902875.
 PR 25-MAR-2004; 2004AU-00901589.
 XX
 XX (UYME) UNITV MELBOURNE.
 PA
 XX Kent SJ;
 PI
 XX
 DR WPI; 2005-031657/03.
 XX
 PT Use of at least one set of peptides in the preparation of a medicament
 PT for modulating an immune response, and for treating cancer or yeast,
 PT viral, bacterial, protozoal and mycoplasma infections.
 XX
 XX Example 4; SEQ ID NO 201, 645bp; English.
 PS
 XX The invention relates to the use of at least one set of peptides in the
 CC preparation of a medicament for modulating an immune response, where
 CC individual peptides of a respective set comprise different portions of an
 CC amino acid sequence corresponding to a single polypeptide of interest and
 CC display partial sequence identity or similarity to at least one other
 CC peptide of the same set of peptides (i.e. they are overlapping). Also
 CC included are an antigen-presenting cell which has been contacted with the
 CC peptides above and thus presents the peptides, a population of such
 CC antigen-presenting cells, a process for producing antigen-presenting
 CC cells for modulating an immune response to a polypeptide of interest, a
 CC method for producing antigen-specific lymphocytes, a composition
 CC comprising at least one set of the peptides (and a carrier and/or
 CC diluent), a method for modulating an immune response to a polypeptide of
 CC interest comprising administering to a patient in need at least one set
 CC of the peptides, a method for treatment and/or prophylaxis of a disease
 CC or condition associated with the presence of a polypeptide of interest
 CC and a composition of matter for modulating an immune response in a
 CC subject to a target antigen. The polypeptide of interest is also a
 CC disease- or condition-associated polypeptide that is a polypeptide
 CC produced by a pathogenic organism or a cancer, and produced by a
 CC pathogenic organism selected from yeast, viruses, bacteria, helminths,
 CC protozoans and mycoplasmas. The disease- or condition-associated
 CC polypeptide is produced by a cancer selected from melanoma, lung cancer,
 CC breast cancer, cervical cancer, prostate cancer, colon cancer, pancreatic
 CC cancer, stomach cancer, bladder cancer, kidney cancer, post transplant
 CC lymphoproliferative disease (PTLD) or Hodgkin's lymphoma. The uncutured
 CC antigen-presenting cells or their precursors are useful in the
 CC preparation of a medicament for the treatment of a disease or condition
 CC in a subject, which disease or condition is associated with the presence
 CC of aberrant expression of a target antigen, where the antigen-presenting
 CC cells or their precursors have not been subjected to activating
 CC conditions but have been contacted with an antigen that corresponds to
 CC the target antigen to express a processed or modified form of the antigen
 CC for presentation to the subject's immune system. The present sequence is
 CC one of a set of overlapping immunogenic peptides derived from an STV
 CC protein.
 CC
 SO Sequence 15 AA;
 XX
 XX
 Query Match 27.0%; Score 31; DB 9; Length 15;
 Best Local Similarity 55.6%; Pred. No. 6.8e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 IPHPNIIHK 10
 ||||| : |

DB 2 IPHPAGIAK 10
 RESULT 69
 AAAY90148
 ID AAAY90148 standard; peptide; 16 AA.
 XX
 XX AAAY90148;
 AC
 XX
 XX 06-AUG-2003 (revised)
 DT 21-SEP-2000 (first entry)
 XX
 XX
 DE Ligand epitope for UPAR #3.
 XX
 XX
 XX Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
 KM adenovirus; hexon HVR5 loop; hexon HI loop; peripheral artery disease;
 KM recombinant adenovirus vector; tumor; restenosis; gene therapy; asthma;
 KM smooth muscle cell proliferation inhibitor; coronary artery disease;
 KM obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
 KM thrombosis; diabetes; tropism-modified virus.
 XX
 XX Synthetic.
 OS
 XX
 XX MO200012738-A1.
 PN
 XX
 XX 09-MAR-2000.
 PD
 XX
 XX 27-AUG-1999; 99WO-IB001524.
 PF
 XX
 XX 27-AUG-1998; 98US-0098028P.
 PR
 XX
 XX (AVERT) AVENTIS PHARMA SA.
 PA
 XX
 XX Vigne E, Dedieu J, Latra M, Yeh P, Perricaudet M;
 PI
 XX WPI; 2000-256653/22.
 DR
 XX
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
 PT vectors having modified hexon HVR5 and HI loops and modified fiber
 PT proteins useful for targeted gene therapy to treat cancer or restenosis.
 PS
 XX Claim 14; Page 69; 128bp; English.
 XX
 CC This sequence represents a ligand epitope for UPAR, and is used as a
 CC targeting sequence. The invention relates to an adenovirus from which at
 CC least a part of the hexon HVR5 or HI loop is replaced with a binding
 CC peptide, or targeting sequence, flanked by connecting amino acid spacers,
 CC to functionally display its binding specificity at the capsid surface.
 CC The invention also relates to a recombinant adenovirus vector where a
 CC binding peptide, or targeting sequence, is connected to the C-terminus of
 CC the fiber by a connecting spacer, or linker, so as to functionally
 CC display its binding specificity at the capsid surface. The adenovirus or
 CC recombinant adenovirus vector can be used to preferentially express a
 CC gene in a target cell, especially a cell that expresses a UPAR. The
 CC targeted adenovirus vector preferably comprises a heterologous gene
 CC encoding a gene for treatment of a tumor or restenosis. The targeted
 CC adenovirus vector is useful for gene therapy treatment of a disease, and
 CC for manufacturing a medicine used in gene therapy treatment of a disease.
 CC The viruses can also be used to inhibit smooth muscle cell proliferation,
 CC to treat peripheral artery diseases, coronary artery diseases, obesity,
 CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
 CC thrombosis, and diabetes. The viruses are particularly targeted against a
 CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
 CC are tropism-modified without adversely impacting productivity of the
 CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
 CC
 SO Sequence 16 AA;
 XX
 XX
 Query Match 27.0%; Score 31; DB 3; Length 16;
 Best Local Similarity 45.5%; Pred. No. 7.4e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IPHPNIIHKYL 12

[illegible]

PR	11-APR-1997;	97EP-00106024.
XX	(WILE-) WILEX BIOTECHNOLOGY GMBH.	
PA	Kessler H, Graeff H, Schmitt M, Megdolen V, Wilhelm OG, Riemer C;	
PI	Bueggle M;	
PI	WPI, 1998-568669/48.	
DR		
XX	New antagonistic peptide(s) derived from urokinase plasminogen activator	
PT	- have high affinity for urokinase receptor, particularly for treatment	
PT	of tumours.	
PS	Example 2; Page 15; 30pp; German.	
XX	This peptide is used in a method which produces cyclic peptides having a	
CC	nine-membered ring in which at least two of the ring-forming amino acids	
CC	are derived from the 22-28 amino acid region of urokinase plasminogen	
CC	activator (uPA). The peptides may also contain D-form residues. Such	
CC	peptides have the formula X21-X22-X23-X24-X25-X26-X27-X28-X29-(X30)n-(Y)m	
CC	where X21-X30 are amino acids, Y = spacer, m and n are each 0 or 1,	
CC	monomers are linked via N-R1-CO or CO-N-R1, R1 = hydrogen, methyl or	
CC	ethyl groups, with a bridge between X21 and X29. The novel peptides are	
CC	uPA antagonists (they inhibit binding of uPA to its receptor, uPAR) so	
CC	are useful for treating diseases involving unregulated expression of uPA	
CC	or uPAR, especially tumours where they reduce invasiveness, metastasis	
CC	and angiogenesis. They can act more generally wherever inhibition of the	
CC	proteolytic activity of uPA is required, e.g. arthritis, inflammation,	
CC	osteoporosis, retinopathy and also for contraception. They can	
CC	additionally act as targeting vehicles (liposomes or viral vectors) for	
CC	uPAR-expressing cells, e.g. for delivering diagnostic markers or	
CC	therapeutic agents, including nucleic acids for gene therapy. Cyclic and	
CC	D-amino acid containing peptides have better affinity for uPAR than known	
CC	compounds and its derivatives are more resistant to degradation	
SQ	Sequence 17 AA:	
Query Match	27.0%; Score 31; DB 2; Length 17;	
Best Local Similarity	45.5%; Pred. No. 7.9e+02;	
Matches	5; Conservative 2; Mismatches 4; Indels 0; Gaps 0	
Oy	2 IPHPNHHKL 12 : 4 MPHSLNFSQYL 14	
Db		
RESULT 74		
AAY79011		
ID	AAY79011 standard; peptide; 17 AA.	
XX		
AC	AAY79011;	
XX		
DT	05-JUN-2000 (first entry)	
DE		
DE	Urokinase receptor antagonist peptide AE78.	
XX		
XX	Antagonist; urokinase plasminogen activator; uPA; uPAR; cancer; plasmin;	
KW	malignant glioma gastric cancer; proteolysis.	
KW	Synthetic.	
XX		
OS		
XX	WO200001802-A2.	
PN		
PD	13-JAN-2000.	
PP	01-JUL-1999; 99WO-DK000377.	
XX		
PR	01-JUL-1998; 98DK-00008674.	
XX		
ZA	(CANC-) CANCERFORSKNINGSPONDET AF 1989.	
PL	Poung M, Ostergaard S, Holm A, Holst-Hansen C, Stephens RW;	

PI Dano K;
 XX
 DR MPI; 2000-171009/15.
 XX
 PT New peptides that antagonize the urokinase receptor, used for treating
 XX cancer by preventing localized conversion of plasminogen to plasmin.
 XX
 PS Example 1; Page 51; 75pp; English.
 XX
 CC This sequence represents a urokinase receptor (UPAR) antagonist peptide.
 CC The peptide inhibits the binding interaction between human urokinase
 CC plasminogen activator (uPA) and its cell surface receptor (UPAR).
 CC Preventing uPA binding to uPAR, reduces the ability of uPA to convert
 CC plasminogen to plasmin, this results in a reduction of localized
 CC proteolysis caused by plasmin. The peptides of the invention are used to
 CC treat cancer, particularly acute myeloid leukaemia, malignant gliomas and
 CC gastric cancer
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 27.0%; Score 31; DB 3; Length 17;
 Best Local Similarity 45.5%; Pred. No. 7.9e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IPHPTNIHKYL 12
 :||| :|||
 Db 4 MPHSLNFSQYL 14
 RESULT 75
 AAB17140
 ID AAB17140 standard; peptide; 17 AA.
 XX
 AC AAB17140;
 XX
 DT 31-OCT-2000 (first entry)
 XX
 DE UKR antagonist peptide sequence SEQ ID NO:196.
 XX
 XX Modified peptide; therapeutic agent; fusion; Fc domain; cancer;
 KM autoimmune disease; cytostatic; antiaesthetic; thrombolytic; VEGF;
 KM immunosuppressive; EPO; TPO; CTLA4; mmetic; IL-1; TNF; antagonist; MMP;
 KM inhibitor; erythropoietin; thrombopoietin; interleukin 1;
 KM cytotoxic T cell lymphocyte antigen 4; tumour necrosis factor;
 KM vascular endothelial growth factor; matrix metalloproteinase; asthma;
 KM thrombosis; pharmaceutical.
 XX
 OS Synthetic.
 XX
 PN WO200024782-A2.
 XX
 PD 04-MAY-2000.
 XX
 PF 25-OCT-1999; 99WO-US025044.
 XX
 PR 23-OCT-1998; 98US-0105371P.
 XX
 PR 22-OCT-1999; 99US-00428082.
 XX
 PA (AMGE-) AMGEN INC.
 XX
 PI Felge U, Liu C, Cheetham J, Boone TC;
 XX
 DR MPI; 2000-350702/30.
 XX
 PT Novel composition of matter comprising an Fc domain and pharmacologically
 PT active peptides, useful for treating cancer and autoimmune diseases.
 XX
 PS Claim 39; Page 261; 608pp; English.
 XX
 CC The present invention describes composition of matter (I) comprising an
 CC Fc domain, pharmacologically active peptides, and linkers. Where (I) is:
 CC (X1)a-F1-(X2)b, where: F1 = an Fc domain; X1 and X2 = are each
 CC independently selected from -(L1)-c-P1, -(L1)c-P1-(L2)d-P2, -(L1)c-P1-

CC (L2)d-P2-(L3)e-P*3, or -(L1)c-P1-(L2)d-P2-(L3)e-P3-(L4)f-P4 where P1, P2,
 CC P3, and P4 = are each independently sequences of pharmacologically active
 CC peptides; L1, L2, L3, and L4 = are each independently linkers; and a, b,
 CC c, d, e, and f = are each independently 0 or 1, provided that at least 1
 CC of a and b is 1. The composition can have cytostatic, antiaesthetic,
 CC thrombolytic and immunosuppressive activities. DNAs, vectors and host
 CC cells from the present invention can be used for producing pharmaceutical
 CC compositions. The compositions are useful for treating cancer, asthma,
 CC thrombosis, or autoimmune diseases. The use of an Fc domain (rather than
 CC a Fcd domain) can provide a longer half-life or incorporate functions
 CC such as Fc receptor binding, protein A binding, complement fixation, and
 CC possibly placental transfer. AAB69443 to AAB69526 and AAB6955 to
 CC AAB18003 represent nucleotide and amino acid sequences used in the
 CC exemplification of the present invention
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 27.0%; Score 31; DB 3; Length 17;
 Best Local Similarity 45.5%; Pred. No. 7.9e+02;
 Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
 QY 2 IPHPTNIHKYL 12
 :||| :|||
 Db 4 MPHSLNFSQYL 14
 RESULT 76
 AAY90149
 ID AAY90149 standard; peptide; 17 AA.
 XX
 AC AAY90149;
 XX
 DT 06-AUG-2003 (revised)
 XX
 DT 21-SEP-2000 (first entry)
 XX
 DE Ligand epitope for UPAR #4.
 XX
 XX Ligand epitope; UPAR; urokinase-type plasminogen activator receptor;
 KM adenovirus; hexon HRV5 loop; hexon HI loop; peripheral artery disease;
 KM recombinant adenovirus vector; tumour; restenosis; gene therapy; asthma;
 KM smooth muscle cell proliferation inhibitor; coronary artery disease;
 KM obesity; neurodegenerative disease; infection; autoimmune disease; HIV;
 KM thrombosis; diabetes; tropism-modified virus.
 XX
 OS Synthetic.
 XX
 PN WO200012738-A1.
 XX
 PD 09-MAR-2000.
 XX
 PF 27-AUG-1999; 99WO-1B001524.
 XX
 PR 27-AUG-1998; 98US-0098028P.
 XX
 PA (AVERT) AVENTIS PHARMA SA.
 XX
 PI Vigne E, Dedieu J, Latta M, Yeh P, Berricaudet M;
 XX
 DR MPI; 2000-256653/22.
 XX
 PT Urokinase-type plasminogen activator receptor (UPAR)-targeted adenovirus
 PT vectors having modified hexon HRV5 and HI loops and modified fiber
 PT proteins useful for targeted gene therapy to treat cancer or restenosis.
 XX
 PS Claim 14; Page 69; 128pp; English.
 XX
 CC This sequence represents a ligand epitope for UPAR, and is used as a
 CC targeting sequence. The invention relates to an adenovirus from which at
 CC least a part of the hexon HRV5 or HI loop is replaced with a binding
 CC peptide, or targeting sequence, flanked by connecting amino acid spacers,
 CC to functionally display its binding specificity at the capsid surface.
 CC The invention also relates to a recombinant adenovirus vector where a
 CC binding peptide, or targeting sequence, is connected to the C-terminus of

CC the fiber by a connecting spacer, or linker, so as to functionally
CC display its binding specificity at the capsid surface. The adenovirus or
CC recombinant adenovirus vector can be used to preferentially express a
CC gene in a target cell, especially a cell that expresses a UPAR. The
CC targeted adenovirus vector preferably comprises a heterologous gene
CC encoding a gene for treatment of a tumour or restenosis. The targeted
CC adenovirus vector is useful for gene therapy treatment of a disease, and
CC for manufacturing a medicine used in gene therapy treatment of a disease.
CC The viruses can also be used to inhibit smooth muscle cell proliferation,
CC to treat peripheral artery diseases, coronary artery diseases, obesity,
CC neurodegenerative diseases, infections, autoimmune diseases, asthma, HIV,
CC thrombosis, and diabetes. The viruses are particularly targeted against a
CC urokinase-type plasminogen activator receptor (UPAR). The adenoviruses
CC are tropism-modified without adversely impacting productivity of the
CC vectors. (Updated on 06-AUG-2003 to correct OS field.)
CC
XX
SQ Sequence 17 AA;
Query Match 27.0%; Score 31; DB 3; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 IHPPTNIHKYL 12
: || | : ||
DB 4 MPHSLNFSQYL 14
RESULT 77
AAB74578 standard; peptide; 17 AA.
XX AAB74578;
XX
DT 05-JUN-2001 (first entry)
XX
XX Context-dependent functional entity recognition domain #2.
XX
KM Context-dependent functional entity; efficacy enhancement; inflammation;
KM selective recognition domain; thrombogenic potential; cancer; infection;
KM arthritis; atherosclerosis; burn.
XX
OS Synthetic.
XX
PN MO200125413-A1.
XX
PD 12-APR-2001.
XX
PF 04-OCT-2000; 2000MO-US027794.
XX
PR 04-OCT-1999; 99US-00411067.
XX
PA (NUVA-) NUVAS LLC.
XX
PI Houston IL;
XX
DR WPI, 2001-258295/26.
XX
XX Enhancing the efficacy of active and diagnostic agents and treating
PT pathological conditions in a subject by administering the agent with a
PT context-dependent functional entity, useful for treating e.g. malignant
PT neoplasms.
XX
PS Claim 10, Page 39, 49pp; English.
XX
CC The present invention describes a method of enhancing the efficacy of an
CC agent by coadministering the agent and a context-dependent functional
CC entity. The latter comprises a substructure with thrombogenic potential
CC and a selective recognition domain. This is useful in the treatment of
CC cancer, arthritis, infections, neovascular glaucoma, inflammatory
CC conditions, dermatitis, endometriosis, atherosclerosis, vascular
CC restenosis and conditions associated with granuloma tissues, such as
CC burns and pyogenic granuloma. The present sequence is an example of a
CC recognition domain for use in the invention

XX
SQ Sequence 17 AA;
Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 IHPPTNIHKYL 12
: || | : ||
DB 4 MPHSLNFSQYL 14
RESULT 78
ABB73284 standard; peptide; 17 AA.
XX ABB73284;
XX
DT 05-APR-2002 (first entry)
XX
XX UTR antagonist peptide SEQ ID NO:196.
XX
XX Modified peptide; mimetic; Fc domain; fusion; immunoglobulin G; IgG; EPO;
KM erythropoietin; TPO; tumour necrosis factor alpha inhibitor;
KM TNP-alpha inhibitor; interleukin 1 antagonist; IL-1 antagonist; TNP;
KM TPO mimetic peptide; EPO mimetic peptide; BMP; VEGF antagonist;
KM MMP inhibitor; antiinflammatory; antitumour; immunosuppressive;
KM cyclostatic; antineumatic; antiarthritis; antidiabetic; ophthalmological;
KM antihaemic; anorectic; antifertility; haemostatic; dermatological;
KM neuroprotective; inflammatory disease; autoimmune disease; tumour growth;
KM cancer; rheumatoid arthritis; diabetic retinopathy; infertility; obesity;
KM sleep disorder; neurological degenerative disease; anaemia;
KM thrombocytopaenia; metastatic tumour; systemic lupus erythematosus;
KM Fanconi's syndrome.
XX
XX Homo sapiens.
OS Synthetic.
XX
PN MO200183525-A2.
XX
PD 08-NOV-2001.
XX
PF 02-MAY-2001; 2001MO-US014310.
XX
PR 03-MAY-2000; 2000US-00563286.
XX
PA (AMGE-) AMGEN INC.
XX
PI Feige U, Liu C, Cheetham JC, Boone TC, Guada JM;
XX
XX WPI, 2002-130313/17.
XX
DR Novel vehicle-peptide molecule or its multimers useful for treating
PT inflammatory and autoimmune diseases, cancer, rheumatoid arthritis,
PT diabetic retinopathy, obesity, sleep disorders and infertility.
XX
XX Claim 39, Page 57, 176pp; English.
XX
XX The present invention describes a vehicle-peptide molecule (I) or its
CC multimers. (I) can have antiinflammatory, antitumour, immunosuppressive,
CC cytostatic, antineumatic, antiarthritis, antidiabetic, ophthalmological,
CC antihaemic, anorectic, antifertility, haemostatic, dermatological and
CC neuroprotective activities. (I) can be used as a therapeutic or
CC prophylactic agent as well as for screening purposes. (I) is useful for
CC diagnosing diseases characterised by dysfunction of their associated
CC protein of interest, for identifying normal or abnormal proteins of
CC interest, as a part of diagnostic kit to detect the presence of their
CC proteins of interest in a biological sample. Additionally, (I) is useful
CC for treating inflammatory and autoimmune diseases, tumour growth, cancer,
CC rheumatoid arthritis, diabetic retinopathy, obesity, sleep disorders,
CC infertility, and neurological degenerative diseases. (I), comprising EPO-
CC mimetic compounds are useful for treating disorders characterised by low
CC red blood cell levels such as anaemia. The TPO-mimetic comprising

CC compounds are useful for treating conditions that involve an existing
CC megakaryocyte/platelet deficiency or an expected megakaryocyte/platelet
CC deficiency, such as thrombocytopenia, aplastic anemia, metastatic
CC tumor which result in thrombocytopenia, systemic lupus erythematosus,
CC and Fanconi's syndrome. ABB72403 to ABB73426 and ABL35695 to ABL35777
CC represent amino acid and nucleic acid sequences used in the
CC exemplification of the present invention
SQ Sequence 17 AA;
Query Match 27.0%; Score 31; DB 5; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 2 IHPHTHKYL 12
: || | : ||
DB 4 MHSLSNFSQYL 14
RESULT 79
ADG25913
ID ADG25913 standard; peptide; 17 AA.
AC ADG25913;
XX
XX
DT 26-FEB-2004 (first entry)
XX
DE INPIONCH03 protein sequence - exon 27.
XX
XX INPIONCH03; INPIONCH04; PKD/REJ cation channel; cardiovascular disease;
KM heart arrhythmia; angina; neurological disorder; psychiatric disorder;
KM Alzheimer's disease; Huntington's disease; diabetes; dermatitis;
KM pulmonary disease; asthma; cystic fibrosis; mucous membrane disorders;
KM COPD; rhinitis; leukemia; ocular disease; glaucoma; retinopathy;
KM immune disorder; renal disease; polycystic kidney disease;
KM fertility disorder; testosterone-related disorder; cancer;
KM gastrointestinal disorders; developmental disorder;
KM muscle tone-related disease; vascular muscle disorder; migraine;
KM pre-eclampsia; hypertension; cardiac arrhythmia;
KM bladder muscle tone disorder; urinary incontinence;
KM urinary tract infection.
XX
XX
OS unidentified.
XX
XX
PN WO2003089469-A2.
XX
PD 30-OCT-2003.
XX
PF 16-APR-2003; 2003WO-GB001655.
XX
PR 16-APR-2002; 2002GB-00008707.
XX
PA (INPH-) INPHARMATICA LTD.
XX
PI Lobley AE, Michalovich D, Allen KE, Reynolds L, Pierron VN;
PI Allen JM;
XX
XX WPI; 2003-845523/78.
DR N-PSDB; ADG25912.
XX
XX
PT New polypeptide of the PKD/REJ family of cation channels, useful for
PT preparing a composition for diagnosing, treating or preventing e.g.,
PT hypertension, angina or psychiatric disorders.
XX
XX
PS Claim 1, SEQ ID NO 54; 104pp; English.
XX
XX The invention comprises the amino acid and coding sequence of two
CC proteins (INPIONCH03 and INPIONCH04) which are members of the PKD/REJ
CC family of cation channels. The proteins of the invention are useful for
CC preparing a composition for diagnosing, treating or preventing:
CC cardiovascular disease (e.g. heart arrhythmia and angina), neurological
CC and psychiatric disorders (e.g. Alzheimer's disease and Huntington's
CC disease), diabetes, dermatitis, pulmonary disease, asthma, cystic

CC fibrosis, mucous membrane disorders, COPD, rhinitis, leukaemia, ocular
CC disease, glaucoma, retinopathy, immune disorder, renal disease,
CC polycystic kidney disease, fertility disorders, testosterone-related
CC disorders, cancer, gastrointestinal disorders, developmental disorders,
CC diseases related to muscle tone, including vascular muscle disorders such
CC as migraine, pre-eclampsia, hypertension and cardiac arrhythmia/s; and
CC bladder muscle tone disorders (e.g. urinary incontinence and urinary
CC tract infection). The present amino acid sequence represents an
CC INPIONCH03 polypeptide of the invention.
SQ Sequence 17 AA;
Query Match 27.0%; Score 31; DB 7; Length 17;
Best Local Similarity 62.5%; Pred. No. 7.9e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DIPHTNTI 8
: || | |
DB 10 DLPHPBAI 17
RESULT 80
ADJ73438
ID ADJ73438 standard; peptide; 17 AA.
AC ADJ73438;
XX
XX
DT 06-MAY-2004 (first entry)
XX
DE Somatostatin (or cortistatin) mimetic peptide sequence SegID 894.
XX
XX mimetic; CDR mimetibody; gene therapy; transgenic; immune;
KM cardiovascular; infectious; malignant; neurological disease; anaemia;
KM immunomodulator; cardiant; antimicrobial; cytostatic; neuroprotective;
KM somatostatin; cortistatin.
XX
XX
OS Synthetic.
XX
XX
PN WO2003084477-A2.
XX
PD 16-OCT-2003.
XX
PF 24-MAR-2003; 2003WO-US009139.
XX
PR 29-MAR-2002; 2002US-0368791P.
XX
PA (CENZ) CENTOCOR INC.
XX
XX Heavner GA, Knight DM, Scallion BJ, Grayeb J;
XX
XX WPI; 2003-804237/75.
DR
XX
XX
PT New CDR mimetibody comprising a portion of a heavy or light chain
PT variable region comprising human framework or ligand binding region,
PT useful for preparing a composition for treating e.g., immune,
PT cardiovascular or neurologic disease.
XX
XX
PS Disclosure, SEQ ID NO 894; 97pp; English.
XX
XX This invention relates to novel mammalian CDR mimetibodies, specific
CC portions or variants thereof. Specifically, it refers to an antibody
CC fragment where a protein has been inserted into, or replaces a portion
CC of, one or more CDR regions, such that each CDR mimetibody comprises at
CC least one portion of a heavy chain or light chain variable region, which
CC itself comprises at least one human framework region and at least one
CC ligand binding region (LBR). The present invention describes human
CC mimetibodies, including modified immunoglobulins and cleavage products
CC that can be useful in gene therapy and the generation of transgenic
CC plants and animals. Furthermore, the CDR mimetibody is useful for
CC preparing compositions for modulating, treating or reducing the symptoms
CC of immune, cardiovascular, infectious, malignant and/or neurologic
CC diseases, as well as anaemia. Accordingly, they exhibit immunomodulator,
CC cardiant, antimicrobial, cytostatic and neuroprotective activities. This

CC peptide sequence is an somatostatin mimetic peptide sequence used to make
CC a mimetibody of the invention.

XX Sequence 17 AA;

SO Query Match 27.0%; Score 31; DB 7; Length 17;

CC Best Local Similarity 45.5%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTNHKYL 12

DB 4 MPHSLNFSQYL 14

RESULT 81

ADJ53072 ID ADJ53072 standard; peptide; 17 AA.

XX ADJ53072;

XX 06-MAY-2004 (first entry)

XX CHI deleted mimetibody-related peptide SegID894.

XX CHI deleted mimetibody; immunosuppressive; cardiovascular; cardiac;
XX hypertensive; neuroprotective; nootropic; antibacterial; virocidic;
XX fungicide; gene therapy; immune disorder; cardiovascular disease;
XX arrhythmia; hypertension; heart failure; neurodegenerative;
XX multiple sclerosis; dementia; Alzheimer's disease; anaemia;
XX cancerous condition; infectious disease; bacterial infection;
XX viral infection; fungal infection.

XX Unidentified.

XX Synthetic.

XX WO2004002417-A2.

XX 08-JAN-2004.

XX 27-JUN-2003; 2003WO-US020347.

XX 28-JUN-2002; 2002US-0392431P.

XX (CENZ) CENTOOR INC.

XX Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;
XX Kutoleski KA;

XX WPI; 2004-082870/08.

XX New CHI-deleted mimetibody polypeptides and nucleic acids, useful for
XX modulating, treating, alleviating, preventing an immune, cardiovascular,
XX or neurodegenerative disease or disorder, anemia, cancer, or infectious
XX diseases.

XX Claim 3; SEQ ID NO 894; 129pp; English.

XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
XX which encode them), compositions, methods and uses. The invention may be
XX useful for the development of compounds with an immunosuppressive,
XX cardiovascular, cardiac, hypotensive, neuroprotective, nootropic,
XX antibacterial, virocidic or fungicide activity. In addition, the disclosed
XX sequences may prove useful for gene therapy. The CHI-deleted mimetibody
XX is useful for diagnosing or treating a disease condition in a cell,
XX tissue, organ or animal, specifically for modulating, treating,
XX alleviating, preventing the incidence or reducing the symptoms of an
XX immune, cardiovascular (for example arrhythmia, hypertension or heart
XX failure), or neurodegenerative (for example multiple sclerosis, dementia
XX or Alzheimer's disease) diseases or disorders, anaemia, cancerous
XX conditions, or infectious diseases (for example bacterial, viral or
XX fungal infection). The present sequence is that of a peptide which may be
XX used during the creation of a mimetibody of the invention.

SO Sequence 17 AA;

XX Query Match 27.0%; Score 31; DB 8; Length 17;

CC Best Local Similarity 45.5%; Pred. No. 7.9e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTNHKYL 12

DB 4 MPHSLNFSQYL 14

RESULT 82

ADJ52033 ID ADJ52033 standard; peptide; 17 AA.

XX ADJ52033;

XX 06-MAY-2004 (first entry)

XX CHI deleted mimetibody-related peptide SegID894.

XX CHI deleted mimetibody; osteopathic; cardiovascular-Gen;
XX dermatological-Gen; auditory; endocrine-Gen; gastrointestinal-Gen;
XX gynaecological-Gen; hepatotropic; haemostatic; immunomodulator;
XX anti-allergic; muscular-Gen; cytostatic; anti-inflammatory; neuroleptic;
XX ophthalmological; nephrotropic; respiratory-Gen; tumour necrosis factor;
XX TNF; cytokine; bone disorder; joint disorder; cardiovascular disorder;
XX dental disorder; oral disorder; dermatological disorder; ear disorder;
XX nose disorder; throat disorder; endocrine disorder; metabolic disorder;
XX gastrointestinal disorder; gynaecological disorder; hepatic disorder;
XX obstructive disorder; haematologic disorder; immunologic disorder;
XX allergic disorder; infectious disorder; musculoskeletal disorder;
XX oncological disorder; neurological disorder; nutritional disorder;
XX ophthalmologic disorder; pediatric disorder; psychiatric disorder;
XX renal disorder; pulmonary disorder.

XX Unidentified.

XX Synthetic.

XX WO2004002424-A2.

XX 08-JAN-2004.

XX 30-JUN-2003; 2003WO-US020495.

XX 28-JUN-2002; 2002US-0392431P.

XX 19-SEP-2002; 2002US-0412144P.

XX (CENZ) CENTOOR INC.

XX Heavner GA, Knight DM, Ghrayeb J, Scallion BJ, Nesspor TC;
XX Kutoleski KA;

XX WPI; 2004-082872/08.

XX New CHI deleted mimetibody polypeptide and nucleic acid, useful for
XX diagnosing, preventing or treating cardiovascular, dermatologic,
XX endocrine, gastrointestinal, gynecologic, infectious, neurologic and
XX nutritional disorders.

XX Claim 15; SEQ ID NO 894; 123pp; English.

XX This invention relates to CHI deleted mimetibodies (and the DNA sequences
XX which encode them), compositions, methods and uses. The invention may be
XX useful for the development of compounds with an osteopathic,
XX cardiovascular-Gen, dermatological-Gen, auditory, endocrine-Gen,
XX gastrointestinal-Gen, gynaecological-Gen, hepatotropic, haemostatic,
XX immunomodulator, anti-allergic, muscular-Gen, cytostatic,
XX anti-inflammatory, neuroleptic, ophthalmological, nephrotropic or
XX respiratory-Gen activity acting as a tumour necrosis factor (TNF)-
XX modulator or cytokine-agonist. The methods and compositions of the
XX present invention are useful for the diagnosis, prevention and/or
XX treatment of diseases or conditions associated with aberrant expression

CC or activity of the CH1 deleted mimetibody, such as a bone or joint,
CC cardiovascular, dental or oral, dermatological, ear, nose or throat,
CC endocrine, metabolic, gastrointestinal, gynaecological, hepatic,
CC obstructive, haematologic, immunological, allergic, infectious,
CC musculoskeletal, oncological, neurological, nutritional, ophthalmologic,
CC pediatric, psychiatric, renal or pulmonary disorders. The present
CC sequence is that of a peptide which may be used during the creation of a
CC mimetibody of the invention.

XX
SQ Sequence 17 AA;

Query Match 27.0%; Score 31; DB 8; Length 17;
Best Local Similarity 45.5%; Pred. No. 7.9e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 THPTNIHKYL 12
:|:|:|:|:
Db 4 MPHSLNFSQYL 14

RESULT 83

ABB39967
ID ABB39967 standard; peptide, 18 AA.

AC ABB39967;

DT 04-FEB-2002 (first entry)

DE Peptide #7473 encoded by human foetal liver single exon probe.

KW Human; foetal liver; gene expression; single exon nucleic acid probe.

OS Homo sapiens.

PN WO200157277-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000669.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-483447/52.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human fetal liver.

PS Claim 27; SEQ ID NO 32602; 639pp + Sequence Listing; English.

XX The invention relates to a single exon nucleic acid probe for measuring
CC human gene expression in a sample derived from human foetal liver. The
CC single exon nucleic acid probes may be used for predicting, measuring and
CC displaying gene expression in samples derived from human fetal liver. The
CC present sequence is a peptide encoded by a single exon nucleic acid probe
CC of the invention. Note: The sequence data for this patent did not form
CC part of the printed specification, but was obtained in electronic format
CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX
SQ Sequence 18 AA;

Query Match 27.0%; Score 31; DB 4; Length 18;
Best Local Similarity 44.4%; Pred. No. 8.5e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TNIHKYIWC 14
:|:|:|:|:
Db 9 SHIHVFLIC 17

RESULT 84

AAM33587
ID AAM33587 standard; protein, 18 AA.

AC AAM33587;

DT 17-OCT-2001 (first entry)

DE Peptide #7624 encoded by probe for measuring placental gene expression.

KW Probe; microarray; human; placenta; antenatal diagnosis;

OS genetic disorder.

PN WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000663.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-488897/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

XX gene expression in human placenta.

PS Claim 27; SEQ ID NO 33856; 654pp; English.

XX The present invention relates to single exon nucleic acid probes (SENP;
CC see A131315-A157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders
XX
SQ Sequence 18 AA;

Query Match 27.0%; Score 31; DB 4; Length 18;
Best Local Similarity 44.4%; Pred. No. 8.5e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 6 TNIHKYIWC 14
:|:|:|:|:
Db 9 SHIHVFLIC 17

RESULT 85

AAM73385
ID AAM73385 standard; protein, 18 AA.

AC AAM73385;

DT 06-NOV-2001 (first entry)

DE Human bone marrow expressed probe encoded protein SEQ ID NO: 33691.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KM microarray; cancer; leukemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488900/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 PS Example 4; SEQ ID NO 33691; 658pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 CC
 CC Sequence 18 AA;
 SQ
 Query Match 27.0%; Score 31; DB 4; Length 18;
 Best Local Similarity 44.4%; Pred. No. 8.5e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 6 TNIHKYIVC 14
 Db 9 SHIHVFLIC 17
 Db
 RESULT 86
 AAM60712
 ID AAM60712 standard; protein; 18 AA.
 XX
 AC AAM60712;
 XX
 DT 05-NOV-2001 (first entry)
 XX
 DE Human brain expressed single exon probe encoded protein SEQ ID NO: 32817.
 XX
 KM Human; brain expressed exon; gene expression analysis; probe; microarray;
 KM Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.
 XX
 OS Homo sapiens.
 XX
 PN WO200157275-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000667.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-483446/52.
 XX
 PT Single exon nucleic acid probes for analyzing gene expression in human
 PT brain.
 XX
 PS Example 4; SEQ ID NO 32817; 650pp + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC brain. They can be used to measure gene expression in brain cell samples,
 CC which may enable the diagnosis and improved treatment of nervous system
 CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
 CC epilepsy and cancers. The present sequence is a protein encoded by one of
 CC the probes of the invention
 CC
 CC Sequence 18 AA;
 SQ
 Query Match 27.0%; Score 31; DB 4; Length 18;
 Best Local Similarity 44.4%; Pred. No. 8.5e+02;
 Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
 QY 6 TNIHKYIVC 14
 Db 9 SHIHVFLIC 17
 Db
 RESULT 87
 ABG55102
 ID ABG55102 standard; peptide; 18 AA.
 XX
 AC ABG55102;
 XX
 DT 25-FEB-2003 (first entry)
 XX
 DE Human liver peptide, SEQ ID NO 33750.
 XX
 KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;
 KM hypercholesterolaemia; coronary heart disease.
 XX
 OS Homo sapiens.
 XX
 PN WO200157273-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000664.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 XX
 DR WPI; 2001-488998/53.
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human adult liver.

XX 17-JUN-2003; 2003BP-00101775.
 PR 17-JUN-2003; 2003US-0479061P.
 XX
 XX (VIBV-) VIB VZW.
 PA (UYGE-) UNIV GENT.
 PI Kas K, Vandekerckhove J, Krols L;
 XX WPI; 2005-057893/06.
 DR
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 PS Example; SEQ ID NO 553; 265pp; English.
 XX
 CC The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a hedgehog pathway peptide combo.
 XX
 SQ Sequence 19 AA;
 QY
 Db 2 IPRPTNIHKYLVCE 15
 4 IPRHQSRRGPRPTCQ 17
 RESULT 90
 ADV52657
 ID ADV52657 standard; peptide; 19 AA.
 XX
 AC ADV52657;
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE Hedgehog pathway peptide SEQ ID NO 154.
 XX
 KW diagnosis; cancer; obesity; diabetes; asthma; inflammation; depression;
 KW food; feedstuff; cosmetics; agriculture; animal breeding;
 KW hedgehog pathway.
 XX
 OS Undefined.
 XX
 PN MO2004111636-A2.
 XX
 PD 23-DEC-2004.
 XX
 PF 17-JUN-2004; 2004MO-BP051158.
 XX

PR 17-JUN-2003; 2003BP-00101775.
 PR 17-JUN-2003; 2003US-0479061P.
 XX
 XX (VIBV-) VIB VZW.
 PA (UYGE-) UNIV GENT.
 PI Kas K, Vandekerckhove J, Krols L;
 XX WPI; 2005-057893/06.
 DR
 XX
 PT Identifying a peptide combo which corresponds with a family of proteins,
 PT useful for diagnosing a variety of diseases, drug development or in
 PT agriculture, comprises generating peptides by applying a digest on the
 PT family of protein.
 XX
 PS Example; SEQ ID NO 154; 265pp; English.
 XX
 CC The invention relates to a method of identifying a peptide combo which
 CC corresponds with a family of proteins where each of the members of the
 CC peptide combo is derived from a unique protein from the family. The
 CC peptide combo is useful for quantifying specific known splice variants of
 CC one or more particular proteins in a sample, for diagnosing complex
 CC genetic diseases such as cancer, obesity, diabetes, asthma and
 CC inflammation, neuropsychiatric disorders such as depression, for
 CC quantifying one to several hundreds of protein disease markers
 CC simultaneously leading to a more accurate diagnostic sub-classification,
 CC for determining the extent of protein modification in a particular sample
 CC of proteins, for tissue-typing analysis, for prenatal testing to detect
 CC the presence of a congenital disease or for quantitating protein levels
 CC diagnostic of a chromosomal abnormality, for diagnosing immune diseases
 CC or neurological diseases, as biomarkers preclinical drug development,
 CC development of improved animal models, biomarkers related with
 CC toxicology, clinical drug development, guidance marketed drugs,
 CC prognostic or diagnostic disease markers, drug target validation and
 CC selection, monitoring protein splicing, drug lead profiling, pathway
 CC analysis, answering basic disease biology questions, and in the fields of
 CC food and feed, cosmetics, agriculture and animal breeding. The present
 CC sequence represents a peptide from a hedgehog pathway peptide combo.
 XX
 SQ Sequence 19 AA;
 QY
 Db 2 IPRPTNIHKYLVCE 15
 4 IPRHQSRRGPRPTCQ 17
 RESULT 91
 AAM85293
 ID AAM85293 standard; peptide; 20 AA.
 XX
 AC AAM85293;
 XX
 DT 16-FEB-1999 (first entry)
 XX
 DE Helper T-cell class II peptide derived from core protein.
 XX
 KW Helper T-cell peptide; human leucocyte antigen; HLA; DR4w4; DR1; DR7;
 KW cytotoxic T lymphocyte; CTL; hepatitis; autoimmune disease;
 KW acquired immune deficiency syndrome; malaria; cancer;
 KW allograft rejection; allergy; Lyme disease; hepatitis;
 KW post-streptococcal endocarditis; glomerulonephritis;
 KW food hypersensitivity.
 XX
 OS Synthetic.
 OS Hepatitis B virus.
 XX
 PN MO9832456-A1.
 XX
 PD 30-JUL-1998.
 XX

PR	06-JUN-1997	97US-0048877P
PR	06-JUN-1997	97US-0048878P
PR	06-JUN-1997	97US-0048880P
PR	06-JUN-1997	97US-0048881P
PR	06-JUN-1997	97US-0048882P
PR	06-JUN-1997	97US-0048883P
PR	06-JUN-1997	97US-0048884P
PR	06-JUN-1997	97US-0048885P
PR	06-JUN-1997	97US-0048892P
PR	06-JUN-1997	97US-0048893P
PR	06-JUN-1997	97US-0048894P
PR	06-JUN-1997	97US-0048895P
PR	06-JUN-1997	97US-0048896P
PR	06-JUN-1997	97US-0048897P
PR	06-JUN-1997	97US-0048910P
PR	06-JUN-1997	97US-0049020P
PR	06-JUN-1997	97US-0049313P
PR	06-JUN-1997	97US-0049314P
PR	06-JUN-1997	97US-0049315P
PR	05-SER-1997	97US-0057584P
PR	05-SER-1997	97US-0057627P
PR	05-SER-1997	97US-0057628P
PR	05-SER-1997	97US-0057629P
PR	05-SER-1997	97US-0057634P
PR	05-SER-1997	97US-0057635P
PR	05-SER-1997	97US-0057642P
PR	05-SER-1997	97US-0057643P
PR	05-SER-1997	97US-0057644P
PR	05-SER-1997	97US-0057645P
PR	05-SER-1997	97US-0057646P
PR	05-SER-1997	97US-0057647P
PR	05-SER-1997	97US-0057648P
PR	05-SER-1997	97US-0057649P
PR	05-SER-1997	97US-0057650P
PR	05-SER-1997	97US-0057651P
PR	05-SER-1997	97US-0057652P
PR	05-SER-1997	97US-0057653P
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PR	05-SER-1997	97US-0057666P
PR	05-SER-1997	97US-0057667P
PR	05-SER-1997	97US-0057668P
PR	05-SER-1997	97US-0057669P
PR	05-SER-1997	97US-0057700P
PR	05-SER-1997	97US-0057712P
PR	05-SER-1997	97US-0057714P
PR	05-SER-1997	97US-0057715P
PR	05-SER-1997	97US-0057716P
PR	05-SER-1997	97US-0057717P
PR	05-SER-1997	97US-0057718P
PR	05-SER-1997	97US-0057719P
PR	18-DEC-1997	97US-0070923P
XA	(HUMA -) HUMAN	GENOME SCI INC.

XX	Young P, Greene JM, Ferrle AM, Ruben SM, Rosen CA, Hu J,
PI	Olsen HS, Ehler R, Brewer LA, Moore PA, Shi Y, Florence C,
PI	Florence K, Lafleur DW, Ni J, Fan P, Wei Y, Fischer CL, Soppet DR,
PI	Li Y, Zeng Z, Kyaw H, Yu G, Feng P, Dillon PJ, Endress GA,
PI	Carter KC,
XX	
DR	WPI, 1999-059865/05.
XX	N-PSDB; AAVB4480.
PT	New isolated human genes and the secreted polypeptides they encode -
PT	useful for diagnosis and treatment of e.g. cancer, neurological
PT	disorders, immune diseases, inflammation or blood disorders.
XX	
PS	Claim 11; Page 520; 772pp; English.
XX	
CC	The invention relates to nucleic acid sequences (AAV64411 to AAVB4633)
CC	encoding human secreted proteins (AAM88534 to AAM88756). The secreted
CC	protein gene sequences are deposited with the ATCC under deposit numbers
CC	ATCC 97979, 97974, 97975, 97976, 97977, 209007, 209008, 209009, 209010,
CC	209011, 209080, 209081, 209082, 209083, 209084, 209085, 209511. Host
CC	cells comprising recombinant vectors containing the nucleic acid
CC	sequences are used for the recombinant production of the secreted
CC	proteins. The polynucleotide and amino acid sequences are useful for are
CC	useful for preventing, treating or ameliorating medical conditions e.g.
CC	by protein or gene therapy. Pathological conditions can be also diagnosed
CC	by determining the amount of the new polypeptides in a sample or by
CC	determining the presence of mutations in the new polynucleotides.
CC	Specific uses are described for each of the polynucleotides, based on
CC	which tissues they are most highly expressed in, and include developing
CC	products for the diagnosis or treatment of cancer, neurodegenerative
CC	disorders, developmental abnormalities and foetal deficiencies, blood
CC	disorders, tumours, leukemias, diseases of the immune system, autoimmune
CC	diseases, hepatic and renal disease, lymphomas, inflammation, allergies,
CC	ischemic shock, Alzheimer's and cognitive disorders, schizophrenia,
CC	restenosis, prostate diseases, obesity, disorders involving osteoclasts
CC	such as osteoporosis, arthritis or malignancies, diseases of testes, lung
CC	or thymus, digestive/endocrine disorders, infections and AIDS. The
CC	polypeptides are also useful for identifying their binding partners. The
CC	present sequence represents human secreted protein (see descriptor line
CC	for gene number and clone identification)
XX	
XX	Sequence 14 AA;
XX	
XX	Query Match
XX	Best Local Similarity 26.5%; Score 30.5; DB 2; Length 14;
XX	Matches 6; Conservative 4; Mismatches 2; Indels 1; Gaps 1;
XX	
QY	6 TNIHKY-LVCESEV 17
XX	: : : : :
DB	1 THITHIILICSV 13
XX	
XX	RESULT 94
XX	ADE70889
ID	ADE70889 standard; peptide: 15 AA.
XX	
AC	ADE70889;
XX	
DT	29-JAN-2004 (first entry)
XX	
DE	Human 161P2F10B protein-related peptide 4894.
XX	
KM	161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
OS	Homo sapiens.
XX	
XX	WO2003040340-A2.
XX	
PD	15-MAY-2003.
XX	
XX	07-NOV-2002; 2002WO-US036002.
XX	

PR 07-NOV-2001; 2001US-00005480.
PR 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
XX
XX Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KM,
PI Morrison RK, Challita-Eid PM;
XX
XX WPI; 2003-441560/41.
XX
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
XX and polypeptides.
XX
XX Claim 13; Page 183; 135pp; English.
XX
XX
CC This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 15 AA;
XX
XX
Query Match 26.5%; Score 30.5; DB 7; Length 15;
Best Local Similarity 47.4%; Pred. No. 8.3e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 7; Gaps 2;
XX
QY 3 PH-PTNIHKYLCESVNGG 20
DB 1 PHRPNTNV-----ESCPG 13
XX
XX
RESULT 95
ADE70286
ID ADE70286 standard; peptide; 15 AA.
XX
XX ADE70286;
AC
XX
DT 29-JAN-2004 (first entry)
XX
XX Human 161P2F10B protein-related peptide 4291.
DE
XX
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KM
XX
XX Homo sapiens.
OS
XX
XX WO2003040340-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 07-NOV-2002; 2002WO-US036002.
PF
XX
XX 07-NOV-2001; 2001US-00005480.
PR
XX 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KM,
PI Morrison RK, Challita-Eid PM;
XX
XX WPI; 2003-441560/41.
XX
XX A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.

XX
XX Claim 13; Page 178; 135pp; English.
PS
XX
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human
CC 161P2F10B protein and which may be used in the development of the
CC compounds of the invention.
XX
SQ Sequence 15 AA;
XX
XX
Query Match 26.5%; Score 30.5; DB 7; Length 15;
Best Local Similarity 47.4%; Pred. No. 8.3e+02;
Matches 9; Conservative 1; Mismatches 2; Indels 7; Gaps 2;
XX
QY 3 PH-PTNIHKYLCESVNGG 20
DB 1 PHRPNTNV-----ESCPG 13
XX
XX
RESULT 96
ADE70871
ID ADE70871 standard; peptide; 15 AA.
XX
XX ADE70871;
AC
XX
DT 29-JAN-2004 (first entry)
XX
XX Human 161P2F10B protein-related peptide 4876.
DE
XX
XX 161P2F10B; cancer; cytostatic; gene therapy; vaccine; human.
KM
XX
XX Homo sapiens.
OS
XX
XX WO2003040340-A2.
PN
XX
XX 15-MAY-2003.
PD
XX
XX 07-NOV-2002; 2002WO-US036002.
PF
XX
XX 07-NOV-2001; 2001US-00005480.
PR
XX 31-JAN-2002; 2002US-00062109.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Raitano AB, Paris M, Hubert RS, Ge W, Morrison KM,
PI Morrison RK, Challita-Eid PM;
XX
XX WPI; 2003-441560/41.
XX
XX
PT A composition for diagnosing, preventing and treating cancer (e.g.
PT prostatic, renal or uterine cancer) comprises 161P2F10B polynucleotides
PT and polypeptides.
XX
XX Claim 13; Page 183; 135pp; English.
XX
XX This invention relates to a novel composition which comprises a substance
CC that modulates the status of a novel human protein (161P2F10B) and its
CC variants having a sequence of 875 amino acids provided in the
CC specification. The protein of the invention is over-expressed in certain
CC cancers. The compounds of the invention may have cytostatic activity and
CC the sequence of the 161P2F10B protein, and the gene which encodes it, may
CC be useful for gene therapy or the development of a vaccine. The
CC composition and methods of the invention are useful in diagnosing,
CC preventing and treating cancer. The present sequence is the amino acid
CC sequence of a peptide which is derived from the sequence of the human

CC 161P210B protein and which may be used in the development of the
 CC compounds of the invention.
 XX
 SQ Sequence 15 AA;

Query Match 26.5%; Score 30.5; DB 7; Length 15;
 Best Local Similarity 47.4%; Pred. No. 8.3e+02;
 Matches 9; Conservative 1; Mismatches 2; Indels 7; Gaps 2;

QY 3 PH-PTNHHKYLVCSSVNGG 20
 |||||
 Db 1 PHRPYNNV-----SSCPGG 13

RESULT 97

ADT92805
 ID ADT92805 standard; peptide; 8 AA.

AC ADT92805;
 XX

DT 13-JAN-2005 (first entry)

DE Consensus peptide mapped onto actin surface.

XX Epitope mapping; tertiary structure; antibody imprinting; actin.

XX Unidentified.

OS WO2004092741-A2.

XX 28-OCT-2004.

PD 14-APR-2004; 2004WO-US011905.

PR 14-APR-2003; 2003US-0462870P.

PA (UYMO-) UNIV MONTANA STATE.

PI Dratz EA, Mumey BM, Jeeaitis AJ;

XX WPI; 2004-795230/78.

PT Mapping discontinuous/surface antibody epitopes on target protein.
 PT comprises binding antibody that binds to target protein with library of
 PT random peptides, computationally aligning peptide sequences to construct
 PT epitope on target protein.

XX Example 2; Page 22; 40pp; English.

XX The invention relates to mapping (M1) discontinuous epitopes on a target
 CC protein. The method of the invention comprises contacting a solid support
 CC having an antibody capable of binding to the target protein, with a
 CC library of random peptides, where the set of probe peptides bind to
 CC antibody, eluting the set of probe peptides, determining the amino acid
 CC sequence of members of the probe peptides, computationally aligning the
 CC probe peptide sequences to the target protein, and constructing a
 CC discontinuous epitope on the target protein. The solid support comprises
 CC a first protein, and is then contacted with a second protein under
 CC conditions, where the first protein binds to the second protein under
 CC solid support is then contacted with a library of random peptides under
 CC conditions, where a set of probe peptides compete with the second protein
 CC for binding to the first protein, eluting the set of probe peptides,
 CC determining the amino acid sequence of the members of the set of probe
 CC peptides, computationally aligning the amino acid sequences of the
 CC members of the set of probe peptides to the target protein, constructing
 CC the binding site on the protein. A computing device for carrying out
 CC (M1), is also disclosed. The method of the invention is useful for
 CC mapping discontinuous antibody or aptamer epitopes on a target protein.
 CC It is also useful for elucidating the tertiary structure of proteins, and
 CC for providing structural information in antibody imprinting, to reveal
 CC distant segments of primary sequence that are in close spatial proximity
 CC on the native, folded protein. The current sequence represents a
 CC consensus peptide that is mapped onto the surface actin. This peptide is

CC from an example of the invention in which the method of the invention is
 CC validated using actin as a model protein.
 XX

SQ Sequence 8 AA;

Query Match 26.1%; Score 30; DB 8; Length 8;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPHPT 6
 :|||
 Db 1 VPHPT 5

RESULT 98

AAM22945
 ID AAM22945 standard; peptide; 9 AA.

AC AAM22945;
 XX

DT 22-OCT-2001 (first entry)

DE HIV peptide SEQ ID NO 830.

XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;

XX human immunodeficiency virus; vaccine.

OS Human immunodeficiency virus.

XX Synthetic.

PN WO200155177-A2.

PD 02-AUG-2001.

PF 29-JAN-2001; 2001WO-DK000059.

PR 28-JAN-2000; 2000EP-00610017.

PR 31-JAN-2000; 2000US-0179333P.

XX (STAT-) STATENS SERUM INST.

XX Fomsgaard A, Brunak S, Buus S, Corbet S, Laemmoller SL, Hansen J;

XX WPI; 2001-476184/51.

XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-
 PT HIV vaccines.

XX Example 4; Page 69; 383pp; English.

XX The invention relates to identification of cytotoxic T cell lymphocyte
 CC (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
 CC are a major protective mechanism against viral diseases. Antibodies may
 CC neutralise extracellular human immunodeficiency virus (HIV) and limit or
 CC prevent infection of cells in the host, but CTL will limit viral
 CC production by killing the cell. The CTL epitopes are useful in medicine,
 CC in the manufacture of vaccines or diagnostic agents

XX Sequence 9 AA;

Query Match 26.1%; Score 30; DB 4; Length 9;
 Best Local Similarity 71.4%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
 |||||
 Db 3 IPHPAGI 9

RESULT 99

AAM22902
 ID AAM22902 standard; peptide; 9 AA.

```

AC AAM22902;
XX
XX 22-OCT-2001 (first entry)
XX
XX HIV peptide SEQ ID NO 787.
XX
XX
XX Cytotoxic T cell lymphocyte; CTL; anti-HIV; viral disease; HIV;
XX human immunodeficiency virus; vaccine.
XX
XX Human immunodeficiency virus.
XX Synthetic.
XX
XX WO200155177-A2.
XX
XX 02-AUG-2001.
XX
XX 29-JAN-2001; 2001WO-DK000059.
XX
XX 28-JAN-2000; 2000EP-00610017.
XX 31-JAN-2000; 2000US-0179333P.
XX
XX (STAT-) STATENS SERUM INST.
XX
XX Fomsgaard A, Brunak S, Buus S, Corbet S, Lauemoller SL, Hansen J;
XX WPI; 2001-476184/51.
XX
XX
XX The generation of cytotoxic T cell lymphocytes epitopes for use in anti-
XX HIV vaccines.
XX
XX Example 4; Page 69; 383pp; English.
XX
XX The invention relates to identification of cytotoxic T cell lymphocyte
XX (CTL) epitopes (AAM22116-AAM23484) that generate anti-HIV activity. CTL
XX are a major protective mechanism against viral diseases. Antibodies may
XX neutralise extracellular human immunodeficiency virus (HIV) and limit or
XX prevent infection of cells in the host, but CTL will limit viral
XX production by killing the cell. The CTL epitopes are useful in medicine,
XX in the manufacture of vaccines or diagnostic agents
XX
XX Sequence 9 AA;
XX
XX Query Match 26.1%; Score 30; DB 4; Length 9;
XX Best Local Similarity 71.4%; Pred. No. 2e+06;
XX Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 2 IHPHNI 8
XX |||||
XX 3 IHPHAGI 9
XX
XX Db
XX
XX RESULT 100
XX ADY92047
XX ID ADY92047 standard; peptide; 9 AA.
XX
XX AC ADY92047;
XX
XX DT 02-JUN-2005 (first entry)
XX
XX DE Human tumor-associated antigen LDHC MHC I epitope peptide - SEQ ID 367.
XX
XX KW tumor-associated antigen; LDHC; lactate dehydrogenase C; gene expression;
XX cell death; cell growth; tumor; cancer; neoplasm; cytostatic.
XX
XX OS Homo sapiens.
XX
XX WO2005026205-A2.
XX
XX 24-MAR-2005.
XX
XX 10-SEP-2004; 2004WO-EP010164.
XX
XX 10-SEP-2003; 2003DE-01041812.

```

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XX
XX (GANY-) GANYMED PHARM AG.
XX
XX Tuerecl O, Sahin U, Koslowski M;
XX
XX WPI; 2005-242374/25.
XX
XX Pharmaceutical composition, with an agent to restrict the expression or
XX activity of an antigen associated with a tumor, incorporates structured
XX nucleic acids.
XX
XX Disclosure; SEQ ID NO 367; 353pp; German.
XX
XX The invention relates to a novel pharmaceutical composition, whereby the
XX composition contains an agent which restricts the expression or activity
XX of an antigen associated with a tumor and the antigen has a sequence,
XX coded by a nucleic acid, where the nucleic acid is selected from SEQ ID
XX NOs: 19-21, 54-57, 1-5, 29, 31-33, 37, 39, 40, 62, 63, 70, 74 or 85-88.
XX The composition of the invention induces cell death and a reduction of
XX cell growth, cell membrane damage or secretion of cytokines. The
XX composition may be useful for the identification of differentially
XX expressed genes in tumors with combined in silico and wet bench studies.
XX The current sequence is that of a human tumor-associated antigen lactate
XX dehydrogenase C (LDHC) MHC class I HLA-B*0702 epitope peptide of the
XX invention which stimulates cytotoxic T-lymphocytes in vivo.
XX
XX Sequence 9 AA;
XX
XX Query Match 26.1%; Score 30; DB 9; Length 9;
XX Best Local Similarity 44.4%; Pred. No. 2e+06;
XX Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 4 HPTNHRKL 12
XX |||||
XX 1 HPTSCHGWI 9
XX
XX Db
XX
XX Search completed: January 20, 2006, 19:05:14
XX Job time : 79.5769 secs

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OW protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 ; Search time 20.9615 seconds
(without alignments)
78.883 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115
Sequence: 1 DHPPTNKHVLCBSVNGS 20

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database :

1: Issued Patents AA:*
2: /cgn2_6/ptodata/1/1aa/5 COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6 COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/H.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTUS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	115	100.0	20	2	US-09-292-225-3
2	109	94.8	19	2	US-09-292-225-11
3	35	30.4	15	2	US-08-595-945-3
4	35	30.4	19	2	US-08-595-945-15
5	35	30.4	20	2	US-09-026-276-20
6	35	30.4	20	2	US-09-964-201A-20
7	32	29.6	15	1	US-07-829-462-6
8	32	27.8	10	2	US-08-159-339A-551
9	32	27.8	15	2	US-09-009-953-109
10	31	27.0	8	1	US-08-529-190B-73
11	31	27.0	16	2	US-09-791-524A-3
12	31	27.0	17	1	US-08-370-567-1
13	31	27.0	17	1	US-08-438-759-1
14	31	27.0	17	1	US-08-538-911-20
15	31	27.0	17	2	US-09-402-641-10
16	31	27.0	17	2	US-09-411-067C-2
17	31	27.0	17	2	US-09-428-082B-196
18	31	27.0	17	2	US-09-155-260C-16
19	31	27.0	17	2	US-09-402-464-1
20	31	27.0	17	2	US-09-791-524A-4
21	31	27.0	17	4	PCT-US94-05591-20
22	31	27.0	17	4	PCT-US94-05684-1
23	31	27.0	20	2	US-09-791-524A-9
24	30	26.1	10	1	US-07-890-422B-19
25	30	26.1	10	2	US-09-139-802-58
26	30	26.1	10	2	US-09-659-786-58
27	30	26.1	10	2	US-08-926-914-58

28	30	26.1	15	2	US-09-300-410A-2	Sequence 2, Appl
29	30	26.1	16	2	US-09-541-345-7	Sequence 7, Appl
30	30	26.1	16	2	US-09-825-517A-7	Sequence 7, Appl
31	29.5	25.7	20	1	US-08-614-935-75	Sequence 75, Appl
32	29.5	25.7	20	2	US-09-130-287-75	Sequence 75, Appl
33	29	25.2	6	1	US-08-192-243-1	Sequence 1, Appl
34	29	25.2	6	1	US-08-448-059-1	Sequence 1, Appl
35	29	25.2	6	2	US-09-295-996B-15	Sequence 15, Appl
36	29	25.2	6	2	US-09-295-846B-18	Sequence 18, Appl
37	29	25.2	6	2	US-09-551-737C-18	Sequence 18, Appl
38	29	25.2	6	2	US-09-295-924B-10	Sequence 10, Appl
39	29	25.2	6	2	US-09-551-738B-15	Sequence 15, Appl
40	29	25.2	11	1	US-07-942-245-495	Sequence 495, App
41	29	25.2	11	1	US-08-024-253-16	Sequence 16, Appl
42	29	25.2	11	2	US-09-649-063-16	Sequence 16, Appl
43	29	25.2	17	2	US-08-918-428D-15	Sequence 15, Appl
44	29	25.2	20	1	US-08-305-871A-11	Sequence 11, Appl
45	29	25.2	20	1	US-08-614-935-26	Sequence 26, Appl
46	29	25.2	20	1	US-08-797-842-7	Sequence 7, Appl
47	29	25.2	20	2	US-09-100-409A-47	Sequence 47, Appl
48	29	25.2	20	2	US-09-130-287-26	Sequence 26, Appl
49	29	25.2	20	2	US-09-009-953-195	Sequence 195, App
50	29	25.2	20	2	US-08-788-822A-14	Sequence 14, Appl
51	29	25.2	20	2	US-09-311-784A-150	Sequence 150, App
52	29	25.2	20	2	US-09-239-043D-2566	Sequence 2566, App
53	29	25.2	20	2	US-09-701-623C-71	Sequence 71, Appl
54	29	25.2	20	2	US-09-674-183-8	Sequence 8, Appl
55	29	25.2	20	2	US-10-666-480-5	Sequence 5, Appl
56	29	25.2	20	2	US-09-618-592-7	Sequence 7, Appl
57	28	24.3	9	2	US-08-159-339A-526	Sequence 526, Appl
58	28	24.3	11	2	US-09-119-507B-51	Sequence 51, Appl
59	28	24.3	11	2	US-08-897-556A-51	Sequence 51, Appl
60	28	24.3	11	2	US-08-947-693-51	Sequence 51, Appl
61	28	24.3	13	1	US-08-147-011-1	Sequence 1, Appl
62	28	24.3	13	1	US-08-480-190-221	Sequence 221, App
63	28	24.3	13	1	US-08-488-379-221	Sequence 221, App
64	28	24.3	13	2	US-08-475-399A-221	Sequence 221, App
65	28	24.3	13	2	US-08-077-255A-221	Sequence 221, App
66	28	24.3	13	4	PCT-US93-07545-221	Sequence 221, App
67	28	24.3	14	1	US-08-480-190-90	Sequence 90, Appl
68	28	24.3	14	1	US-08-480-190-220	Sequence 220, App
69	28	24.3	14	1	US-08-488-379-90	Sequence 90, Appl
70	28	24.3	14	1	US-08-488-379-220	Sequence 220, App
71	28	24.3	14	1	US-08-475-399A-90	Sequence 90, Appl
72	28	24.3	14	2	US-08-475-399A-220	Sequence 220, App
73	28	24.3	14	2	US-08-077-255A-90	Sequence 90, Appl
74	28	24.3	14	2	US-08-077-255A-220	Sequence 220, App
75	28	24.3	14	4	PCT-US93-07545-220	Sequence 220, App
76	28	24.3	14	4	PCT-US93-07545-220	Sequence 220, App
77	28	24.3	15	1	US-08-480-190-88	Sequence 88, Appl
78	28	24.3	15	1	US-08-480-190-89	Sequence 89, Appl
79	28	24.3	15	1	US-08-488-379-88	Sequence 88, Appl
80	28	24.3	15	1	US-08-488-379-89	Sequence 89, Appl
81	28	24.3	15	2	US-09-009-953-110	Sequence 110, App
82	28	24.3	15	2	US-08-475-399A-88	Sequence 88, Appl
83	28	24.3	15	2	US-08-475-399A-89	Sequence 89, Appl
84	28	24.3	15	2	US-08-077-255A-88	Sequence 88, Appl
85	28	24.3	15	4	US-08-077-255A-89	Sequence 89, Appl
86	28	24.3	15	4	PCT-US93-07545-88	Sequence 88, Appl
87	28	24.3	15	4	PCT-US93-07545-89	Sequence 89, Appl
88	28	24.3	16	1	US-08-480-190-85	Sequence 85, Appl
89	28	24.3	16	1	US-08-480-190-86	Sequence 86, Appl
90	28	24.3	16	1	US-08-480-190-87	Sequence 87, Appl
91	28	24.3	16	1	US-08-488-379-85	Sequence 85, Appl
92	28	24.3	16	1	US-08-488-379-86	Sequence 86, Appl
93	28	24.3	16	1	US-08-488-379-87	Sequence 87, Appl
94	28	24.3	16	2	US-08-810-009-51	Sequence 51, Appl
95	28	24.3	16	2	US-08-475-399A-85	Sequence 85, Appl
96	28	24.3	16	2	US-08-475-399A-86	Sequence 86, Appl
97	28	24.3	16	2	US-08-475-399A-87	Sequence 87, Appl
98	28	24.3	16	2	US-09-776-490-51	Sequence 51, Appl
99	28	24.3	16	2	US-08-077-255A-85	Sequence 85, Appl
100	28	24.3	16	2	US-08-077-255A-86	Sequence 86, Appl

ALIGNMENTS

RESULT 1

US-09-292-225-3
; Sequence 3, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-3

Query Match 100.0%; Score 115; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 7.4e-12;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DHPPTNHHKYLVCESVNG 20
Db 1 DHPPTNHHKYLVCESVNG 20

RESULT 2

US-09-292-225-11
; Sequence 11, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-11

Query Match 94.8%; Score 109; DB 2; Length 19;

Best Local Similarity 100.0%; Pred. No. 6.5e-11;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DHPPTNHHKYLVCESVNG 19
Db 1 DHPPTNHHKYLVCESVNG 19

RESULT 3

US-08-595-945-3
; Sequence 3, Application US/08595945
; Patent No. 6143509
; GENERAL INFORMATION:
; APPLICANT: DOWELL, BARRY L.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: QIU, XIAOXING
; APPLICANT: LITUA, HANS
; APPLICANT: PIIRONEN, TIMO P.
; APPLICANT: VIHINEN, MAUNO A.
; APPLICANT: PETERSSON, KIM S. I.
; TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES
; TITLE OF INVENTION: AND USES THEREOF
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSER: ABBOTT LABORATORIES
; STREET: 100 ABBOTT PARK ROAD
; CITY: ABBOTT PARK
; STATE: IL
; COUNTRY: USA
; ZIP: 60064-3500
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/595,945
; FILING DATE: 06-FEB-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BECKER, CHERYL L.
; REGISTRATION NUMBER: 35,441
; REFERENCE/DOCKET NUMBER: 5875.US.01
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 847-935-1729
; TELEFAX: 847-938-2623
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-595-945-3

Query Match 30.4%; Score 35; DB 2; Length 15;
Best Local Similarity 36.4%; Pred. No. 45;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

Qy 4 HPTNHHKYLVC 14
Db 5 HPOKTKFMFLC 15

RESULT 4

US-08-595-945-15
; Sequence 15, Application US/08595945
; Patent No. 6143509
; GENERAL INFORMATION:
; APPLICANT: DOWELL, BARRY L.
; APPLICANT: BRIDON, DOMINIQUE P.
; APPLICANT: QIU, XIAOXING
; APPLICANT: LITUA, HANS

APPLICANT: PIIRONEN, TIMO P.
APPLICANT: VIHINEN, MAURO A.
APPLICANT: PETERSON, KIM S.I.
TITLE OF INVENTION: PROSTATE SPECIFIC ANTIGEN PEPTIDES
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/595,945
FILING DATE: 06-FEB-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BECKER, CHERYL L.
REGISTRATION NUMBER: 35,441
REFERENCE/DOCKET NUMBER: 5875.US.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 847-935-1729
TELEFAX: 847-938-2623
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-595-945-15

Query Match 30.4%; Score 35; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 58;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHIKYLVC 14
DB 9 HPQKVTKFMLC 19

RESULT 5
US-09-026-276-20
Sequence 20, Application US/09026276
Patent No. 6319503
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Tramontano, Alfonso
APPLICANT: Pilon, Aprille L.
APPLICANT: Lohmas, Gerald L.
APPLICANT: Roberts, Steven P
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6319503 09\026,276
CURRENT APPLICATION NUMBER: US/09/026,276
FILING DATE: 1998-02-19
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-026-276-20

Query Match 30.4%; Score 35; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 61;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHIKYLVC 14
DB 7 HPQKVTKFMLC 17

RESULT 6
US-09-964-201A-20
Sequence 20, Application US/09964201A
Patent No. 6660271
GENERAL INFORMATION:
APPLICANT: Kenten, John H
APPLICANT: Tramontano, Alfonso
APPLICANT: Pilon, Aprille L.
APPLICANT: Lohmas, Gerald L.
APPLICANT: Roberts, Steven P
TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
FILE REFERENCE: U.S. Patent Application No. 6660271 09\026,276
CURRENT APPLICATION NUMBER: US/09/964,201A
FILING DATE: 2002-05-21
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 20
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-964-201A-20

Query Match 30.4%; Score 35; DB 2; Length 20;
Best Local Similarity 36.4%; Pred. No. 61;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHIKYLVC 14
DB 7 HPQKVTKFMLC 17

RESULT 7
US-07-829-462-6
Sequence 6, Application US/07829462
Patent No. 5453489
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki I.
APPLICANT: Morla, Alex
TITLE OF INVENTION: NOVEL FRAGMENTS OF FIBRONECTIN AND
METHODS TO MODULATE THE ROLE OF FIBRONECTIN IN
TITLE OF INVENTION: EXTRACELLULAR MATRIX ASSEMBLY
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSER: CAMPBELL AND FLORES
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: USA
ZIP: 92132
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/829,462
FILING DATE: 19920131
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: CAMPBELL, CATHERYN A.
REGISTRATION NUMBER: 31,547
REFERENCE/DOCKET NUMBER: P-LA 9179
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619-535-8949
TELEFAX: 619-535-8949
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids

TYPE: AMINO ACID
TOPOLOGY: linear
US-07-829-462-6

Query Match 29.6%; Score 34; DB 1; Length 15;
Best Local Similarity 45.5%; Pred. No. 65;
Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

Qy 3 PPHPTNHYLV 13
Db 3 PPSHSKIL 13

RESULT 8

US-08-159-339A-551
Sequence 551, Application US/08159339A
Patent No. 6037135
GENERAL INFORMATION:
APPLICANT: Kubo, Ralph T.
APPLICANT: Grey, Howard M.
APPLICANT: Sette, Alessandro
APPLICANT: Celis, Eateban
TITLE OF INVENTION: HLA Binding peptides and their
TITLE OF INVENTION: Uses
NUMBER OF SEQUENCES: 1254
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/159,339A
FILING DATE: 28-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
FILING DATE: 07-AUG-1992
APPLICATION NUMBER: US 08/027,746
FILING DATE: 05-MAR-1993
APPLICATION NUMBER: US 08/103,396
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 016623-005030US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
TELEX:
INFORMATION FOR SEQ ID NO: 551:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-159-339A-551

Query Match 27.8%; Score 32; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 88;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTNIHK 10
Db 2 IPHPAGLKK 10

RESULT 9

US-09-009-953-109
Sequence 109, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 016623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 109:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 109:
US-09-009-953-109

Query Match 27.8%; Score 32; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 1,4e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTNIHK 10
Db 6 IPHPAGLKK 14

RESULT 10

US-08-529-190B-73
Sequence 73, Application US/08529190B
Patent No. 5833991
GENERAL INFORMATION:
APPLICANT: Masucci, Maria G.
TITLE OF INVENTION: GLYCINE-CONTAINING SEQUENCES
CONFERRING INVISIBILITY TO THE IMMUNE SYSTEM
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
ADDRESSER: Banner & Witcoff, Ltd.
STREET: One Financial Center
CITY: Boston
STATE: MA
COUNTRY: USA

ZIP: 02111
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Wordperfect 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/529,190B
FILING DATE: 15-SEP-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE9501324-9
FILING DATE: 10-APR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US08/522,595
FILING DATE: 01-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Williams, Ph. D., Kathleen A
REGISTRATION NUMBER: 34,380
REFERENCE/DOCKET NUMBER: 3255/53015
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-345-9100
TELEFAX: 617-345-9111
INFORMATION FOR SEQ ID NO: 73:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-529-190B-73

Query Match 27.0%; Score 31; DB 1; Length 8;
Best Local Similarity 71.4%; Pred. No. 4.6e+05;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKLYVC 14
|||
Db 1 IHRYLRC 7

RESULT 11
US-09-791-524A-3
Sequence 3, Application US/09791524A
Patent No. 6911199
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery of Heterologous Genes
FILE REFERENCE: P26,992-B USA
CURRENT APPLICATION NUMBER: US/09/791,524A
PRIOR FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1999-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 155
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 16
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524A-3

Query Match 27.0%; Score 31; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKL 12
:|:|:|
Db 4 MPHSLNFSQYL 14

RESULT 12

US-08-370-567-1
Sequence 1, Application US/08370567
Patent No. 5656726
GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Doyle, Michael
APPLICANT: Goodson, Robert
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/370,567
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/061,514
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-08-370-567-1

Query Match 27.0%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKL 12
:|:|:|
Db 4 MPHSLNFSQYL 14

RESULT 13
US-08-438-759-1
Sequence 1, Application US/08438759
Patent No. 5679782
GENERAL INFORMATION:
APPLICANT: Rosenberg, Steven
APPLICANT: Goodson, Robert
APPLICANT: Doyle, Michael
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/438,759
FILING DATE:
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/370,567
FILING DATE:
APPLICATION NUMBER: US/08/061,514
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-438-759-1

Query Match 27.0%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12
DB 4 MPHSLNFSQYL 14

RESULT 14
US-08-538-911-20
Sequence 20, Application US/08538911
Patent No. 5750344
GENERAL INFORMATION:
APPLICANT: Doyle, Michael
TITLE OF INVENTION: Method For Selection Of Biologically
TITLE OF INVENTION: Active Peptide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRES:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/538,911
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/069,352
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0407.001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706

TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
US-08-538-911-20

Query Match 27.0%; Score 31; DB 1; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12
DB 4 MPHSLNFSQYL 14

RESULT 15
US-09-402-641-10
Sequence 10, Application US/09402641
Patent No. 6528619
GENERAL INFORMATION:
APPLICANT: BURGIE, Markus
APPLICANT: GRABER, Heinrich
APPLICANT: KESSLER, Horst
APPLICANT: MAGDOLEN, Viktor Robert
APPLICANT: KOENIG, Bernhard
APPLICANT: KOPIITZ, Marcus
APPLICANT: RIEMER, Christoph
APPLICANT: SCHMITT, Manfred
APPLICANT: WEIDLE, Ulrich
APPLICANT: WILHELM, Olaf
TITLE OF INVENTION: INHIBITORS FOR UROKINASE RECEPTOR
FILE REFERENCE: Case 20367US
CURRENT APPLICATION NUMBER: US/09/402,641
CURRENT FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: EP97106024.9
PRIOR FILING DATE: 1997-04-11
PRIOR APPLICATION NUMBER: PCT/EP98/02178
PRIOR FILING DATE: 1998-04-14
NUMBER OF SEQ ID NOS: 10
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 10
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: clone-20 peptide
US-09-402-641-10

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYL 12
DB 4 MPHSLNFSQYL 14

RESULT 16
US-09-411-067C-2
Sequence 2, Application US/09411067C
Patent No. 6576610
GENERAL INFORMATION:
APPLICANT: NUVAS, LLC
APPLICANT: HOUSTON, L.L.
TITLE OF INVENTION: USE OF A CONTEXT-DEPENDENT FUNCTIONAL ENTITY TO ENHANCE THE EFFI
FILE REFERENCE: NUVAS1140
CURRENT APPLICATION NUMBER: US/09/411,067C

;; CURRENT FILING DATE: 2002-05-07
;; NUMBER OF SEQ ID NOS: 5
;; SOFTWARE: PatentIn version 3.0
;; SEQ ID NO 2
;; LENGTH: 17
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-411-067C-2

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 17
US-09-428-082B-196
; Sequence 196, Application US/09428082B
; Patent No. 6660843
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/09/428, 082B
; CURRENT FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURES:
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-09-428-082B-196

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 18
US-09-155-260C-16
; Sequence 16, Application US/09155260C
; Patent No. 6794358
; GENERAL INFORMATION:
; APPLICANT: ROSENBERG, STEVE
; APPLICANT: DOYLE, MICHAEL
; APPLICANT: CHAPMAN, HAROLD
; TITLE OF INVENTION: PEPTIDE LIGANDS OF THE UROKINASE RECEPTOR
; FILE REFERENCE: 014024-0284102
; CURRENT APPLICATION NUMBER: US/09/155,260C
; CURRENT FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: PCT/US97/05199
; PRIOR FILING DATE: 1997-03-28
; PRIOR APPLICATION NUMBER: 08/623,361
; PRIOR FILING DATE: 1996-03-28
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 16
; LENGTH: 17
; TYPE: PRT

;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; OTHER INFORMATION: peptide ligand
US-09-155-260C-16

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 19
US-09-402-464-1
; Sequence 1, Application US/09402464
; Patent No. 6872702
; GENERAL INFORMATION:
; APPLICANT: Kessler, Horst
; APPLICANT: Graeff, Heinrich
; APPLICANT: Schmitt, Manfred
; APPLICANT: Magdolen, Viktor
; APPLICANT: Wilhelm, Olaf G.
; APPLICANT: Riemer, Christoph
; APPLICANT: Burgle, Markus
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor
; FILE REFERENCE: 100564-09040
; CURRENT APPLICATION NUMBER: US/09/402,464
; CURRENT FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: EP 97 106 024.9
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-402-464-1

Query Match 27.0%; Score 31; DB 2; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 20
US-09-791-524A-4
; Sequence 4, Application US/09791524A
; Patent No. 6911199
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharmaceuticals Products Inc.
; TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery of Heterologous Genes
; FILE REFERENCE: P26, 992-B USA
; CURRENT APPLICATION NUMBER: US/09/791,524A
; CURRENT FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: PCT/IB99/01524
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: US 60/098,028
; PRIOR FILING DATE: 1998-08-27
; NUMBER OF SEQ ID NOS: 165
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Adenovirus
US-09-791-524A-4

Query Match 27.0%; Score 31; DB 2; Length 17;

Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHXYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 21

PCT-US94-05591-20
Sequence 20, Application PC/TUS9405591
GENERAL INFORMATION:
APPLICANT: Doyle, Michael V.
TITLE OF INVENTION: Method For Selection Of Biologically
TITLE OF INVENTION: Active Peptide Sequences
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05591
FILING DATE: 19-MAY-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0407.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ. ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05591-20

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHXYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 22

PCT-US94-05684-1
Sequence 1, Application PC/TUS9405684
GENERAL INFORMATION:
APPLICANT: Chiron Corporation
TITLE OF INVENTION: Peptide Inhibitors of Urokinase Receptor
TITLE OF INVENTION: Activity
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/05684
FILING DATE: 19 MAY 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 0941.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEFAX: 510-655-3542
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
PCT-US94-05684-1

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHXYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 23
US-09-791-524A-9
Sequence 9, Application US/09791524A
Patent No. 6911199
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
FILE REFERENCE: P26,992-B USA
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: PCT/IB99/01524
PRIOR FILING DATE: 1998-08-27
PRIOR APPLICATION NUMBER: US 60/098,028
NUMBER OF SEQ. ID NOS: 165
SOFTWARE: PatentIn version 3.2
SEQ. ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524A-9

Query Match 27.0%; Score 31; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 2.7e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNIHXYL 12
: || | : ||
Db 6 MPHSLNFSQYL 16

RESULT 24
US-07-890-422B-19
Sequence 19, Application US/07890422B
Patent No. 5602102
GENERAL INFORMATION:
APPLICANT: THIELS, DWAIN L.
APPLICANT: LIPSKY, PETER E.
APPLICANT: MCGUIRE, MICHAEL J.

TITLE OF INVENTION: DIPEPTIDYL PEPTIDASE-I
TITLE OF INVENTION: INHIBITORS AND USES THEREOF
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: ARNOLD, WHITE & DUNKER
STREET: P.O. BOX 4433
CITY: HOUSTON
STATE: TEXAS
COUNTRY: USA
ZIP: 77210
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/890,422B
FILING DATE: 19920529
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MAYFIELD, DENISE L.
REGISTRATION NUMBER: 33,732
REFERENCE/DOCKET NUMBER: UTSD:296/MAY
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512-320-7200
TELEFAX: 512-474-7577
TELEX: NOT APPLICABLE
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acid residues
TYPE: AMINO ACID
TOPOLOGY: linear
US-07-890-422B-19

Query Match 26.1%; Score 30; DB 1; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCESVNGG 20
DB 3 VCEKRIIG 10

RESULT 25
US-09-139-802-58
Sequence 58, Application US/09139802
Patent No. 6180084
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/139,802
CURRENT FILING DATE: 1998-08-25
EARLIER APPLICATION NUMBER: 08/926,914
EARLIER FILING DATE: 1997-09-10
EARLIER APPLICATION NUMBER: 08/710,067
EARLIER FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-139-802-58

Query Match 26.1%; Score 30; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19
DB 1 CEGVNG 6

RESULT 26
US-09-659-786-58
Sequence 58, Application US/09659786
Patent No. 6491894
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/09/659,786
CURRENT FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-659-786-58

Query Match 26.1%; Score 30; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVNG 19
DB 1 CEGVNG 6

RESULT 27
US-08-926-914-58
Sequence 58, Application US/08926914
Patent No. 6576239
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Pasqualini, Renata
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
TITLE OF INVENTION: Derived Therefrom, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESS:
ADDRESSEE: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815

REFERENCE/DOCKET NUMBER: P-LJ 2725
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: both
MOLECULE TYPE: peptide
US-08-926-914-58

Query Match 26.1%; Score 30; DB 2; Length 10;
Best Local Similarity 83.3%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEEVNG 19
| | | |
| | | |
DB 1 CEEVNG 6

RESULT 28
US-09-300-410A-2
Sequence 2, Application US/09300410A
Patent No. 6414113
GENERAL INFORMATION:
APPLICANT: SATO, Atsuehi
APPLICANT: JINGAMI, HISAO
TITLE OF INVENTION: PEPTIDES BINDING TO BONE MARROW STROMAL CELL ANTIGEN
FILE REFERENCE: 99-0449*/JC/00177
CURRENT APPLICATION NUMBER: US/09/300,410A
CURRENT FILING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-300-410A-2

Query Match 26.1%; Score 30; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 TWIKY 11
| | | |
| | | |
DB 6 TWIKY 11

RESULT 29
US-09-541-345-7
Sequence 7, Application US/09541345
Patent No. 6774209
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC ANTIGEN (CEA)
FILE REFERENCE: Sequence Listing DYX-016.0 US
Patent No. 6774209
CURRENT APPLICATION NUMBER: US/09/541,345
CURRENT FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 107
SEQ ID NO 7
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: CEA binding
US-09-541-345-7

Query Match 26.1%; Score 30; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNG 20
| | | |
| | | |
DB 3 VCEKTTGG 10

RESULT 30
US-09-825-517A-7
Sequence 7, Application US/09825517A
Patent No. 6919424
GENERAL INFORMATION:
APPLICANT: Rondon, Isaac J
APPLICANT: Ladner, Robert C
TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRYONIC
TITLE OF INVENTION: ANTIGEN (CEA)
FILE REFERENCE: DYX-016.1 (3421.1005-001)
CURRENT APPLICATION NUMBER: US/09/825,517A
CURRENT FILING DATE: 2003-03-24
PRIOR APPLICATION NUMBER: US 09/541,345
PRIOR FILING DATE: 2000-04-03
NUMBER OF SEQ ID NOS: 151
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 7
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CEA binding polypeptide
US-09-825-517A-7

Query Match 26.1%; Score 30; DB 2; Length 16;
Best Local Similarity 62.5%; Pred. No. 3.1e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNG 20
| | | |
| | | |
DB 3 VCEKTTGG 10

RESULT 31
US-08-614-935-75
Sequence 75, Application US/08614935
Patent No. 5804201
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156

TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-08-614-935-75

Query Match 25.7%; Score 29.5; DB 1; Length 20;
Best Local Similarity 77.8%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 NIHK-YLVC 14
| | | | |
Db 4 NWHKHYLVC 12

RESULT 32
US-09-130-287-75
Sequence 75, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
TITLE OF INVENTION: ANTIGEN 5
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRES:
ADDRESSEE: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-09-130-287-75

Query Match 25.7%; Score 29.5; DB 2; Length 20;
Best Local Similarity 77.8%; Pred. No. 4.7e+02;
Matches 7; Conservative 0; Mismatches 1; Indels 1; Gaps 1;

QY 7 NIHK-YLVC 14
| | | | |
Db 4 NWHKHYLVC 12

RESULT 33
US-08-192-243-1
Sequence 1, Application US/08192243
Patent No. 5459130
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: De loof, Arnold
APPLICANT: Byllemans, Dany
TITLE OF INVENTION: No. 5459130el Methode and Compositions for
TITLE OF INVENTION: the Control of the Flesh Fly
NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRES:
ADDRESSEE: Ted W. Whitlock
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/192,243
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Whitlock, Ted W.
REGISTRATION NUMBER: 36,965
REFERENCE/DOCKET NUMBER: UF137
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 6 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-08-192-243-1

Query Match 25.2%; Score 29; DB 1; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | | | |
Db 1 NPTNTH 6

RESULT 34
US-08-448-059-1
Sequence 1, Application US/08448059
Patent No. 5501976
GENERAL INFORMATION:
APPLICANT: Borovsky, Dov
APPLICANT: De loof, Arnold
APPLICANT: Byllemans, Dany
TITLE OF INVENTION: No. 5501976el Methods and Compositions for
TITLE OF INVENTION: the Control of the Flesh Fly

NUMBER OF SEQUENCES: 1
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Ted W. Whitlock
 STREET: 2421 N.W. 41st Street, Suite A-1
 CITY: Gainesville
 STATE: FL
 COUNTRY: USA
 ZIP: 32606
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/448,059
 FILING DATE:
 CLASSIFICATION: 435
 ATTORNEY/AGENT INFORMATION:
 NAME: Whitlock, Ted W.
 REGISTRATION NUMBER: 36,965
 REFERENCE/DOCKET NUMBER: UF137
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 904-375-8100
 TELEFAX: 904-372-5800
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 6 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 US-08-448-059-1

Query Match 25.2%; Score 29; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9
 :|||:|
 DB 1 NPTNTH 6

RESULT 35
 US-09-295-996B-15
 Sequence 15, Application US/09295996B
 Patent No. 6413530
 GENERAL INFORMATION:
 APPLICANT: Borovsky, Dov
 TITLE OF INVENTION: PESTICIDAL PEPTIDES
 FILE REFERENCE: UF-230
 CURRENT APPLICATION NUMBER: US/09/295,996B
 CURRENT FILING DATE: 1999-04-21
 NUMBER OF SEQ ID NOS: 60
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 15
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: TMOP peptide
 US-09-295-996B-15

Query Match 25.2%; Score 29; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9
 :|||:|
 DB 1 NPTNTH 6

RESULT 36
 US-09-295-846B-18
 Sequence 18, Application US/09295846B
 Patent No. 6562590
 GENERAL INFORMATION:
 APPLICANT: Borovsky, Dov
 TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
 FILE REFERENCE: UF-223
 CURRENT APPLICATION NUMBER: US/09/295,846B
 CURRENT FILING DATE: 1999-04-21
 NUMBER OF SEQ ID NOS: 59
 SOFTWARE: Patentin Ver. 2.0
 SEQ ID NO 18
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: TMOP peptide
 US-09-295-846B-18

Query Match 25.2%; Score 29; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9
 :|||:|
 DB 1 NPTNTH 6

RESULT 37
 US-09-551-737C-18
 Sequence 18, Application US/09551737C
 Patent No. 6566129
 GENERAL INFORMATION:
 APPLICANT: Borovsky, Dov
 APPLICANT: Schlesinger, Yaagov
 APPLICANT: Nauwelaers, Sabine M. I.
 TITLE OF INVENTION: Transformed Cells Useful for the Control of Pests
 FILE REFERENCE: UF-223C1
 CURRENT APPLICATION NUMBER: US/09/551,737C
 CURRENT FILING DATE: 2000-04-18
 PRIOR APPLICATION NUMBER: US 09/295,846
 PRIOR FILING DATE: 1999-04-21
 NUMBER OF SEQ ID NOS: 71
 SOFTWARE: Patentin version 3.1
 SEQ ID NO 18
 LENGTH: 6
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: TMOP peptide
 US-09-551-737C-18

Query Match 25.2%; Score 29; DB 2; Length 6;
 Best Local Similarity 66.7%; Pred. No. 4.6e+05;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNTH 9
 :|||:|
 DB 1 NPTNTH 6

RESULT 38
 US-09-295-924B-10
 Sequence 10, Application US/09295924B
 Patent No. 6593299
 GENERAL INFORMATION:
 APPLICANT: John, Bennett
 APPLICANT: Alan, Brandt
 APPLICANT: Dov, Borovski
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR CONTROLLING PESTS
 FILE REFERENCE: 4137-120
 CURRENT APPLICATION NUMBER: US/09/295,924B

/ CURRENT FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 10
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Truncated TMOF
US-09-295-924B-10

Query Match 25.2%; Score 29; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNIIH 9
: |||: |
Db 1 NPTNLIH 6

RESULT 39
US-09-551-738B-15
/ Sequence 15, Application US/09551738B
/ Patent No. 6635265
/ GENERAL INFORMATION:
/ APPLICANT: Borovsky, Dov
/ TITLE OF INVENTION: Materials and Methods Useful for the Control of Insect Larvae
/ FILE REFERENCE: UF-224C1
/ CURRENT APPLICATION NUMBER: US/09/551,738B
/ CURRENT FILING DATE: 2000-04-18
/ PRIOR APPLICATION NUMBER: US 09/296,113
/ PRIOR FILING DATE: 1999-04-21
/ NUMBER OF SEQ ID NOS: 63
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 15
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: TMOF peptide
US-09-551-738B-15

Query Match 25.2%; Score 29; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNIIH 9
: |||: |
Db 1 NPTNLIH 6

RESULT 40
US-07-942-245-495
/ Sequence 495, Application US/07942245
/ Patent No. 5639641
/ GENERAL INFORMATION:
/ APPLICANT: PEDERSEN, Jan T.
/ APPLICANT: SEARLE, Stephen M. J.
/ APPLICANT: REES, Anthony R.
/ APPLICANT: ROGUSKA, Michael A.
/ APPLICANT: GUILD, Braydon C.
/ TITLE OF INVENTION: SURFACE RESIDUE VENERING OF RODENT
/ TITLE OF INVENTION: ANTIBODIES
/ NUMBER OF SEQUENCES: 522
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Sushrue, Mlon, Zlun, Macpeak & Seas
/ STREET: 2100 Pennsylvania Avenue, N.W.
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: United States
/ ZIP: 20037-3202
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk

/ COMPUTER: HP 9000/700 Workstation
/ OPERATING SYSTEM: UNIX
/ SOFTWARE: In house
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/942,245
/ FILING DATE: 09-SEP-1992
/ CLASSIFICATION: 530
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 293-7060
/ TELEFAX: (202) 293-7860
/ TELEX: 6491103
/ INFORMATION FOR SEQ ID NO: 495:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULAR TYPE: peptide
US-07-942-245-495

Query Match 25.2%; Score 29; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NHHYKL 12
: |||: |
Db 5 NHHYKL 10

RESULT 41
US-08-024-253-16
/ Sequence 16, Application US/08024253
/ Patent No. 5785968
/ GENERAL INFORMATION:
/ APPLICANT: KIMACHI, Kazuhiko
/ APPLICANT: MABDA, Hiroaki
/ APPLICANT: NISHIYAMA, Kiyoko
/ APPLICANT: TOKIYOSHI, Sachio
/ APPLICANT: TOHYA, Yukinobu
/ APPLICANT: MIRAMI, Takeshi
/ TITLE OF INVENTION: ANTI-FELINE CALICIVIRUS RECOMBINANT
/ TITLE OF INVENTION: ANTIBODY AND GENE FRAGMENT ENCODING THE SAME
/ NUMBER OF SEQUENCES: 23
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: WEGNER, CANTOR, MUELLER & PLAYER
/ STREET: 1233 20th Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: U.S.A.
/ ZIP: 20036-8218
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/024,253
/ FILING DATE: 19930301
/ CLASSIFICATION: 424
/ PRIOR APPLICATION NUMBER: JP 79189/1992
/ FILING DATE: 28-FEB-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CANTOR, Herbert I.
/ REGISTRATION NUMBER: 24,392
/ REFERENCE/DOCKET NUMBER: P-500-23744
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (202) 887-0400
/ TELEFAX: (202) 835-0605
/ TELEX: 440706 WEGHR
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid

TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-024-253-16

Query Match 25.2%; Score 29; DB 1; Length 11;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NHHKYL 12
DB 5 NHHNYL 10

RESULT 42
US-09-649-063-16
Sequence 16, Application US/09649063
Patent No. 6600022
GENERAL INFORMATION:
APPLICANT: TORIGOE, Kakuji
USHIO, Shimpel
KUNIKATA, Toashio
KURIMOTO, Masahiko
TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/649,063
FILING DATE: 29-Aug-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/996,140
FILING DATE: <Unknown>
APPLICATION NUMBER: JP 52,526/1997
FILING DATE: 21-FEB-1997
APPLICATION NUMBER: JP 163,490/1997
FILING DATE: 6-JUN-1997
APPLICATION NUMBER: JP 215,490/1997
FILING DATE: 28-JUL-1997
ATTORNEY/AGENT INFORMATION:
NAME: BROWDY, Roger L.
REGISTRATION NUMBER: 25,618
REFERENCE/DOCKET NUMBER: TORIGOE=2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal fragment
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-09-649-063-16

Query Match 25.2%; Score 29; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 NHHKYL 12
DB 5 NHHNYL 10

RESULT 43
US-08-918-428D-15
Sequence 15, Application US/08918428D
Patent No. 6432636
GENERAL INFORMATION:
APPLICANT: Grace Marresh and Alan Snow
TITLE OF INVENTION: Therapeutic and Diagnostic Applications
of Perlecan Domain I Splice Variants
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrick M. Dwyer
STREET: 1818 Westlake Avenue N, Suite 114
CITY: Seattle
STATE: WA (Washington)
COUNTRY: United States of America
ZIP: 98109

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette - 3.50 Inch, 1.44 Mb storage
COMPUTER: IBM PC
OPERATING SYSTEM: PC-DOS (Windows NT '95)
SOFTWARE: WordPerfect 9
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/918,428D
FILING DATE: 26-August-1997
CLASSIFICATION:
PRIOR APPLICATION DATA: n/a
ATTORNEY/AGENT INFORMATION:
NAME: Dwyer, Patrick M.
REGISTRATION NUMBER: 32,411
REFERENCE/DOCKET NUMBER: PROTEO.P02
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 343-7074
TELEFAX: (206) 343-7085
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-918-428D-15

Query Match 25.2%; Score 29; DB 2; Length 17;
Best Local Similarity 43.8%; Pred. No. 4.8e+02;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 PTNHHKYLVCESVNG 20
DB 1 PTPGHSAPVPSKIHGG 16

RESULT 44
US-08-305-871A-11
Sequence 11, Application US/08305871A
Patent No. 5736142
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Gaeta, Federico
APPLICANT: Grey, Howard M.
APPLICANT: Sidney, John
APPLICANT: Alexander, Jeffrey L.
TITLE OF INVENTION: Alteration of Immune Response Using Pan
DR-Binding Peptides
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/305,871A
 FILING DATE: 14-SEP-1994
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 08/121,101
 FILING DATE: 14-SEP-1993
 ATTORNEY/AGENT INFORMATION:
 NAME: Baselian, Kevin L.
 REGISTRATION NUMBER: 34,774
 REFERENCE/DOCKET NUMBER: 14137-0062-10
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 INFORMATION FOR SEQ ID NO: 11:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-305-871A-11

Query Match 25.2%; Score 29; DB 1; Length 20;
 Best Local Similarity 33.3%; Pred. No. 5.7e+02;
 Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHTHIKYLC 14
 |||
 Db 1 PPHTHLRQALYC 12

RESULT 45
 US-08-614-935-26
 Sequence 26, Application US/08614935
 Patent No. 5804201
 GENERAL INFORMATION:
 APPLICANT: Kling, Te P.
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
 TITLE OF INVENTION: ANTIGEN 5
 NUMBER OF SEQUENCES: 81
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: David A. Jackson, Esq.
 STREET: 411 Hackensack Ave, Continental Plaza, 4th
 STREET: Floor
 CITY: Hackensack
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07601
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/614,935
 FILING DATE: 11-MAR-1996
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Jackson Esq., David A.
 REGISTRATION NUMBER: 26,742
 REFERENCE/DOCKET NUMBER: 600-1-156
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 201-487-5800
 TELEFAX: 201-343-1684
 INFORMATION FOR SEQ ID NO: 26:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 ANTI-SENSE: NO
 FRAGMENT TYPE: internal
 US-08-614-935-26

Query Match 25.2%; Score 29; DB 1; Length 20;
 Best Local Similarity 60.0%; Pred. No. 5.7e+02;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNGG 20
 |||||
 Db 9 YLVCSNTGPGG 18

RESULT 46
 US-08-797-842-7
 Sequence 7, Application US/08797842
 Patent No. 5932706
 GENERAL INFORMATION:
 APPLICANT: Mertens, Koenraad et al
 TITLE OF INVENTION: Antibodies specific for a haemostatic protein,
 TITLE OF INVENTION: their use for isolating intact protein, haemostatic compo
 TITLE OF INVENTION: of proteolytic cleavage products of the protein
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Michaelson and Wallace
 STREET: Parkway 109 Office Center, 328 Newman Springs
 STREET: Road, P. O. Box 8489
 CITY: Red Bank
 STATE: New Jersey
 COUNTRY: USA
 ZIP: 07701

COMPUTER READABLE FORM:
 MEDIUM TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
 COMPUTER: IBM PC
 OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11
 SOFTWARE: Microsoft Word for Windows 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/797,842
 FILING DATE: 10-Feb-1997
 CLASSIFICATION: 530
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/381,891
 FILING DATE: February 8, 1995
 ATTORNEY/AGENT INFORMATION:
 NAME: Michaelson, Peter L.
 REGISTRATION NUMBER: 30090
 REFERENCE/DOCKET NUMBER: Stiteling-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908) 530-6671
 TELEFAX: (908) 530-6584
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 US-08-797-842-7

Query Match 25.2%; Score 29; DB 1; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KYLYC 14
 |||||
 Db 4 KYLYC 8

RESULT 47
US-09-100-409A-47
Sequence 47, Application US/09100409A
Patent No. 6090388
GENERAL INFORMATION:
APPLICANT: Wang, Chang Y1
TITLE OF INVENTION: PEPTIDE COMPOSITION FOR
PREVENTION AND TREATMENT OF HIV INFECTION AND
TITLE OF INVENTION: IMMUNE DISORDERS
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSER: MORGAN & FINNEGAN
STREET: 345 Park Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10154-0054
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/100,409A
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME:
REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 1151-4154
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-409A-47

Query Match 25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHYIKHYLVLC 14
DB 1 PPHYIKHYLVLC 12

RESULT 48
US-09-130-287-26
Sequence 26, Application US/09130287
Patent No. 6106844
GENERAL INFORMATION:
APPLICANT: King, Te P.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES OF VESPID
TITLE OF INVENTION: ANTIGEN 5
NUMBER OF SEQUENCES: 81
CORRESPONDENCE ADDRESS:
ADDRESSER: David A. Jackson, Esq.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
FLOOR
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/130,287
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/614,935
FILING DATE: 11-MAR-1996
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-156 DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: Internal
US-09-130-287-26

Query Match 25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNGG 20
DB 9 YLVCSVNGG 18

RESULT 49
US-09-009-953-195
Sequence 195, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: PASCSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300


```

;
; TELEEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 195:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 195:
US-09-009-953-195

Query Match      25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHPTNKHLYVC 14
DB      1 PPHHTALRQAILC 12

RESULT 50
US-08-788-822A-14
; Sequence 14, Application US/08788822A
; Patent No. 6413935
; GENERAL INFORMATION:
; APPLICANT: Alexander, Jeffrey L.
; APPLICANT: Deftrees, Shawn
; APPLICANT: Sette, Alessandro
; TITLE OF INVENTION: Induction of Immune Response Against
; TITLE OF INVENTION: Desired Determinants
; NUMBER OF SEQUENCES: 30
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,822A
; FILING DATE: 23-JAN-1997
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/010,510
; FILING DATE: 24-JAN-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Baelian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 014137-009210US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-788-822A-14

Query Match      25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHPTNKHLYVC 14
DB      1 PPHHTALRQAILC 12
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;
; RESULT 51
; US-09-311-784A-150
; Sequence 150, Application US/09311784A
; Patent No. 6534482
; GENERAL INFORMATION:
; APPLICANT: Pike, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Bpimmune Inc.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 39963-20022.01
; CURRENT APPLICATION NUMBER: US/09/311,784A
; CURRENT FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-09-311-784A-150

Query Match      25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHPTNKHLYVC 14
DB      1 PPHHTALRQAILC 12

RESULT 52
US-09-239-043D-2566
; Sequence 2566, Application US/09239043D
; Patent No. 6689363
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Vitello, Maria A.
; APPLICANT: Livingston, Brian D.
; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph T.
; APPLICANT: Grey, Howard M.
; APPLICANT: Chesnut, Robert
; APPLICANT: Bpimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0060007
; CURRENT APPLICATION NUMBER: US/09/239,043D
; CURRENT FILING DATE: 1999-01-27
; PRIOR APPLICATION NUMBER: US 09/189,702
; PRIOR FILING DATE: 1998-11-10
; PRIOR APPLICATION NUMBER: US 08/978,291
; PRIOR FILING DATE: 1997-11-25
; PRIOR APPLICATION NUMBER: US 08/820,360
; PRIOR FILING DATE: 1997-03-12
; PRIOR APPLICATION NUMBER: US 60/013,363
; PRIOR FILING DATE: 1996-03-13
; PRIOR APPLICATION NUMBER: US 08/461,603
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; PRIOR APPLICATION NUMBER: US 08/344,824
```

```
/ PRIOR FILING DATE: 1994-11-23
/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/197,484
/ PRIOR FILING DATE: 1994-02-16
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2566
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-09-239-043D-2566

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNTHKYLVC 14
        ||| : : :|
Db      1 PPHNTHLRQAIIIC 12

RESULT 53
US-09-701-623C-71
/ Sequence 71, Application US/09701623C
/ Patent No. 6811782
/ GENERAL INFORMATION:
/ APPLICANT: Wang Ph.D., Chang Y1
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ FILE REFERENCE: 11514151US1
/ CURRENT APPLICATION NUMBER: US/09/701,623C
/ CURRENT FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959
/ PRIOR FILING DATE: 1999-06-21
/ PRIOR APPLICATION NUMBER: 09/100,287
/ PRIOR FILING DATE: 1998-06-20
/ NUMBER OF SEQ ID NOS: 91
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 71
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-09-701-623C-71

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNTHKYLVC 14
        ||| : : :|
Db      1 PPHNTHLRQAIIIC 12

RESULT 54
US-09-674-183-8
/ Sequence 8, Application US/09674183
/ Patent No. 6855321
/ GENERAL INFORMATION:
/ APPLICANT: RAPPUOLI, Rino
/ APPLICANT: GRANDI, Guido
/ TITLE OF INVENTION: POLYPEPTIDE CARRIER PROTEIN
/ FILE REFERENCE: PP00362.102 / 2302-0362
/ CURRENT APPLICATION NUMBER: US/09/674,183
/ CURRENT FILING DATE: 2000-11-14
/ PRIOR APPLICATION NUMBER: PCT/IB99/00844
/ PRIOR FILING DATE: 1999-04-27
/ PRIOR APPLICATION NUMBER: GB9808932.9
```

```
/ PRIOR FILING DATE: 1998-04-27
/ NUMBER OF SEQ ID NOS: 20
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 8
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: T-cell epitope HBVnc
US-09-674-183-8

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNTHKYLVC 14
        ||| : : :|
Db      1 PPHNTHLRQAIIIC 12

RESULT 55
US-10-666-480-5
/ Sequence 5, Application US/10666480
/ Patent No. 6919426
/ GENERAL INFORMATION:
/ APPLICANT: Boone, Thomas C
/ APPLICANT: Wild, Kenneth D
/ APPLICANT: Stiney, Karen C
/ APPLICANT: Min, Hosung
/ APPLICANT: Kimmel, Bruce
/ TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
/ FILE REFERENCE: A-82705
/ CURRENT APPLICATION NUMBER: US/10/666,480
/ CURRENT FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/412,524
/ PRIOR FILING DATE: 2002-09-19
/ NUMBER OF SEQ ID NOS: 286
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
US-10-666-480-5

Query Match          25.2%; Score 29; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 PTNTHKYLVC 13
        ||| : : :|
Db      10 PSNIDRYML 18

RESULT 56
US-09-618-592-7
/ Sequence 7, Application US/09618592
/ Patent No. RE38202
/ GENERAL INFORMATION:
/ APPLICANT: Mertens, Koenraad et al
/ TITLE OF INVENTION: Antibodies specific for a haemostatic protein,
/ their use for isolating intact protein, haemostatic composi
/ of proteolytic cleavage products of the protein
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSER: Michaelson and Wallace
STREET: Parkway 109 Office Center, 328 Newman Springs
CITY: Red Bank
STATE: New Jersey
COUNTRY: USA
ZIP: 07701
COMPUTER READABLE FORM:
```

MEDIUM TYPE: 3 1/2" 1.44 MByte IBM compatible diskette
 COMPUTER: IBM PC
 OPERATING SYSTEM: MS-DOS, Windows for Workgroups 3.11
 SOFTWARE: Microsoft Word for Windows 6
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/618,592
 FILING DATE: 17-Jul-2000
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 08/797,842
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Michaelson, Peter J.
 REGISTRATION NUMBER: 30090
 REFERENCE/DOCKET NUMBER: Sitching-5
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (908)530-6671
 TELEFAX: (908)530-6584
 INFORMATION FOR SEQ ID NO: 7:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 20 amino acids
 TYPE: amino acid
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 HYPOTHETICAL: NO
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:
 US-09-618-592-7

Query Match 25.2%; Score 29; DB 5; Length 20;
 Best Local Similarity 100.0%; Pred. No. 5.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 KYLYC 14
 |||||
 DB 4 KYLYC 8

RESULT 57
 US-08-159-339A-526
 Sequence 526, Application US/08159339A
 Patent No. 6037135
 GENERAL INFORMATION:
 APPLICANT: Kubo, Ralph T.
 APPLICANT: Grey, Howard M.
 APPLICANT: Sette, Alessandro
 APPLICANT: Celis, Balleban
 TITLE OF INVENTION: HLA Binding peptides and Their
 TITLE OF INVENTION: Uses
 NUMBER OF SEQUENCES: 1254
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: Townsend and Townsend and Crew LLP
 STREET: Two Embarcadero Center, Eighth Floor
 CITY: San Francisco
 STATE: CA
 COUNTRY: USA
 ZIP: 94111-3834
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: Paratsq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/159,339A
 FILING DATE: 29-NOV-1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/926,666
 FILING DATE: 07-AUG-1992
 APPLICATION NUMBER: US 08/027,746
 FILING DATE: 05-MAR-1993
 APPLICATION NUMBER: US 08/103,396
 FILING DATE: 06-AUG-1993

ATTORNEY/AGENT INFORMATION:
 NAME: Weber, Ellen Lauver
 REGISTRATION NUMBER: 32,762
 REFERENCE/DOCKET NUMBER: 018623-0050300S
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 576-0200
 TELEFAX: (415) 576-0300
 TELEX:
 INFORMATION FOR SEQ ID NO: 526:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 9 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-159-339A-526

Query Match 24.3%; Score 28; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 4.6e+05;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
 |||||
 DB 2 IPHPAGL 8

RESULT 58
 US-09-119-507B-51
 Sequence 51, Application US/09119507B
 Patent No. 6548642
 GENERAL INFORMATION:
 APPLICANT: Kieliszewski, Marcia J.
 TITLE OF INVENTION: No. 6548642el Synthetic Genes for Plant Gums
 FILE REFERENCE: OHU-03417
 CURRENT APPLICATION NUMBER: US/09/119,507B
 CURRENT FILING DATE: 1998-07-20
 NUMBER OF SEQ ID NOS: 118
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 51
 LENGTH: 11
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 NAME/KEY: SITE
 LOCATION: (8)
 OTHER INFORMATION: The Proline at this position is a hydroxyproline.
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 US-09-119-507B-51

Query Match 24.3%; Score 28; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 4.3e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNIHK 10
 |||||
 DB 5 HPTPYVK 11

RESULT 59
 US-08-897-556A-51
 Sequence 51, Application US/08897556A
 Patent No. 6570062
 GENERAL INFORMATION:
 APPLICANT: KIELISZEWSKI, MARCIA J.
 TITLE OF INVENTION: SYNTHETIC GENES FOR PLANT GUMS AND OTHER
 NUMBER OF SEQUENCES: 106
 CORRESPONDENCE ADDRESSES:
 ADDRESSES: MEDLEN & CARROLL, LLP
 STREET: 220 Montgomery Street, Suite 2200
 CITY: San Francisco
 STATE: California

```
/ COUNTRY: United States of America
/ ZIP: 94104
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/897,556A
/ FILING DATE: 21-JUL-1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: CARROLL, PETER G.
/ REGISTRATION NUMBER: 32,837
/ REFERENCE/DOCKET NUMBER: OHU-02908
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (415) 397-8338
/ TELEFAX: (415) 705-8410
/ INFORMATION FOR SEQ ID NO: 51:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: not relevant
/ TOPOLOGY: unknown
/ MOLECULAR TYPE: protein
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 8
/ OTHER INFORMATION: /note="The Proline at this
/ OTHER INFORMATION: position is a hydroxyproline."
US-08-897-556A-51
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Query Match      24.3%; Score 28; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 HPTNHR 10
      |||::|
Db      5 HPTPVYK 11

RESULT 60
US-09-547-693-51
/ Sequence 51, Application US/09547693
/ Patent No. 6639050
/ GENERAL INFORMATION:
/ APPLICANT: Kleiszewski, Marcia
/ TITLE OF INVENTION: Synthetic Genes for Plant Gums and Other Hydroxyproline-Rich
/ FILE REFERENCE: OHU-04089
/ CURRENT APPLICATION NUMBER: US/09/547,693
/ CURRENT FILING DATE: 2000-04-12
/ NUMBER OF SEQ ID NOS: 236
/ SOFTWARE: Patentin version 3.0
/ SEQ ID NO 51
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial/Unknown
/ FEATURE:
/ NAME/KEY: misc.feature
/ OTHER INFORMATION: Synthetic
/ NAME/KEY: SITE
/ LOCATION: (8)..(8)
/ OTHER INFORMATION: The Proline at this position is a hydroxyproline.
US-09-547-693-51
```

```
Query Match      24.3%; Score 28; DB 2; Length 11;
Best Local Similarity 57.1%; Pred. No. 4.3e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      4 HPTNHR 10
      |||::|
Db      5 HPTPVYK 11
```

```
RESULT 61
US-08-147-011-1
/ Sequence 1, Application US/08147011
/ Patent No. 5478724
/ GENERAL INFORMATION:
/ APPLICANT: Morse, Stephen S.
/ APPLICANT: Gelman, Irwin H.
/ TITLE OF INVENTION: Lentivirus-Specific Nucleotide Probes
/ NUMBER OF SEQUENCES: 8
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Kilpatrick & Cody
/ STREET: 100 Peachtree Street
/ CITY: Atlanta
/ STATE: Georgia
/ COUNTRY: US
/ ZIP: 30303
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/147,011
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/746,706
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patricia L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: RU100
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 404-572-6508
/ TELEFAX: 404-572-6555
/ INFORMATION FOR SEQ ID NO: 1:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ HYPOTHETICAL: NO
/ ANTI-SENSE: NO
/ FRAGMENT TYPE: Internal
/ ORIGINAL SOURCE:
/ ORGANISM: lentivirus
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 4
/ OTHER INFORMATION: /note="X" at position 4 is A, P,
/ OTHER INFORMATION: or G."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 7
/ OTHER INFORMATION: /note="X" at position 7 is K or
/ OTHER INFORMATION: A."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 9
/ OTHER INFORMATION: /note="X" at position 9 is K or
/ OTHER INFORMATION: R."
/ FEATURE:
/ NAME/KEY: Modified-site
/ LOCATION: 10
/ OTHER INFORMATION: /note="X" at position 10 is K or
/ OTHER INFORMATION: R."
/ FEATURE:
/ NAME/KEY: Modified-site
```

LOCATION: 11
OTHER INFORMATION: /note= "X" at position 11 is S or
OTHER INFORMATION: R."
FEATURE:
NAME/KEY: Modified-site
LOCATION: 12
OTHER INFORMATION: /note= "X" at position 12 is V or
OTHER INFORMATION: I."
US-08-147-011-1

Query Match 24.3%; Score 28; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 PHEPTIHK 10
DB 1 PHEPTIHK 8

RESULT 62

US-08-480-190-221
Sequence 221, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Mario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-221

Query Match 24.3%; Score 28; DB 1; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVGESVNG 20
DB 2 HKYLVGESVTHG 13

RESULT 63

US-08-488-379-221
Sequence 221, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Mario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 221:
SEQUENCE CHARACTERISTICS:
LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-221

Query Match 24.3%; Score 28; DB 1; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVGESVNG 20
DB 2 HKYLVGESVTHG 13

RESULT 64

US-08-475-399A-221
Sequence 221, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Mario A.A.
APPLICANT: Hedley, Mary L.

```

/ APPLICANT: Stern, Lawrence J.
/ APPLICANT: Strominger, Jack L.
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 276
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: Windows95
/ SOFTWARE: FastSeq for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,399A
/ FILING DATE: 07-JUN-1995
/ PRIORITY APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: 15-JUN-1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: 11-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Fraser, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 00246/168003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-507
/ TELEFAX: 617/542-890
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 221:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ US-08-475-399A-221

Query Match      24.3% Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      9 HKYVCESYNGG 20
DB      2 HKYVACEVTHQG 13

RESULT 65
US-08-077-255A-221
/ Sequence 221, Application US/08077255A
/ Patent No. 6696061
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Darío A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 555X
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)

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/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/077,255A
/ FILING DATE: June 15, 1993
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 221:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 13
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/ US-08-077-255A-221

Query Match      24.3% Score 28; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY      9 HKYVCESYNGG 20
DB      2 HKYVACEVTHQG 13

RESULT 66
PCT-US93-07545-221
/ Sequence 221, Application PC/TUS9307545
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chicz
/ APPLICANT: Darío A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 273
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 MB
/ COMPUTER: IBM PS/2 Model 502 or 555X
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US93/07545
/ FILING DATE: 19930811
/ CLASSIFICATION:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 221:
/ SEQUENCE CHARACTERISTICS:

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LENGTH: 13
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-221

Query Match 24.3%; Score 28; DB 4; Length 13;
Best Local Similarity 41.7%; Pred. No. 5.2e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20
DB 2 HKYVACEVTHG 13

RESULT 67
US-08-480-190-90
Sequence 90, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-90

Query Match 24.3%; Score 28; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 9 HKYLVCEVNG 20
DB 3 HKYVACEVTHG 14

RESULT 68
US-08-480-190-220
Sequence 220, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-220

Query Match 24.3%; Score 28; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 9 HKYLVCEVNG 20
DB 2 HKYVACEVTHG 13

RESULT 69
US-08-488-379-90
Sequence 90, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274

```
/
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,379
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 90:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-488-379-90

Query Match          24.3% Score 28; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      9 HKVLCESVNG 20
Db      3 HKVACEVTHG 14

RESULT 70
US-08-488-379-220
/ Sequence 220, Application US/08488379
/ Patent No. 5880103
/ GENERAL INFORMATION:
/ APPLICANT: Robert G. Urban
/ APPLICANT: Roman M. Chiciz
/ APPLICANT: Dario A. A. Vignali
/ APPLICANT: Mary L. Hedley
/ APPLICANT: Lawrence J. Stern
/ APPLICANT: Jack L. Strominger
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 274
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: Massachusetts
/ COUNTRY: U.S.A.
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
/ OPERATING SYSTEM: MS-DOS (Version 5.0)
/ SOFTWARE: WordPerfect (Version 5.1)
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/488,379
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/
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: June 15, 1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: August 11, 1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Clark, Paul T.
/ REGISTRATION NUMBER: 30,162
/ REFERENCE/DOCKET NUMBER: 00246/168001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (617) 542-5070
/ TELEFAX: (617) 542-8906
/ TELEX: 200154
/ INFORMATION FOR SEQ ID NO: 220:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 14
/ TYPE: amino acid
/ STRANDEDNESS:
/ TOPOLOGY: linear
/
US-08-488-379-220

Query Match          24.3% Score 28; DB 1; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy      9 HKVLCESVNG 20
Db      2 HKVACEVTHG 13

RESULT 71
US-08-475-399A-90
/ Sequence 90, Application US/08475399A
/ Patent No. 6509033
/ GENERAL INFORMATION:
/ APPLICANT: Urban, Robert G.
/ APPLICANT: Chiciz, Roman M.
/ APPLICANT: Vignali, Dario A.A.
/ APPLICANT: Hedley, Mary L.
/ APPLICANT: Stern, Lawrence J.
/ APPLICANT: Strominger, Jack L.
/ TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
/ NUMBER OF SEQUENCES: 276
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Fish & Richardson, P.C.
/ STREET: 225 Franklin Street
/ CITY: Boston
/ STATE: MA
/ COUNTRY: US
/ ZIP: 02110-2804
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: IBM Compatible
/ SOFTWARE: PastsEQ for Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,399A
/ FILING DATE: 07-JUN-1995
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/077,255
/ FILING DATE: 15-JUN-1993
/ APPLICATION NUMBER: 07/925,460
/ FILING DATE: 11-AUG-1992
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Frazer, Janis K.
/ REGISTRATION NUMBER: 34,819
/ REFERENCE/DOCKET NUMBER: 00246/168003
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 617/542-507
/ TELEFAX: 617/542-890
/ TELEX: 200154
```


INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-90

Query Match 24.3%; Score 28; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20
DB 3 HKYVACEVTHG 14

RESULT 72
US-08-475-399A-220
Sequence 220, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chiciz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Frazer, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-220

Query Match 24.3%; Score 28; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20
DB 2 HKYVACEVTHG 13

RESULT 73

US-08-077-255A-90
Sequence 90, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chiciz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 555X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-90

Query Match 24.3%; Score 28; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20
DB 3 HKYVACEVTHG 14

RESULT 74
US-08-077-255A-220
Sequence 220, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chiciz
APPLICANT: Vignali, Dario A. A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street

CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-220

Query Match 24.3% Score 28; DB 2; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 HKVLCESVNGG 20
Db 2 HKVACEVTHQG 13

RESULT 75
PCT-US93-07545-90
Sequence 90, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 90:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-90

Query Match 24.3% Score 28; DB 4; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

Qy 9 HKVLCESVNGG 20
Db 3 HKVACEVTHQG 14

RESULT 76
PCT-US93-07545-220
Sequence 220, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSER: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 220:
SEQUENCE CHARACTERISTICS:
LENGTH: 14
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-220

Query Match 24.3% Score 28; DB 4; Length 14;
Best Local Similarity 41.7%; Pred. No. 5.6e+02;

Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNG 20
DB 2 HKYVACEVTHG 13

RESULT 77
US-08-480-190-88
Sequence 88, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-88

Query Match 24.3%; Score 28; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 66+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNG 20
DB 2 HKYVACEVTHG 13

RESULT 78
US-08-480-190-89
Sequence 89, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:

APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: Wordperfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-89

Query Match 24.3%; Score 28; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 66+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNG 20
DB 1 HKYVACEVTHG 12

RESULT 79
US-08-488-379-88
Sequence 88, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-88

Query Match 24.3% Score 28; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYVCSVNGS 20
DB 2 HKVYVCEVTHQG 13

RESULT 80
US-08-488-379-89
Sequence 89, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Mario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-89

Query Match 24.3% Score 28; DB 1; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKVYVCSVNGS 20
DB 1 HKVYVCEVTHQG 12

RESULT 81
US-09-009-953-110
Sequence 110, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Paste-Seq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 110:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 110:
US-09-009-953-110
Query Match 24.3% Score 28; DB 2; Length 15;

Best Local Similarity 57.1%; Pred. No. 6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
DB 8 IPHAPGL 14

RESULT 82

US-08-475-399A-88
Sequence 88, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignall, Darlo A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-88

Query Match 24.3%; Score 28; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSYVNG 20
DB 2 HKYVACEVTHQG 13

RESULT 83

US-08-475-399A-89
Sequence 89, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignall, Darlo A.A.

APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-89

Query Match 24.3%; Score 28; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSYVNG 20
DB 1 HKYVACEVTHQG 12

RESULT 84

US-08-077-255A-88
Sequence 88, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignall
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: MS-DOS (Version 5.0)

SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-88

Query Match 24.3%; Score 28; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCSVNGG 20
DB 2 HKVACEVTHQG 13

RESULT 85
US-08-077-255A-89
Sequence 89, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154

INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-077-255A-89

Query Match 24.3%; Score 28; DB 2; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCSVNGG 20
DB 1 HKVACEVTHQG 12

RESULT 86
PCT-US93-07545-88
Sequence 88, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 88:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-88

Query Match 24.3%; Score 28; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCSVNGG 20
DB 2 HKVACEVTHQG 13

RESULT 87
PCT-US93-07545-89
Sequence 89, Application PC/TUS9307545
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 273
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07545
FILING DATE: 19930811
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 89:
SEQUENCE CHARACTERISTICS:
LENGTH: 15
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
PCT-US93-07545-89

Query Match 24.3%; Score 28; DB 4; Length 15;
Best Local Similarity 41.7%; Pred. No. 6e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNGG 20
DB 1 HKYVACEVTHQG 12

RESULT 88
US-08-480-190-85
Sequence 85, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston

STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-85

Query Match 24.3%; Score 28; DB 1; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCSVNGG 20
DB 2 HKYVACEVTHQG 13

RESULT 89
US-08-480-190-86
Sequence 86, Application US/08480190
Patent No. 5827516
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/480,190
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255

FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-86

Query Match 24.3% Score 28; DB 1; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCESYNG 20
|||:
Db 1 HKYVACEVTHQG 12

RESULT 90
US-08-480-190-87
Sequence 87, Application US/08480190
Patent No. 5827516

GENERAL INFORMATION:

APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/480,190

FILING DATE:

CLASSIFICATION: 424

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255

FILING DATE: June 15, 1993

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 87:

SEQUENCE CHARACTERISTICS:
LENGTH: 16

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-480-190-87

Query Match 24.3% Score 28; DB 1; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCESYNG 20
|||:
Db 3 HKYVACEVTHQG 14

RESULT 91
US-08-488-379-85

Sequence 85, Application US/08488379
Patent No. 5880103

GENERAL INFORMATION:

APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/488,379

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/077,255

FILING DATE: June 15, 1993

APPLICATION NUMBER: 07/925,460

FILING DATE: August 11, 1992

ATTORNEY/AGENT INFORMATION:

NAME: Clark, Paul T.

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 00246/168001

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 85:

SEQUENCE CHARACTERISTICS:

LENGTH: 16

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear
US-08-488-379-85

Query Match 24.3% Score 28; DB 1; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCESYNG 20
|||:
Db 2 HKYVACEVTHQG 13

RESULT 92
US-08-488-379-86
Sequence 86, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignelli
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-86
Query Match 24.3%; Score 28; DB 1; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 9 HKYVACEVTHQG 20
DB 1 HKYVACEVTHQG 12
RESULT 93
US-08-488-379-87
Sequence 87, Application US/08488379
Patent No. 5880103
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Darlo A. A. Vignelli
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,379
FILING DATE:
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: June 15, 1993
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 16
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-488-379-87
Query Match 24.3%; Score 28; DB 1; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 9 HKYVACEVTHQG 20
DB 3 HKYVACEVTHQG 14
RESULT 94
US-08-810-009-51
Sequence 51, Application US/08810009
Patent No. 6211437
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
APPLICANT: Jhal, Gurmukh S.
APPLICANT: Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6211437ch Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/810,009
FILING DATE: 04-MAR-1997
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:

NAME: Sprull, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-810-009-51

Query Match 24.3%; Score 28; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 6.5e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DHPPTNIH 9
|:|:|:
Db 7 DLTHETVH 15

RESULT 95
US-08-475-399A-85
Sequence 85, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-85

Query Match 24.3%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20
|||:|:
Db 2 HKYVACEVTHQG 13

RESULT 96
US-08-475-399A-86
Sequence 86, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.
APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: PASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 86:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-86

Query Match 24.3%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYVCESYNG 20
|||:|:
Db 1 HKYVACEVTHQG 12

RESULT 97
US-08-475-399A-87
Sequence 87, Application US/08475399A
Patent No. 6509033
GENERAL INFORMATION:
APPLICANT: Urban, Robert G.
APPLICANT: Chicz, Roman M.

APPLICANT: Vignali, Dario A.A.
APPLICANT: Hedley, Mary L.
APPLICANT: Stern, Lawrence J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 276
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson, P.C.
STREET: 225 Franklin Street
CITY: Boston
STATE: MA
COUNTRY: US
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,399A
FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/077,255
FILING DATE: 15-JUN-1993
APPLICATION NUMBER: 07/925,460
FILING DATE: 11-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00246/168003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-507
TELEFAX: 617/542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO: 87:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-475-399A-87

Query Match 24.3%; Score 28; DB 2; Length 16;
Best Local Similarity 41.7%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCEVNG 20
DB 3 HKYVACEVTHG 14

RESULT 98
US-09-776-490-51
Sequence 51, Application US/09776490
Patent No. 6599725
GENERAL INFORMATION:
APPLICANT: Briggs, Steven P.
Johal, Gurmukh S.
Gray, John
TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR CONTROLLING
CELL DEATH AND DISEASE RESISTANCE IN PLANTS
NUMBER OF SEQUENCES: 65
CORRESPONDENCE ADDRESS:
ADDRESSEE: BELL, SELTZER, PARK & GIBSON
STREET: P.O. Drawer 34009
CITY: Charlotte
STATE: No. 6599725th Carolina
COUNTRY: USA
ZIP: 28234
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/776,490
FILING DATE: 02-Feb-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/810,009
FILING DATE: 04-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Spullin, W. Murray
REGISTRATION NUMBER: 32,943
REFERENCE/DOCKET NUMBER: 5718-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
TELEX: 575102
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 51:
US-09-776-490-51

Query Match 24.3%; Score 28; DB 2; Length 16;
Best Local Similarity 44.4%; Pred. No. 6.5e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIHPPTNH 9
DB 7 DLTHETVH 15

RESULT 99
US-08-077-255A-85
Sequence 85, Application US/08077255A
Patent No. 6696061
GENERAL INFORMATION:
APPLICANT: Robert G. Urban
APPLICANT: Roman M. Chicz
APPLICANT: Dario A. A. Vignali
APPLICANT: Mary L. Hedley
APPLICANT: Lawrence J. Stern
APPLICANT: Jack L. Strominger
TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
STATE: Massachusetts
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 MB
COMPUTER: IBM PS/2 Model 502 or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/077,255A
FILING DATE: June 15, 1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/925,460
FILING DATE: August 11, 1992
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00246/168001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906

Search completed: January 20, 2006, 19:14:12
 Job time : 21.9615 secs

TELEX: 200154
 INFORMATION FOR SEQ ID NO: 85:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-077-255A-85

Query Match 24.3%; Score 28; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCESVNGG 20
 DB 2 HKYVACEVTHOG 13

RESULT 100
 US-08-077-255A-86
 Sequence 86, Application US/08077255A
 Patent No. 6696061
 GENERAL INFORMATION:
 APPLICANT: Robert G. Urban
 APPLICANT: Roman M. Chicz
 APPLICANT: Dario A. A. Vignali
 APPLICANT: Mary L. Hedley
 APPLICANT: Lawrence J. Stern
 APPLICANT: Jack L. Strominger
 TITLE OF INVENTION: IMMUNOMODULATORY PEPTIDES
 NUMBER OF SEQUENCES: 274
 CORRESPONDENCE ADDRESSES:
 ADDRESSEE: Fish & Richardson
 STREET: 225 Franklin Street
 CITY: Boston
 STATE: Massachusetts
 COUNTRY: U.S.A.
 ZIP: 02110-2804
 COMPUTER READABLE FORM:
 MEDIUM TYPE: 3.5" Diskette, 1.44 MB
 COMPUTER: IBM PS/2 Model 502 or 55SX
 OPERATING SYSTEM: MS-DOS (Version 5.0)
 SOFTWARE: WordPerfect (Version 5.1)
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/077,255A
 FILING DATE: June 15, 1993
 CLASSIFICATION: 424
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 07/925,460
 FILING DATE: August 11, 1992
 ATTORNEY/AGENT INFORMATION:
 NAME: Clark, Paul T.
 REGISTRATION NUMBER: 30,162
 REFERENCE/DOCKET NUMBER: 00246/168001
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 542-5070
 TELEFAX: (617) 542-8906
 TELEX: 200154
 INFORMATION FOR SEQ ID NO: 86:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 16
 TYPE: amino acid
 STRANDEDNESS:
 TOPOLOGY: linear
 US-08-077-255A-86

Query Match 24.3%; Score 28; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 6.5e+02;
 Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 9 HKYLVCESVNGG 20
 DB 1 HKYVACEVTHOG 12

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ; Search time 72.1154 Seconds
(without alignments)
115.878 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115

Sequence: 1 DHPPTNHRKYLVCESVNGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Published Applications AA Main:*

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2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*

3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*

4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*

5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*

6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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2	109	94.8	19	4	US-10-218-743-11
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4	35	30.4	7	5	US-09-554-385-54
5	35	30.4	7	5	US-10-512-512-54
6	35	30.4	7	5	US-10-235-043-54
7	35	30.4	20	3	US-09-564-201A-20
8	35	30.4	20	4	US-10-681-389-20
9	35	30.4	20	4	US-10-681-388-20
10	32	27.8	10	4	US-10-200-708-47
11	32	27.8	10	4	US-10-200-708-95
12	32	27.8	10	4	US-10-200-708-117
13	32	27.8	10	4	US-10-200-708-119
14	32	27.8	10	4	US-10-200-708-671
15	32	27.8	14	4	US-10-417-895A-36
16	32	27.8	14	5	US-10-808-187-2265
17	32	27.8	14	5	US-10-807-807-2265
18	32	27.8	15	4	US-10-103-395-109
19	32	27.8	16	4	US-10-062-710-19
20	32	27.8	17	4	US-10-442-909-32
21	32	27.8	20	4	US-10-385-649A-9
22	32	27.8	20	6	US-11-008-653-128
23	31.5	27.4	17	4	US-10-430-685-95
24	31	27.0	12	4	US-10-706-391-29
25	31	27.0	15	3	US-09-966-782A-58
26	31	27.0	15	4	US-10-254-905-58
27	31	27.0	16	3	US-09-791-524-3

28	31	27.0	17	3	US-09-791-524-4	Sequence 4, Appl1
29	31	27.0	17	4	US-10-609-217-196	Sequence 196, App
30	31	27.0	17	4	US-10-632-388-196	Sequence 196, App
31	31	27.0	17	4	US-10-651-723-196	Sequence 196, App
32	31	27.0	17	4	US-10-645-761-196	Sequence 196, App
33	31	27.0	17	4	US-10-666-696-196	Sequence 196, App
34	31	27.0	17	4	US-10-653-048-196	Sequence 196, App
35	31	27.0	17	4	US-10-756-289-1	Sequence 1, Appl1
36	31	27.0	17	5	US-10-821-544-16	Sequence 196, App
37	31	27.0	17	5	US-10-645-784-196	Sequence 196, App
38	31	27.0	18	3	US-09-664-761-44227	Sequence 9, Appl1
39	31	27.0	20	3	US-10-182-252A-787	Sequence 787, App
40	30	26.1	9	4	US-10-182-252A-830	Sequence 830, App
41	30	26.1	10	3	US-09-765-086-58	Sequence 58, Appl1
42	30	26.1	10	3	US-09-573-822C-160	Sequence 58, Appl1
43	30	26.1	10	4	US-10-264-374-58	Sequence 58, Appl1
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58	29.5	25.7	10	4	US-10-005-480A-164	Sequence 164, App
59	29.5	25.7	10	4	US-10-005-480A-164	Sequence 164, App
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61	29	25.2	8	4	US-10-485-758-89	Sequence 89, Appl1
62	29	25.2	9	3	US-09-826-290-41	Sequence 41, Appl1
63	29	25.2	9	3	US-09-826-290-41	Sequence 41, Appl1
64	29	25.2	9	3	US-09-791-393-7	Sequence 7, Appl1
65	29	25.2	9	3	US-09-791-393-7	Sequence 7, Appl1
66	29	25.2	9	4	US-10-264-309-239	Sequence 239, App
67	29	25.2	9	4	US-10-182-252A-232	Sequence 232, App
68	29	25.2	9	4	US-10-182-252A-759	Sequence 759, App
69	29	25.2	9	4	US-10-182-252A-832	Sequence 832, App
70	29	25.2	9	5	US-10-182-252A-866	Sequence 866, App
71	29	25.2	11	2	US-08-596-140-16	Sequence 239, App
72	29	25.2	11	4	US-10-169-351-80	Sequence 16, Appl1
73	29	25.2	11	4	US-10-239-656-9	Sequence 80, Appl1
74	29	25.2	11	5	US-10-879-994-59	Sequence 59, Appl1
75	29	25.2	12	4	US-10-411-869A-36	Sequence 36, Appl1
76	29	25.2	15	4	US-10-283-940-59	Sequence 59, Appl1
77	29	25.2	15	6	US-11-022-454-59	Sequence 59, Appl1
78	29	25.2	16	4	US-10-219-834-123	Sequence 123, App
79	29	25.2	17	4	US-10-244-151-15	Sequence 15, Appl1
80	29	25.2	18	3	US-09-988-493-136	Sequence 136, App
81	29	25.2	19	4	US-10-481-180-280	Sequence 280, App
82	29	25.2	20	3	US-09-466-035-84	Sequence 84, Appl1
83	29	25.2	20	4	US-10-103-395-195	Sequence 195, App
84	29	25.2	20	4	US-10-225-567A-2221	Sequence 2221, App
85	29	25.2	20	4	US-10-029-386-33390	Sequence 33390, A
86	29	25.2	20	4	US-10-371-525-150	Sequence 150, App
87	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
88	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
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90	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
91	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
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93	29	25.2	20	4	US-10-371-645-150	Sequence 150, App
94	29	25.2	20	5	US-10-654-601-2566	Sequence 2566, App
95	29	25.2	20	6	US-11-127-702-5	Sequence 5, Appl1
96	28.5	24.8	13	4	US-10-469-304-106	Sequence 106, App
97	28.5	24.8	13	4	US-10-469-304-107	Sequence 107, App
98	28	24.3	9	4	US-10-133-210-83	Sequence 83, Appl1
99	28	24.3	9	4	US-10-442-909-4	Sequence 4, Appl1
100	28	24.3	9	4	US-10-182-252A-758	Sequence 758, App

ALIGNMENTS

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RESULT 1
US-10-218-743-3
; Sequence 3, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 3
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-3

Query Match      100.0%; Score 115; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1,6e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIPHPTNHHKYLVCESVNG 20
Db      1 DIPHPTNHHKYLVCESVNG 20

RESULT 2
US-10-218-743-11
; Sequence 11, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 11
; LENGTH: 19
; TYPE: PRT
```

```
; ORGANISM: Dermatophagoides farinae
US-10-218-743-11

Query Match      94.8%; Score 109; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 1,3e-09;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1 DIPHPTNHHKYLVCESVNG 19
Db      1 DIPHPTNHHKYLVCESVNG 19

RESULT 3
US-09-864-761-38552
; Sequence 38552, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecmca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 38552
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005099.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.7
```

```
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN HEPA, SIGNAL = 1.8
/ OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.9
/ OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.8
/ OTHER INFORMATION: SWISSPROT HIT: P53820, EVALU8.80e+00
US-09-664-761-38552
```

Query Match 32.6%; Score 37.5; DB 3; Length 20;

Best Local Similarity 42.9%; Pred. No. 1.4e+02; Matches 6; Conservative 5; Mismatches 2; Indels 1; Gaps 1;

Qy 2 PHPTN1HKYLCV 15
Db 8 LPHR-HSHTLTLQ 20

RESULT 4

```
US-09-954-385-54
/ Sequence 54, Application US/09954385
/ Publication No. US20030100467A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Aehle, Wolfgang
/ APPLICANT: Baldwin, Toby L.
/ APPLICANT: Van Gastel, Franciscus J.C.
/ APPLICANT: Janssen, Giselle G.
/ APPLICANT: Murray, Christopher J.
/ APPLICANT: Wang, Huaming
/ APPLICANT: Winetzk, Deborah S.
/ TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
/ FILE REFERENCE: GC690
```

```
/ CURRENT APPLICATION NUMBER: US/09/954,385
/ CURRENT FILING DATE: 2001-09-12
/ NUMBER OF SEQ ID NOS: 433
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
/ SEQ ID NO 54
```

```
/ LENGTH: 7
```

```
/ TYPE: PRT
```

```
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: binding peptide
```

```
US-09-954-385-54
```

Query Match 30.4%; Score 35; DB 3; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHPTN1 8
Db 1 PHPTNL 6

RESULT 5

```
US-10-912-512-54
```

```
/ Sequence 54, Application US/10912512
```

```
/ Publication No. US20050042684A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Aehle, Wolfgang
/ APPLICANT: Baldwin, Toby L.
/ APPLICANT: Van Gastel, Franciscus J.C.
/ APPLICANT: Janssen, Giselle G.
/ APPLICANT: Murray, Christopher J.
/ APPLICANT: Wang, Huaming
/ APPLICANT: Winetzk, Deborah S.
/ TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-peptide
/ FILE REFERENCE: GC690
```

```
/ CURRENT APPLICATION NUMBER: US/10/912,512
```

```
/ CURRENT FILING DATE: 2004-08-05
```

```
/ PRIOR APPLICATION NUMBER: US/09/954,385
```

```
/ PRIOR FILING DATE: 2001-09-12
```

```
/ NUMBER OF SEQ ID NOS: 433
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
/ SEQ ID NO 54
```

```
/ LENGTH: 7
```

```
/ TYPE: PRT
```

```
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: binding peptide
```

```
US-10-912-512-54
```

Query Match 30.4%; Score 35; DB 5; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHPTN1 8
Db 1 PHPTNL 6

RESULT 6

```
US-10-235-043-54
```

```
/ Sequence 54, Application US/10235043
```

```
/ Publication No. US20050058996A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Aehle, Wolfgang
/ APPLICANT: Baldwin, Toby M.
/ APPLICANT: Van Gastel, Franciscus J.C.
/ APPLICANT: Janssen, Giselle G.
/ APPLICANT: Murray, Christopher J.
/ APPLICANT: Wang, Huaming
/ APPLICANT: Winetzk, Deborah S.
/ TITLE OF INVENTION: Binding Phenol Oxidizing Enzyme-Peptide
/ FILE REFERENCE: GC690-2
```

```
/ CURRENT APPLICATION NUMBER: US/10/235,043
```

```
/ CURRENT FILING DATE: 2002-09-03
```

```
/ NUMBER OF SEQ ID NOS: 446
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
```

```
/ SEQ ID NO 54
```

```
/ LENGTH: 7
```

```
/ TYPE: PRT
```

```
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
```

```
/ OTHER INFORMATION: binding peptide
```

```
US-10-235-043-54
```

Query Match 30.4%; Score 35; DB 5; Length 7;

Best Local Similarity 83.3%; Pred. No. 1.7e+06; Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 3 PHPTN1 8
Db 1 PHPTNL 6

RESULT 7

```
US-09-964-201A-20
```

```
/ Sequence 20, Application US/09964201A
```

```
/ Publication No. US20030091575A1
```

```
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Kenten, John H.
/ APPLICANT: Tramontano, Alfonso
/ APPLICANT: Pilon, April L.
/ APPLICANT: Lohmas, Gerald L.
/ APPLICANT: Roberts, Steven P.
/ TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM
/ FILE REFERENCE: U.S. Patent Application No. US20030091575A1 091026,276
```

```
/ CURRENT APPLICATION NUMBER: US/09/964,201A
```

```
/ CURRENT FILING DATE: 2002-05-21
```

```
/ NUMBER OF SEQ ID NOS: 35
```

```
/ SOFTWARE: Patentin Ver. 2.0
```

```
/ SEQ ID NO 20
```

```
/ LENGTH: 20
```

```
/ TYPE: PRT
```

/ ORGANISM: Homo sapiens
US-09-964-201A-20

Query Match 30.4%; Score 35; DB 3; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHKYIVC 14
||| : ||| :
DB 7 HQKVTKFMLC 17

RESULT 8

US-10-681-389-20
/ Sequence 20, Application US/10681389
/ Publication No. US20040115218A1

/ GENERAL INFORMATION:

/ APPLICANT: Kenten, John H

/ APPLICANT: Tramonano, Alfonso

/ APPLICANT: Pilon, Aprille L

/ APPLICANT: Lohmas, Gerald L

/ APPLICANT: Roberts, Steven F

/ TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM

/ FILE REFERENCE: U.S. Patent Application No. 09\026,276

/ CURRENT FILING DATE: 2003-10-07

/ PRIOR APPLICATION NUMBER: US/10/681,389

/ PRIOR FILING DATE: 2002-05-21

/ NUMBER OF SEQ ID NOS: 35

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 20

/ LENGTH: 20

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-681-389-20

Query Match 30.4%; Score 35; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHKYIVC 14
||| : ||| :
DB 7 HQKVTKFMLC 17

RESULT 9

US-10-681-388-20
/ Sequence 20, Application US/10681388
/ Publication No. US20040170643A1

/ GENERAL INFORMATION:

/ APPLICANT: Kenten, John H

/ APPLICANT: Tramonano, Alfonso

/ APPLICANT: Pilon, Aprille L

/ APPLICANT: Lohmas, Gerald L

/ APPLICANT: Roberts, Steven F

/ TITLE OF INVENTION: HEAT-SHOCK FUSION-BASED VACCINE SYSTEM

/ FILE REFERENCE: U.S. Patent Application No. 09\026,276

/ CURRENT FILING DATE: 2003-10-07

/ PRIOR APPLICATION NUMBER: US/10/681,388

/ PRIOR FILING DATE: 2002-05-21

/ NUMBER OF SEQ ID NOS: 35

/ SOFTWARE: PatentIn Ver. 2.0

/ SEQ ID NO 20

/ LENGTH: 20

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-681-388-20

Query Match 30.4%; Score 35; DB 4; Length 20;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNIHKYIVC 14
||| : ||| :
DB 7 HQKVTKFMLC 17

RESULT 10

US-10-200-708-47
/ Sequence 47, Application US/10200708
/ Publication No. US20030180314A1

/ GENERAL INFORMATION:

/ APPLICANT: Degroot, Anne S.

/ TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES

/ FILE REFERENCE: 17999-001

/ CURRENT FILING DATE: 2002-07-22

/ PRIOR APPLICATION NUMBER: US/09/351,036

/ PRIOR FILING DATE: 1999-07-09

/ PRIOR APPLICATION NUMBER: 60/092,346

/ PRIOR FILING DATE: 1998-07-10

/ PRIOR APPLICATION NUMBER: 60/115,145

/ PRIOR FILING DATE: 1999-01-08

/ PRIOR APPLICATION NUMBER: 60/130,677

/ PRIOR FILING DATE: 1999-04-23

/ NUMBER OF SEQ ID NOS: 672

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 95

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Human immunodeficiency virus

US-10-200-708-95

Query Match 27.8%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
||| : ||| :
DB 2 IPHPAGLKK 10

QY 4 HPTNIHKYIVC 14
||| : ||| :
DB 7 HQKVTKFMLC 17

RESULT 11

US-10-200-708-95
/ Sequence 95, Application US/10200708
/ Publication No. US20030180314A1

/ GENERAL INFORMATION:

/ APPLICANT: Degroot, Anne S.

/ TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES

/ FILE REFERENCE: 17999-001

/ CURRENT FILING DATE: 2002-07-22

/ PRIOR APPLICATION NUMBER: US/10/200,708

/ PRIOR FILING DATE: 2002-07-22

/ PRIOR APPLICATION NUMBER: US/09/351,036

/ PRIOR FILING DATE: 1999-07-09

/ PRIOR APPLICATION NUMBER: 60/092,346

/ PRIOR FILING DATE: 1998-07-10

/ PRIOR APPLICATION NUMBER: 60/115,145

/ PRIOR FILING DATE: 1999-01-08

/ PRIOR APPLICATION NUMBER: 60/130,677

/ PRIOR FILING DATE: 1999-04-23

/ NUMBER OF SEQ ID NOS: 672

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 47

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Human immunodeficiency virus

US-10-200-708-47

Query Match 27.8%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
||| : ||| :
DB 1 IPHPAGLKK 9

RESULT 11

US-10-200-708-95
/ Sequence 95, Application US/10200708
/ Publication No. US20030180314A1

/ GENERAL INFORMATION:

/ APPLICANT: Degroot, Anne S.

/ TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES

/ FILE REFERENCE: 17999-001

/ CURRENT FILING DATE: 2002-07-22

/ PRIOR APPLICATION NUMBER: US/10/200,708

/ PRIOR FILING DATE: 2002-07-22

/ PRIOR APPLICATION NUMBER: US/09/351,036

/ PRIOR FILING DATE: 1999-07-09

/ PRIOR APPLICATION NUMBER: 60/092,346

/ PRIOR FILING DATE: 1998-07-10

/ PRIOR APPLICATION NUMBER: 60/115,145

/ PRIOR FILING DATE: 1999-01-08

/ PRIOR APPLICATION NUMBER: 60/130,677

/ PRIOR FILING DATE: 1999-04-23

/ NUMBER OF SEQ ID NOS: 672

/ SOFTWARE: PatentIn Ver. 2.1

/ SEQ ID NO 95

/ LENGTH: 10

/ TYPE: PRT

/ ORGANISM: Human immunodeficiency virus

US-10-200-708-95

Query Match 27.8%; Score 32; DB 4; Length 10;
Best Local Similarity 55.6%; Pred. No. 4.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10
||| : ||| :
DB 2 IPHPAGLKK 10

RESULT 12

US-10-200-708-117
 ; Sequence 117, Application US/10200708
 ; Publication No. US20030180314A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Degroot, Anne S.
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
 ; FILE REFERENCE: 17999-001
 ; CURRENT APPLICATION NUMBER: US/10/200,708
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: US/09/351,036
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/092,346
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/115,145
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 60/130,677
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 117
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-200-708-117

Query Match 27.8%; Score 32; DB 4; Length 10;
 Best Local Similarity 55.6%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNHHK 10
 DB 2 IHPAGLKK 10

RESULT 13

US-10-200-708-119
 ; Sequence 119, Application US/10200708
 ; Publication No. US20030180314A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Degroot, Anne S.
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
 ; FILE REFERENCE: 17999-001
 ; CURRENT APPLICATION NUMBER: US/10/200,708
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: US/09/351,036
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/092,346
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/115,145
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 60/130,677
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 119
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-200-708-119

Query Match 27.8%; Score 32; DB 4; Length 10;
 Best Local Similarity 55.6%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNHHK 10
 DB 1 IHPAGLKK 9

RESULT 14

US-10-200-708-671

; Sequence 671, Application US/10200708
 ; Publication No. US20030180314A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Degroot, Anne S.
 ; TITLE OF INVENTION: HIV VACCINE CANDIDATE PEPTIDES
 ; FILE REFERENCE: 17999-001
 ; CURRENT APPLICATION NUMBER: US/10/200,708
 ; CURRENT FILING DATE: 2002-07-22
 ; PRIOR APPLICATION NUMBER: US/09/351,036
 ; PRIOR FILING DATE: 1999-07-09
 ; PRIOR APPLICATION NUMBER: 60/092,346
 ; PRIOR FILING DATE: 1998-07-10
 ; PRIOR APPLICATION NUMBER: 60/115,145
 ; PRIOR FILING DATE: 1999-01-08
 ; PRIOR APPLICATION NUMBER: 60/130,677
 ; PRIOR FILING DATE: 1999-04-23
 ; NUMBER OF SEQ ID NOS: 672
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 671
 ; LENGTH: 10
 ; TYPE: PRT
 ; ORGANISM: Human immunodeficiency virus
 US-10-200-708-671

Query Match 27.8%; Score 32; DB 4; Length 10;
 Best Local Similarity 55.6%; Pred. No. 4.6e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNHHK 10
 DB 2 IHPAGLKK 10

RESULT 15

US-10-417-895A-36
 ; Sequence 36, Application US/10417895A
 ; Publication No. US20040033569A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Crea, Roberto
 ; TITLE OF INVENTION: "DOPING" IN WALK-THROUGH MUTAGENESIS
 ; FILE REFERENCE: 1551.2002-001
 ; CURRENT APPLICATION NUMBER: US/10/417,895A
 ; CURRENT FILING DATE: 2003-04-16
 ; PRIOR APPLICATION NUMBER: 60/373,686
 ; PRIOR FILING DATE: 2002-04-17
 ; NUMBER OF SEQ ID NOS: 86
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 36
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: variant peptide for second complementarity
 ; OTHER INFORMATION: determining region of Fv region of an
 ; OTHER INFORMATION: immunoglobulin
 US-10-417-895A-36

Query Match 27.8%; Score 32; DB 4; Length 14;
 Best Local Similarity 55.6%; Pred. No. 6.6e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHHKL 12
 DB 4 HPTQHHDLV 12

RESULT 16

US-10-808-187-2265
 ; Sequence 2265, Application US/10808187
 ; Publication No. US20050009009A1
 ; GENERAL INFORMATION:

```

; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLS, JOHN
; TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
; FILE REFERENCE: V9661.0078
; CURRENT APPLICATION NUMBER: US/10/808,187
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08
; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/468,139
; PRIOR FILING DATE: 2003-05-05
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/471,200
; PRIOR FILING DATE: 2003-05-16
; NUMBER OF SEQ ID NOS: 2476
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2265
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-808-187-2265

Query Match      27.8%; Score 32; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 HPTNTH 9
      |||||
      9 HPTTTH 14

Db

RESULT 17
US-10-807-807-2265
; Sequence 2265, Application US/10807807
; Publication No. US20050181357A1
; GENERAL INFORMATION:
; APPLICANT: LEUNG, FREDERICK C.
; APPLICANT: PEIRIS, JOSEPH S. M.
; APPLICANT: YUEN, KWOK YUNG
; APPLICANT: POON, LIT MAN
; APPLICANT: GUAN, YI
; APPLICANT: CHAN, KWOK HUNG
; APPLICANT: NICHOLS, JOHN M.
; TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
; FILE REFERENCE: V9661.0077
; CURRENT APPLICATION NUMBER: US/10/807,807
; CURRENT FILING DATE: 2004-03-24
; PRIOR APPLICATION NUMBER: 60/457,031
; PRIOR FILING DATE: 2003-03-24
; PRIOR APPLICATION NUMBER: 60/457,730
; PRIOR FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: 60/459,931
; PRIOR FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: 60/460,357
; PRIOR FILING DATE: 2003-04-03
; PRIOR APPLICATION NUMBER: 60/461,265
; PRIOR FILING DATE: 2003-04-08

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; PRIOR APPLICATION NUMBER: 60/462,805
; PRIOR FILING DATE: 2003-04-14
; PRIOR APPLICATION NUMBER: 60/464,886
; PRIOR FILING DATE: 2003-04-23
; PRIOR APPLICATION NUMBER: 60/465,738
; PRIOR FILING DATE: 2003-04-25
; PRIOR APPLICATION NUMBER: 60/470,935
; PRIOR FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 2487
; SOFTWARE: PatentIn ver. 3.2
; SEQ ID NO 2265
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Human severe acute respiratory system virus
US-10-807-807-2265

Query Match      27.8%; Score 32; DB 5; Length 14;
Best Local Similarity 83.3%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      4 HPTNTH 9
      |||||
      9 HPTTTH 14

Db

RESULT 18
US-10-103-395-109
; Sequence 109, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: BEIMMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; FILE REFERENCE: 39963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 109
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-109

Query Match      27.8%; Score 32; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 7.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy      2 IHPNTHK 10
      |||||
      6 IHPAGLKK 14

Db

RESULT 19
US-10-062-710-19
; Sequence 19, Application US/10062710
; Publication No. US20030049253A1
; GENERAL INFORMATION:
; APPLICANT: Li, Frank Q.
; APPLICANT: Chu, Yong-Biang
; APPLICANT: Qiu, Jian-Tai
; TITLE OF INVENTION: Polymeric Conjugates for Delivery of

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/ TITLE OF INVENTION: MHC-Recognized Epitopes
/ TITLE OF INVENTION: Via Peptide Vaccines
/ FILE REFERENCE: 3781-001-27
/ CURRENT APPLICATION NUMBER: US/10/062,710
/ PRIOR FILING DATE: 2002-02-05
/ PRIOR APPLICATION NUMBER: US 60/310,498
/ PRIOR FILING DATE: 2001-08-08
/ NUMBER OF SEQ ID NOS: 232
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 19
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HIV Helper-T Cell Epitopes
US-10-062-710-19

Query Match 27.8%; Score 32; DB 4; Length 16;
Best Local Similarity 55.6%; Pred. No. 7.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10
Db 8 IHPHAGLKK 16

RESULT 20
US-10-442-909-32
/ Sequence 32, Application US/10442909
/ Publication No. US20040001845A1
/ GENERAL INFORMATION:
/ APPLICANT: Alfeld, Marcus
/ APPLICANT: Yu, Xu
/ APPLICANT: Walker, Bruce
/ APPLICANT: Addo, Marylyn
/ TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
/ FILE REFERENCE: 24028-010
/ CURRENT APPLICATION NUMBER: US/10/442,909
/ PRIOR FILING DATE: 2003-05-20
/ PRIOR APPLICATION NUMBER: 60/382,120
/ PRIOR FILING DATE: 2002-05-20
/ NUMBER OF SEQ ID NOS: 77
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 32
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Human Immunodeficiency virus type 1
US-10-442-909-32

Query Match 27.8%; Score 32; DB 4; Length 17;
Best Local Similarity 55.6%; Pred. No. 8.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10
Db 8 IHPHAGLKK 16

RESULT 21
US-10-285-649A-9
/ Sequence 9, Application US/10285649A
/ Publication No. US20030106089A1
/ GENERAL INFORMATION:
/ APPLICANT: McBride, Kevin
/ APPLICANT: Stealder, David M.
/ APPLICANT: Bear, Julie
/ APPLICANT: Perez-Grau, Luis
/ TITLE OF INVENTION: COTTON FIBER TRANSCRIPTIONAL FACTORS
/ FILE REFERENCE: 15615/03/US
/ CURRENT APPLICATION NUMBER: US/10/285,649A
/ PRIOR FILING DATE: 2003-02-07
/ PRIOR APPLICATION NUMBER: US 08/984,099
/ PRIOR FILING DATE: 1997-12-03

/ PRIOR APPLICATION NUMBER: PCT/US96/09897
/ PRIOR FILING DATE: 1996-06-07
/ PRIOR APPLICATION NUMBER: US 08/480,178
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: IBM PC; Windows 2000; Microsoft Word 2000
/ SEQ ID NO 9
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Gossypium Hirsutum
US-10-285-649A-9

Query Match 27.8%; Score 32; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 9.6e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IHPPTNIHKYLCE 15
Db 6 LPPTPTNKLCTSD 19

RESULT 22
US-11-008-653-128
/ Sequence 128, Application US/11008653
/ Publication No. US20050175627A1
/ GENERAL INFORMATION:
/ APPLICANT: Schneider, Joerg
/ TITLE OF INVENTION: HIV Pharmaccines
/ FILE REFERENCE: 3742.1001-000
/ CURRENT APPLICATION NUMBER: US/11/008,653
/ PRIOR FILING DATE: 2004-12-09
/ PRIOR APPLICATION NUMBER: PCT/GB2004/004038
/ PRIOR FILING DATE: 2004-09-23
/ PRIOR APPLICATION NUMBER: GB 0325011.5
/ PRIOR FILING DATE: 2003-10-27
/ PRIOR APPLICATION NUMBER: GB 0322637.0
/ PRIOR FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: GB 0322402.9
/ PRIOR FILING DATE: 2003-09-24
/ NUMBER OF SEQ ID NOS: 174
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 128
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: peptide from pol pool 2
US-11-008-653-128

Query Match 27.8%; Score 32; DB 6; Length 20;
Best Local Similarity 55.6%; Pred. No. 9.6e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPPTNIHK 10
Db 5 IHPHAGLKK 13

RESULT 23
US-10-430-685-95
/ Sequence 95, Application US/10430685
/ Publication No. US20040039543A1
/ GENERAL INFORMATION:
/ APPLICANT: Keck, Peter
/ TITLE OF INVENTION: COMPUTER METHOD AND APPARATUS FOR CLASSIFYING OBJECTS
/ FILE REFERENCE: 63040-010210
/ CURRENT APPLICATION NUMBER: US/10/430,685
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: PCT/US01/44000
/ PRIOR FILING DATE: 2001-11-06
/ PRIOR APPLICATION NUMBER: 60/246,196
/ PRIOR FILING DATE: 2000-11-06
/ NUMBER OF SEQ ID NOS: 240

/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Adenovirus
US-09-791-524-3

Query Match 27.0%; Score 31; DB 3; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNHHKYL 12
: || | : ||
DB 4 MPHSLNFSQYL 14

RESULT 28
US-09-791-524-4
/ Sequence 4, Application US/09791524
/ Publication No. US20030143209A1
/ GENERAL INFORMATION:
/ APPLICANT: Aventis Pharmaceuticals Products Inc.
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: A3319A
/ CURRENT APPLICATION NUMBER: US/09/791.524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: 60/09828
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 150
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Adenovirus
US-09-791-524-4

Query Match 27.0%; Score 31; DB 3; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNHHKYL 12
: || | : ||
DB 4 MPHSLNFSQYL 14

RESULT 29
US-10-609-217-196
/ Sequence 196, Application US/10609217
/ Publication No. US2004004188A1
/ GENERAL INFORMATION:
/ APPLICANT: FEIG, ULRICH
/ APPLICANT: LIU, CHUAN-PA
/ APPLICANT: CHEETHAM, JANET C.
/ APPLICANT: BOONE, THOMAS CHARLES
/ TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
/ FILE REFERENCE: A-527
/ CURRENT APPLICATION NUMBER: US/10/609.217
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: US/09/428.082B
/ PRIOR FILING DATE: 1999-10-22
/ PRIOR APPLICATION NUMBER: 60/105.371
/ PRIOR FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 1133
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 196
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-10-609-217-196

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNHHKYL 12
: || | : ||
DB 4 MPHSLNFSQYL 14

RESULT 30
US-10-632-388-196
/ Sequence 196, Application US/10632388
/ Publication No. US20040053845A1
/ GENERAL INFORMATION:
/ APPLICANT: FEIG, ULRICH
/ APPLICANT: LIU, CHUAN-PA
/ APPLICANT: CHEETHAM, JANET C.
/ APPLICANT: BOONE, THOMAS CHARLES
/ TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
/ FILE REFERENCE: A-527
/ CURRENT APPLICATION NUMBER: US/10/632.388
/ PRIOR FILING DATE: 2003-07-31
/ PRIOR APPLICATION NUMBER: US/09/428.082B
/ PRIOR FILING DATE: 1999-10-22
/ PRIOR APPLICATION NUMBER: 60/105.371
/ PRIOR FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 1133
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 196
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-10-632-388-196

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNHHKYL 12
: || | : ||
DB 4 MPHSLNFSQYL 14

RESULT 31
US-10-651-723-196
/ Sequence 196, Application US/10651723
/ Publication No. US20040057953A1
/ GENERAL INFORMATION:
/ APPLICANT: FEIG, ULRICH
/ APPLICANT: LIU, CHUAN-PA
/ APPLICANT: CHEETHAM, JANET C.
/ APPLICANT: BOONE, THOMAS CHARLES
/ TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
/ FILE REFERENCE: A-527
/ CURRENT APPLICATION NUMBER: US/10/651.723
/ PRIOR FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: US/09/428.082B
/ PRIOR FILING DATE: 1999-10-22
/ PRIOR APPLICATION NUMBER: 60/105.371
/ PRIOR FILING DATE: 1998-10-23
/ NUMBER OF SEQ ID NOS: 1133
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 196
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-10-651-723-196

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IHPPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 32

US-10-645-761-196
; Sequence 196, Application US/10645761
; Publication No. US20040071712A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/645,761
; CURRENT FILING DATE: 2003-08-18
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-10-645-761-196

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 IHPPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 33

US-10-666-696-196
; Sequence 196, Application US/10666696
; Publication No. US20040077022A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; APPLICANT: GUDAS, JEAN MARIE
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527A
; CURRENT APPLICATION NUMBER: US/10/666,696
; CURRENT FILING DATE: 2003-09-19
; PRIOR APPLICATION NUMBER: US/09/563,286C
; PRIOR FILING DATE: 2000-05-03
; PRIOR APPLICATION NUMBER: 09/428,082
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1157
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-10-666-696-196

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 IHPPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 34

US-10-653-048-196
; Sequence 196, Application US/10653048
; Publication No. US2004008778A1
; GENERAL INFORMATION:
; APPLICANT: FEIGE, ULRICH
; APPLICANT: LIU, CHUAN-FA
; APPLICANT: CHEETHAM, JANET C.
; APPLICANT: BOONE, THOMAS CHARLES
; TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
; FILE REFERENCE: A-527
; CURRENT APPLICATION NUMBER: US/10/653,048
; CURRENT FILING DATE: 2003-08-29
; PRIOR APPLICATION NUMBER: US/09/428,082B
; PRIOR FILING DATE: 1999-10-22
; PRIOR APPLICATION NUMBER: 60/105,371
; PRIOR FILING DATE: 1998-10-23
; NUMBER OF SEQ ID NOS: 1133
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 196
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: UKR ANTAGONIST PEPTIDE
US-10-653-048-196

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
Qy 2 IHPPTNIHKYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 35

US-10-756-289-1
; Sequence 1, Application US/10756289
; Publication No. US20040138110A1
; GENERAL INFORMATION:
; APPLICANT: Kessler, Horst
; APPLICANT: Graeff, Heinrich
; APPLICANT: Schmitt, Manfred
; APPLICANT: Magdalena, Viktor
; APPLICANT: Wilhelm, Olaf G.
; APPLICANT: Riemer, Christoph
; APPLICANT: Burgle, Markus
; TITLE OF INVENTION: Inhibitors for Urokinase Receptor
; FILE REFERENCE: 100564-09040
; CURRENT APPLICATION NUMBER: US/10/756,289
; CURRENT FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: US/09/402,464
; PRIOR FILING DATE: 2000-01-07
; PRIOR APPLICATION NUMBER: EP 97 106 024.9
; PRIOR FILING DATE: 1997-04-11
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-756-289-1

Query Match 27.0%; Score 31; DB 4; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTNHYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 36
US-10-821-544-16
Sequence 16, Application US/10821544
Publication No. US20040265797A1
GENERAL INFORMATION:
APPLICANT: ROSENBERG, STEVE
APPLICANT: DOYLE, MICHAEL
APPLICANT: CHAPMAN, HAROLD
TITLE OF INVENTION: PEPTIDE LIGANDS OF THE UOKINASE RECEPTOR
FILE REFERENCE: 014024-0284102
CURRENT APPLICATION NUMBER: US/10/821,544
PRIOR FILING DATE: 2004-04-09
PRIOR APPLICATION NUMBER: US/09/155,260C
PRIOR FILING DATE: 1998-09-23
PRIOR FILING DATE: 1997-03-28
PRIOR APPLICATION NUMBER: PCT/US97/05199
PRIOR FILING DATE: 1996-03-28
NUMBER OF SEQ ID NOS: 76
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 16
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-821-544-16

Query Match 27.0%; Score 31; DB 5; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTNHYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 37
US-10-645-784-196
Sequence 196, Application US/10645784
Publication No. US20050123548A1
GENERAL INFORMATION:
APPLICANT: PEIGE, ULRICH
APPLICANT: LIU, CHUAN-FA
APPLICANT: CHEETHAM, JANET C.
APPLICANT: BOONE, THOMAS CHARLES
APPLICANT: GUIDAS, JEAN MARIE
TITLE OF INVENTION: MODIFIED PEPTIDES AS THERAPEUTIC AGENTS
FILE REFERENCE: A-527A
CURRENT APPLICATION NUMBER: US/10/645,784
PRIOR FILING DATE: 2003-08-18
PRIOR APPLICATION NUMBER: US/09/563,286
PRIOR FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: 09/428,082
PRIOR FILING DATE: 1999-10-22
PRIOR APPLICATION NUMBER: 60/105,371
PRIOR FILING DATE: 1998-10-23
NUMBER OF SEQ ID NOS: 1157
SOFTWARE: PatentIn version 3.1
SEQ ID NO 196
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: UKR ANTAGONIST PEPTIDE

US-10-645-784-196

Query Match 27.0%; Score 31; DB 5; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPHTNHYL 12
: || | : ||
Db 4 MPHSLNFSQYL 14

RESULT 38
US-09-864-761-44227
Sequence 44227, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeomica-X-1
CURRENT APPLICATION NUMBER: US/09/864,761
CURRENT FILING DATE: 2001-05-23
PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 09/632,366
PRIOR FILING DATE: 2000-08-03
PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: PCT/US01/00666
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00667
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00664
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00669
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00668
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00663
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00662
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00661
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00670
PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: US 60/234,687
PRIOR FILING DATE: 2000-09-21
PRIOR APPLICATION NUMBER: US 09/608,408
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/774,203
PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 44227
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005827.3
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.84
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.67
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.95
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.74

OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.65
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.79
US-09-864-761-44227

Query Match 27.0%; Score 31; DB 3; Length 18;
Best Local Similarity 44.4%; Pred. No. 1.2e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 6 TNIHKYLC 14
Db 9 SHHWPLIC 17

RESULT 39
US-09-791-524-9

Sequence 9, Application US/09791524
Publication No. US20030143209A1
GENERAL INFORMATION:
APPLICANT: Aventis Pharmaceuticals Products Inc.
TITLE OF INVENTION: Targeted Adenovirus Vectors for Delivery of Heterologous Genes
FILE REFERENCE: A33194
CURRENT APPLICATION NUMBER: US/09/791,524
CURRENT FILING DATE: 2001-02-22
PRIOR APPLICATION NUMBER: 60/09828
PRIOR FILING DATE: 1998-08-27
NUMBER OF SEQ ID NOS: 150
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 20
TYPE: PRT
ORGANISM: Adenovirus
US-09-791-524-9

Query Match 27.0%; Score 31; DB 3; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 2 IPHPTIHKYL 12
Db 6 MPHSLNFSQYL 16

RESULT 40
US-10-182-252A-787

Sequence 787, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 787
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-787

Query Match 26.1%; Score 30; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8
Db 3 IPHPAGI 9

RESULT 41
US-10-182-252A-830

Sequence 830, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUS, SOREN
APPLICANT: CORBET, SYLVIE
APPLICANT: LAUEMOLLER, SANNE LISE
APPLICANT: HANSEN, JAN
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 830
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-830

Query Match 26.1%; Score 30; DB 4; Length 9;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 IPHPTNI 8
Db 3 IPHPAGI 9

RESULT 42
US-09-765-086-58

Sequence 58, Application US/09765086
Patent No. US20010046498A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
APPLICANT: Paqualini, Renata
APPLICANT: Wadli, Arap
APPLICANT: Bredesen, Dale E.
APPLICANT: Bledy, H. Michael
TITLE OF INVENTION: Chimeric Prostate-Homing Peptides With
TITLE OF INVENTION: Pro-Apoptotic Activity
FILE REFERENCE: P-ID 3844
CURRENT APPLICATION NUMBER: US/09/765,086
CURRENT FILING DATE: 2001-01-17
PRIOR APPLICATION NUMBER: US 09/489,582
PRIOR FILING DATE: 2000-01-21
NUMBER OF SEQ ID NOS: 235
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 58
LENGTH: 10
TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: synthetic peptide
US-09-765-086-58

Query Match 26.1%; Score 30; DB 3; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEEVNG 19
DB 1 CEEVNG 6

RESULT 43
US-09-573-822C-160
Sequence 160, Application US/09573822C
Publication No. US2003019901A1
GENERAL INFORMATION:
APPLICANT: Proteom Ltd
TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
FILE REFERENCE: Microbe patent
CURRENT APPLICATION NUMBER: US/09/573,822C
CURRENT FILING DATE: 2000-05-18
NUMBER OF SEQ ID NOS: 804
SOFTWARE: ProPatent version 1.0
SEQ ID NO 160
LENGTH: 10
TYPE: PRT
ORGANISM: mycoplasma genitalium
FEATURE:
OTHER INFORMATION: Sequence located in MG445 at 158-167 and may interact with Sequen
US-09-573-822C-160

Query Match 26.1%; Score 30; DB 3; Length 10;
Best Local Similarity 71.4%; Pred. No. 9.3e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCEVYN 18
DB 4 LVCEVYN 10

RESULT 44
US-10-264-374-58
Sequence 58, Application US/10264374
Publication No. US20030113320A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
FILE REFERENCE: P-LJ 3203
CURRENT APPLICATION NUMBER: US/10/264,374
CURRENT FILING DATE: 2002-10-03
PRIOR APPLICATION NUMBER: US/09/139,802
PRIOR FILING DATE: 1998-08-25
PRIOR APPLICATION NUMBER: 08/926,914
PRIOR FILING DATE: 1997-09-10
PRIOR APPLICATION NUMBER: 08/710,067
PRIOR FILING DATE: 1996-09-10
NUMBER OF SEQ ID NOS: 226
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 58
LENGTH: 10
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-264-374-58

Query Match 26.1%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEEVNG 19
DB 1 CEEVNG 6

RESULT 45
US-10-375-992-58
Sequence 58, Application US/10375992
Publication No. US20030152578A1
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
DERIVED THEREFROM, and Methods of Using Same
NUMBER OF SEQUENCES: 199
CORRESPONDENCE ADDRESSES:
ADDRESSER: Campbell & Flores
STREET: 4370 La Jolla Village Drive, Suite 700
CITY: San Diego
STATE: California
COUNTRY: United States
ZIP: 92122
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/375,992
FILING DATE: 27-Feb-2003
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/926,914
FILING DATE: 10-SEP-1997
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGISTRATION NUMBER: 31,815
REFERENCE/DOCKET NUMBER: P-LJ 2725
TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 535-9001
TELEFAX: (619) 535-8949
INFORMATION FOR SEQ ID NO: 58:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 58:
US-10-375-992-58

Query Match 26.1%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CEEVNG 19
DB 1 CEEVNG 6

RESULT 46
US-10-264-374-58
Sequence 58, Application US/10264374
Publication No. US20040096441A3
GENERAL INFORMATION:
APPLICANT: Ruoslahti, Erkki
TITLE OF INVENTION: NGR Receptor and Methods of Identifying Tumor Homing
TITLE OF INVENTION: Molecules That Home to Angiogenic Vasculature Using
US-10-264-374-58

/ TITLE OF INVENTION: Same
/ FILE REFERENCE: P-LJ 3203
/ CURRENT APPLICATION NUMBER: US/10/264,374
/ CURRENT FILING DATE: 2002-10-03
/ PRIOR APPLICATION NUMBER: US/09/139,802
/ PRIOR FILING DATE: 1998-08-25
/ PRIOR APPLICATION NUMBER: 08/926,914
/ PRIOR FILING DATE: 1997-09-10
/ PRIOR APPLICATION NUMBER: 08/710,067
/ PRIOR FILING DATE: 1996-09-10
/ NUMBER OF SEQ ID NOS: 226
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 58
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-264-374-58
Query Match 26.1%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 CEEVNG 19
DB 1 CEEVNG 6
RESULT 47
US-10-375-992-58
/ Sequence 58, Application US/10375992
/ Publication No. US20040131623A9
/ GENERAL INFORMATION:
/ APPLICANT: Ruoslahti, Erkki
/ Paasqualini, Renata
/ TITLE OF INVENTION: Tumor Homing Molecules, Conjugates
/ Derived Therefrom, and Methods of Using Same
/ NUMBER OF SEQUENCES: 199
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Campbell & Flores
/ STREET: 4370 La Jolla Village Drive, Suite 700
/ CITY: San Diego
/ STATE: California
/ COUNTRY: United States
/ ZIP: 92122
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/375,992
/ FILING DATE: 27-Feb-2003
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/08/926,914
/ FILING DATE: 10-SEP-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Campbell, Cathryn A.
/ REGISTRATION NUMBER: 31,815
/ REFERENCE/DOCKET NUMBER: P-LJ 2725
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (619) 535-9001
/ TELEFAX: (619) 535-8949
/ INFORMATION FOR SEQ ID NO: 58:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 10 amino acids
/ TYPE: amino acid
/ TOPOLOGY: both
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 58:

US-10-375-992-58
Query Match 26.1%; Score 30; DB 4; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 CEEVNG 19
DB 1 CEEVNG 6
RESULT 48
US-10-838-289-549
/ Sequence 549, Application US/10838289
/ Publication No. US20050058603A1
/ GENERAL INFORMATION:
/ APPLICANT: Gao, Jiming
/ APPLICANT: Ai, Hua
/ TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
/ TITLE OF INVENTION: NANOSHIELDS
/ FILE REFERENCE: CMRU-P01-040
/ CURRENT APPLICATION NUMBER: US/10/838,289
/ CURRENT FILING DATE: 2004-05-03
/ PRIOR APPLICATION NUMBER: US 60/502,429
/ PRIOR FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: US 60/467,389
/ PRIOR FILING DATE: 2003-05-02
/ NUMBER OF SEQ ID NOS: 756
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 549
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Tumor targeting peptide
US-10-838-289-549
Query Match 26.1%; Score 30; DB 5; Length 10;
Best Local Similarity 83.3%; Pred. No. 9.3e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 14 CEEVNG 19
DB 1 CEEVNG 6
RESULT 49
US-10-490-911-4
/ Sequence 4, Application US/10490911
/ Publication No. US20040253636A1
/ GENERAL INFORMATION:
/ APPLICANT: Soloviev, Mikhail
/ APPLICANT: Terret, Jonathan Alexander
/ TITLE OF INVENTION: A METHOD OF PROTEIN ANALYSIS
/ FILE REFERENCE: 2543-1-035
/ CURRENT APPLICATION NUMBER: US/10/490,911
/ CURRENT FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER: GB 0123295.8
/ PRIOR FILING DATE: 2001-09-27
/ PRIOR APPLICATION NUMBER: US 60/326177
/ PRIOR FILING DATE: 2001-09-27
/ NUMBER OF SEQ ID NOS: 10
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 4
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homosapiens
/ FEATURE:
/ NAME/KEY: MOD RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: biotinylated at N-terminus
US-10-490-911-4

Query Match 26.1%; Score 30; DB 5; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 7 NIKYLVCSVNGG 20
 |||
 1 NPHQY----SVEGG 10

RESULT 50

US-10-946-647-769
 ; Sequence 769, Application US/10946647
 ; Publication No. US20050186217A1
 ; GENERAL INFORMATION:
 ; APPLICANT: EMERY, DARYL A.
 ; APPLICANT: STRAUB, DARREN E.
 ; TITLE OF INVENTION: COMPOSITIONS PRODUCED USING ENTERIC PATHOGENS AND METHODS OF USE
 ; FILE REFERENCE: 293.00340101
 ; CURRENT APPLICATION NUMBER: US/10/946,647
 ; CURRENT FILING DATE: 2004-09-20
 ; PRIOR APPLICATION NUMBER: 60/504,119
 ; PRIOR FILING DATE: 2003-09-19
 ; NUMBER OF SEQ ID NOS: 1448
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 769
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 US-10-946-647-769

Query Match 26.1%; Score 30; DB 5; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 IHPPTNIHKY 11
 |||
 1 IYPPTESQNY 10

RESULT 51

US-09-825-517A-7
 ; Sequence 7, Application US/09825517A
 ; Publication No. US20030203415A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rondon, Isaac J
 ; APPLICANT: Ladner, Robert C
 ; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRIONIC
 ; FILE REFERENCE: DTX-016.1 (3421.1005-001)
 ; CURRENT APPLICATION NUMBER: US/09/825,517A
 ; CURRENT FILING DATE: 2003-03-24
 ; PRIOR APPLICATION NUMBER: US 09/541,345
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 151
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: CEA binding polypeptide
 US-09-825-517A-7

Query Match 26.1%; Score 30; DB 3; Length 16;
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNGG 20
 |||
 3 VCEKTTGG 10

RESULT 52

US-10-148-671-10
 ; Sequence 10, Application US/10148671
 ; Publication No. US20030186419A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Jensenius, Jens Christian
 ; APPLICANT: Thiel, Steffen
 ; TITLE OF INVENTION: MASP-3, A complement-fixing enzyme, and uses for it
 ; FILE REFERENCE: 10/148,671
 ; CURRENT APPLICATION NUMBER: US/10/148,671
 ; CURRENT FILING DATE: 2000-11-30
 ; PRIOR APPLICATION NUMBER: PCT/DK00/00659
 ; PRIOR FILING DATE: 2000-11-30
 ; NUMBER OF SEQ ID NOS: 26
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 10
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens (fig. 4, cd13 and cd14)
 US-10-148-671-10

Query Match 26.1%; Score 30; DB 4; Length 16;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTNIHKYLV 13
 |||
 6 PANIMMYLV 14

RESULT 53

US-11-045-477-7
 ; Sequence 7, Application US/11045477
 ; Publication No. US20050201934A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Rondon, Isaac J
 ; APPLICANT: Ladner, Robert C
 ; TITLE OF INVENTION: BINDING PEPTIDES FOR CARCINOEMBRIONIC
 ; FILE REFERENCE: DTX-016.1 (3421.1005-001)
 ; CURRENT APPLICATION NUMBER: US/11/045,477
 ; CURRENT FILING DATE: 2005-01-26
 ; PRIOR APPLICATION NUMBER: US/09/825,517
 ; PRIOR FILING DATE: 2001-04-03
 ; PRIOR APPLICATION NUMBER: US 09/541,345
 ; PRIOR FILING DATE: 2000-04-03
 ; NUMBER OF SEQ ID NOS: 151
 ; SOFTWARE: PastSeq for Windows Version 4.0
 ; SEQ ID NO 7
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: CEA binding polypeptide
 US-11-045-477-7

Query Match 26.1%; Score 30; DB 6; Length 16;
 Best Local Similarity 62.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 13 VCESVNGG 20
 |||
 3 VCEKTTGG 10

RESULT 54

US-10-280-066-34
 ; Sequence 34, Application US/10280066
 ; Publication No. US20030180718A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Pillucola, Renuka C.
 ; APPLICANT: Brissette, Renee
 ; APPLICANT: Spruyt, Michael

```
/ APPLICANT: Dedova, Olga
/ APPLICANT: Blume, Arthur J.
/ APPLICANT: Prendergast, John
/ APPLICANT: Goldstein, Neil I
/ TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
/ FILE REFERENCE: 2598-4009051
/ CURRENT APPLICATION NUMBER: US/10/280,066
/ CURRENT FILING DATE: 2002-10-24
/ PRIOR APPLICATION NUMBER: 60/345,471
/ PRIOR FILING DATE: 2001-10-24
/ NUMBER OF SEQ ID NOS: 537
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 34
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Escherichia coli
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ OTHER INFORMATION: DGI-2-20F-PP-B42
US-10-280-066-34

Query Match          26.1%; Score 30; DB 4; Length 20;
Best Local Similarity 55.6%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      12 LVCESVNGG 20
Db      5 VVCRPVSGG 13

RESULT 55
US-10-776-013-463
/ Sequence 463, Application US/10776013
/ Publication No. US20040226056A1
/ GENERAL INFORMATION:
/ APPLICANT: MYRIAD GENETICS, INC.
/ APPLICANT: Roch, Jean-Marc
/ APPLICANT: Bartel, Paul
/ APPLICANT: Heichman, Karen
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
/ TITLE OF INVENTION: DISEASES
/ FILE REFERENCE: 1600.24
/ CURRENT APPLICATION NUMBER: US/10/776,013
/ CURRENT FILING DATE: 2004-02-09
/ PRIOR APPLICATION NUMBER: 09/948994
/ PRIOR FILING DATE: 2001-09-10
/ PRIOR APPLICATION NUMBER: 09/466139
/ PRIOR FILING DATE: 1999-12-21
/ PRIOR APPLICATION NUMBER: 60/113534
/ PRIOR FILING DATE: 1998-12-22
/ PRIOR APPLICATION NUMBER: 60/124120
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/141243
/ PRIOR FILING DATE: 1999-06-30
/ PRIOR APPLICATION NUMBER: 09/975072
/ PRIOR FILING DATE: 2001-10-12
/ PRIOR APPLICATION NUMBER: 60/240790
/ PRIOR FILING DATE: 2000-10-17
/ PRIOR APPLICATION NUMBER: 10/194967
/ PRIOR FILING DATE: 2002-07-15
/ PRIOR APPLICATION NUMBER: 60/304775
/ PRIOR FILING DATE: 2001-07-13
/ NUMBER OF SEQ ID NOS: 695
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-776-013-463

Query Match          26.1%; Score 30; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPRPTNIH 9
Db      11 LSPPTRIH 18

RESULT 56
US-10-062-109A-123
/ Sequence 123, Application US/10062109A
/ Publication No. US20030165505A1
/ GENERAL INFORMATION:
/ APPLICANT: Agensys
/ APPLICANT: Chaillica-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
/ TITLE OF INVENTION: Cancer
/ FILE REFERENCE: 51158-20062.01
/ CURRENT APPLICATION NUMBER: US/10/062,109A
/ CURRENT FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-062-109A-123

Query Match          25.7%; Score 29.5; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY      2 IPRPTNI 8
Db      2 IPRPTNV 9

RESULT 57
US-10-005-480A-123
/ Sequence 123, Application US/10005480A
/ Publication No. US20030191073A1
/ GENERAL INFORMATION:
/ APPLICANT: Agensys
/ APPLICANT: Chaillica-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
/ TITLE OF INVENTION: Cancer
/ FILE REFERENCE: 51158-20062.00
/ CURRENT APPLICATION NUMBER: US/10/005,480A
/ CURRENT FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-005-480A-123

Query Match          25.7%; Score 29.5; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;
```

QY 2 IPH-PTNI 8
|||
Db 2 IPRPTNV 9

RESULT 58
US-10-062-109A-164
; Sequence 164, Application US/100622109A
; Publication No. US20030165505A1
; GENERAL INFORMATION:
; APPLICANT: Agenysys
; APPLICANT: Chailita-Bld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.01
; CURRENT APPLICATION NUMBER: US/10/062,109A
; CURRENT FILING DATE: 2002-01-31
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-062-109A-164

Query Match 25.7%; Score 29.5; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
|||
Db 3 IPRPTNV 10

RESULT 59
US-10-005-480A-164
; Sequence 164, Application US/10005480A
; Publication No. US20030191073A1
; GENERAL INFORMATION:
; APPLICANT: Agenysys
; APPLICANT: Chailita-Bld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
; FILE REFERENCE: 51158-20062.00
; CURRENT APPLICATION NUMBER: US/10/005,480A
; CURRENT FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: PastSeq for Windows Version 4.0
; SEQ ID NO 164
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-005-480A-164

Query Match 25.7%; Score 29.5; DB 4; Length 10;
Best Local Similarity 75.0%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8

Db 3 IPRPTNV 10

RESULT 60
US-10-485-758-89
; Sequence 89, Application US/10485758
; Publication No. US20050129681A1
; GENERAL INFORMATION:
; APPLICANT: Varner, Judith A.
; TITLE OF INVENTION: Methods for Inhibiting Angiogenesis
; FILE REFERENCE: UCSD-07325
; CURRENT APPLICATION NUMBER: US/10/485,758
; CURRENT FILING DATE: 2004-02-03
; PRIOR FILING DATE: 2001-08-06
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn Version 3.1
; SEQ ID NO 89
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-485-758-89

Query Match 25.7%; Score 29.5; DB 5; Length 17;
Best Local Similarity 62.5%; Pred. No. 2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPRPTNI 9
|||
Db 3 LPH-MLH 9

RESULT 61
US-10-285-394-408
; Sequence 408, Application US/10285394
; Publication No. US20030228583A1
; GENERAL INFORMATION:
; APPLICANT: AMACHER, DAVID E.
; APPLICANT: PASULO, LISA M.
; APPLICANT: HERATH, HERATH MUDIYANSelage ATHULA CHANDRASIRI
; APPLICANT: HOLT, GORDON DUANE
; APPLICANT: STIGER, THOMAS R.
; TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
; FILE REFERENCE: POA-003.01
; CURRENT APPLICATION NUMBER: US/10/285,394
; CURRENT FILING DATE: 2003-02-07
; PRIOR FILING DATE: 2001-10-31
; NUMBER OF SEQ ID NOS: 412
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 408
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-285-394-408

Query Match 25.2%; Score 29; DB 4; Length 8;
Best Local Similarity 71.4%; Pred. No. 1.7e+06;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 YLVGESV 17
|||
Db 1 YTVCDGV 7

RESULT 62
US-09-826-290-41
; Sequence 41, Application US/09826290
; Patent No. US2002016468A1
; GENERAL INFORMATION:
; APPLICANT: Durham, L. Kathryn
; APPLICANT: Friedman, David L.

```
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Kimmel, Lida H.
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Potter, David M.
/ APPLICANT: Rohlf, Christian
/ APPLICANT: Silber, B. Michael
/ APPLICANT: Stigler, Thomas R.
/ APPLICANT: Sunderland, P. Trey
/ APPLICANT: Townsend, Robert Reid
/ APPLICANT: White, Frost
/ APPLICANT: Williams, Stephen A.
/ TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and
/ TITLE OF INVENTION: Uses Therefor, Including Diagnosis and Treatment of
/ TITLE OF INVENTION: Alzheimer's Disease
/ FILE REFERENCE: 2572-1-001 N2
/ CURRENT APPLICATION NUMBER: US/09/826,230
/ CURRENT FILING DATE: 2001-04-30
/ PRIOR APPLICATION NUMBER: US 60/194,504
/ PRIOR FILING DATE: 2000-04-03
/ PRIOR APPLICATION NUMBER: US 60/253,647
/ PRIOR FILING DATE: 2000-11-28
/ NUMBER OF SEQ ID NOS: 492
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 41
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-826-290-41
```

```
Query Match      25.2%; Score 29; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 LVCESVNG 19
Db      1 LICSELNG 8
```

```
RESULT 63
US-09-791-393-7
/ Sequence 7, Application US/09791389
/ Publication No. US20030032200A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Rohlf, Christian
/ TITLE OF INVENTION: Proteins, Genes and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
/ FILE REFERENCE: 2543-1-001 N1
/ CURRENT APPLICATION NUMBER: US/09/791,393
/ CURRENT FILING DATE: 2002-01-02
/ EARLIER APPLICATION NUMBER: GB 0004412.3
/ EARLIER FILING DATE: 2000-02-24
/ EARLIER APPLICATION NUMBER: GB 0030050.9
/ EARLIER FILING DATE: 2000-12-08
/ EARLIER APPLICATION NUMBER: US 60/254,830
/ EARLIER FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-791-393-7
```

```
Query Match      25.2%; Score 29; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 LVCESVNG 19
Db      1 LICSELNG 8
```

```
RESULT 64
US-09-791-389-7
/ Sequence 7, Application US/09791389
/ Publication No. US20030032773A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Rohlf, Christian
/ APPLICANT: Terrett, Jonathan Alexander
/ APPLICANT: Tyson, Kerry Louise
/ TITLE OF INVENTION: Proteins, Genes and Their Use for
/ TITLE OF INVENTION: Diagnosis and Treatment of Bipolar Affective Disorder (BAD)
/ FILE REFERENCE: 2543-1-001 N2
/ CURRENT APPLICATION NUMBER: US/09/791,389
/ CURRENT FILING DATE: 2001-02-23
/ PRIOR APPLICATION NUMBER: GB 0004412.3
/ PRIOR FILING DATE: 2000-02-24
/ PRIOR APPLICATION NUMBER: GB 0030050.9
/ PRIOR FILING DATE: 2000-12-08
/ PRIOR APPLICATION NUMBER: US 60/254,830
/ PRIOR FILING DATE: 2000-12-12
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-791-389-7
```

```
Query Match      25.2%; Score 29; DB 3; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      12 LVCESVNG 19
Db      1 LICSELNG 8
```

```
RESULT 65
US-10-264-309-239
/ Sequence 239, Application US/10264309
/ Publication No. US20040022794A1
/ GENERAL INFORMATION:
/ APPLICANT: DURHAM, L. KATHRYN
/ APPLICANT: FRIDMAN, DAVID L.
/ APPLICANT: HERATH, HERATH
/ APPLICANT: KIMMEL, LIDA H.
/ APPLICANT: PAREKH, RAJESH B.
/ APPLICANT: POTTER, DAVID M.
/ APPLICANT: ROHLF, CHRISTIAN
/ APPLICANT: SILBER, B. MICHAEL
/ APPLICANT: SNYDER, PETER J.
/ APPLICANT: SOARES, HOLLY D.
/ APPLICANT: STIGLER, THOMAS R.
/ APPLICANT: SUNDERLAND, P. TREY
/ APPLICANT: TOWNSEND, ROBERT R.
/ APPLICANT: WHITE, W. FROST
/ APPLICANT: WILLIAMS, STEPHEN A.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
/ TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
/ FILE REFERENCE: POA-002.01
/ CURRENT APPLICATION NUMBER: US/10/264,309
/ CURRENT FILING DATE: 2002-10-03
/ PRIOR APPLICATION NUMBER: 60/326,708
/ PRIOR FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: Patentin Version 2.1
/ SEQ ID NO 239
/ LENGTH: 9
/ TYPE: PRT
```

ORGANISM: Homo sapiens
US-10-264-309-239

Query Match 25.2%; Score 29; DB 4; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCSYNG 19
DB 1 LICSELNG 8

RESULT 66

US-10-182-252A-232
Sequence 232, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUIIS, SOREN
APPLICANT: CORBERT, SYLVIE
APPLICANT: LAUBMOLLER, SANNE LISE
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 232
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-232

Query Match 25.2%; Score 29; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPPTNI 8
DB 3 IHPAGV 9

RESULT 67

US-10-182-252A-759
Sequence 759, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUIIS, SOREN
APPLICANT: CORBERT, SYLVIE
APPLICANT: LAUBMOLLER, SANNE LISE
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28

PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31

NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 759

LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-759

Query Match 25.2%; Score 29; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPPTNI 8
DB 3 IHPAGV 9

RESULT 68

US-10-182-252A-832
Sequence 832, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUIIS, SOREN
APPLICANT: CORBERT, SYLVIE
APPLICANT: LAUBMOLLER, SANNE LISE
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/179,333
PRIOR FILING DATE: 2000-01-31
NUMBER OF SEQ ID NOS: 1388
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 832
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-832

Query Match 25.2%; Score 29; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IHPPTNI 8
DB 3 IHPAGV 9

RESULT 69

US-10-182-252A-866
Sequence 866, Application US/10182252A
Publication No. US20040072162A1
GENERAL INFORMATION:
APPLICANT: FOMSGAARD, ANDERS
APPLICANT: BRUNAK, SOREN
APPLICANT: BUIIS, SOREN
APPLICANT: CORBERT, SYLVIE
APPLICANT: LAUBMOLLER, SANNE LISE
TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
FILE REFERENCE: 030307/0205
CURRENT APPLICATION NUMBER: US/10/182,252A
CURRENT FILING DATE: 2003-04-10
PRIOR APPLICATION NUMBER: PCT/DK01/00059
PRIOR FILING DATE: 2001-01-29
PRIOR APPLICATION NUMBER: EP 00610017.6
PRIOR FILING DATE: 2000-01-28

```
/ TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
/ FILE OF INVENTION: CONTROL OF HIV INFECTIONS
/ FILE REFERENCE: 030307/0205
/ CURRENT APPLICATION NUMBER: US/10/182,252A
/ CURRENT FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/DK01/00059
/ PRIOR FILING DATE: 2001-01-29
/ PRIOR APPLICATION NUMBER: EP 00610017.6
/ PRIOR FILING DATE: 2000-01-28
/ PRIOR APPLICATION NUMBER: US 60/179,333
/ PRIOR FILING DATE: 2000-01-31
/ NUMBER OF SEQ ID NOS: 1388
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 866
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-866
```

```
Query Match          25.2%; Score 29; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IHPPTNI 8
      |||||
DB      3 IHPHAGV 9
```

```
RESULT 70
US-10-264-309-239
/ Sequence 239, Application US/10264309
/ Publication No. US20050163789A9
/ GENERAL INFORMATION:
/ APPLICANT: DURHAM, L. KATHRYN
/ APPLICANT: FRIEDMAN, DAVID L.
/ APPLICANT: HERATH, HERATH
/ APPLICANT: KIMMEL, LIDA H.
/ APPLICANT: PAREKH, RAJESH B.
/ APPLICANT: POTTER, DAVID M.
/ APPLICANT: ROHLF, CHRISTIAN
/ APPLICANT: SILBER, B. MICHAEL
/ APPLICANT: SNYDER, PETER J.
/ APPLICANT: SOARES, HOLLY D.
/ APPLICANT: STIGER, THOMAS R.
/ APPLICANT: SUNDERLAND, P. TREV
/ APPLICANT: TOWNSEND, ROBERT R.
/ APPLICANT: WHITE, W. FROST
/ APPLICANT: WILLIAMS, STEPHEN A.
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES, POLYPEPTIDES AND USES THEREFOR,
/ TITLE OF INVENTION: INCLUDING DIAGNOSIS AND TREATMENT OF ALZHEIMER'S DISEASE
/ FILE REFERENCE: POA-002.01
/ CURRENT APPLICATION NUMBER: US/10/264,309
/ CURRENT FILING DATE: 2002-10-03
/ PRIOR APPLICATION NUMBER: 60/326,708
/ PRIOR FILING DATE: 2001-10-03
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Version 2.1
/ SEQ ID NO 239
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-264-309-239
```

```
Query Match          25.2%; Score 29; DB 5; Length 9;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      12 LVCEVING 19
      |||||
DB      1 LICSELNG 8
```

```
RESULT 71
US-08-996-140-16
/ Sequence 16, Application US/08996140
/ Publication No. US20030190318A1
/ GENERAL INFORMATION:
/ APPLICANT: TORIGOE, Kakuji
/ APPLICANT: USHIO, Shimpel
/ APPLICANT: KUNIKATA, Toshio
/ APPLICANT: KURIMOTO, Masashi
/ TITLE OF INVENTION: INTERLEUKIN-18 RECEPTOR PROTEINS
/ NUMBER OF SEQUENCES: 31
/ CORRESPONDENCE ADDRESSES:
/ ADDRESSER: BROWDY AND NEIMARK
/ STREET: 419 Seventh Street, N.W., Suite 300
/ CITY: Washington
/ STATE: D.C.
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent In Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/996,140
/ FILING DATE: 22-DEC-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 356,426/1996
/ FILING DATE: 26-DEC-1996
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 52,526/1997
/ FILING DATE: 21-FEB-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 163,490/1997
/ FILING DATE: 6-JUN-1997
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: JP 215,490/1997
/ FILING DATE: 28-JUL-1997
/ ATTORNEY/AGENT INFORMATION:
/ NAME: BROWDY, Roger L.
/ REGISTRATION NUMBER: 25,618
/ REFERENCE/DOCKET NUMBER: TORIGOE=2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-628-5197
/ TELEFAX: 202-737-3528
/ INFORMATION FOR SEQ ID NO: 16:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 11 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ FRAGMENT TYPE: Internal fragment
US-08-996-140-16
```

```
Query Match          25.2%; Score 29; DB 2; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIKHTYL 12
      |||||
DB      5 NIKHTYL 10
```

```
RESULT 72
US-10-169-351-80
/ Sequence 80, Application US/10169351
/ Publication No. US20030157090A1
/ GENERAL INFORMATION:
/ APPLICANT: BENVENUTO, EUGENIO
/ APPLICANT: FRANCONI, ROSSELLA
/ APPLICANT: DESIDERIO, ANGIOLA
/ APPLICANT: TAVLADORAKI, PARASKEVI
```



```
/ TITLE OF INVENTION: STABILIZING PEPTIDES, POLYPEPTIDES AND ANTIBODIES
/ TITLE OF INVENTION: WHICH INCLUDE THEM
/ FILE REFERENCE: 4161-4
/ CURRENT APPLICATION NUMBER: US/10/169,351
/ PRIOR FILING DATE: 2002-10-23
/ PRIOR APPLICATION NUMBER: PCT/IT00/00554
/ PRIOR FILING DATE: 2000-12-29
/ PRIOR APPLICATION NUMBER: IT RM99A000803
/ PRIOR FILING DATE: 1999-12-30
/ NUMBER OF SEQ ID NOS: 118
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 80
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ US-10-169-351-80
```

```
Query Match      25.2%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 73
US-10-239-656-9
/ Sequence 9, Application US/10239656
/ Publication No. US20040038339A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: KUPER, PETER
/ APPLICANT: RIETHMULLER, GERT
/ APPLICANT: LUTTERBUSH, RALF
/ APPLICANT: BORSCHERT, KATRIN
/ APPLICANT: KISCHEL, ROMAN
/ APPLICANT: MAYER, MONIKA
/ APPLICANT: HOFMEISTER, ROBERT
/ TITLE OF INVENTION: MULTIFUNCTIONAL POLYPEPTIDES COMPRISING A BINDING SITE
/ TITLE OF INVENTION: TO AN EPIPOPE OF THE NKG2D RECEPTOR COMPLEX
/ FILE REFERENCE: 029976/0106
/ CURRENT APPLICATION NUMBER: US/10/239,656
/ PRIOR FILING DATE: 2003-03-06
/ PRIOR APPLICATION NUMBER: PCT/EP01/03414
/ PRIOR FILING DATE: 2001-03-26
/ PRIOR APPLICATION NUMBER: EP 00106467.4
/ PRIOR FILING DATE: 2000-03-24
/ NUMBER OF SEQ ID NOS: 92
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO 9
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic Anti-NKG2D
/ OTHER INFORMATION: hybridoma 11B2D10 variable light chain CDRI
/ US-10-239-656-9
```

```
Query Match      25.2%; Score 29; DB 4; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 74
US-10-879-994-59
/ Sequence 59, Application US/10879994
```

```
/ Publication No. US2005002175A1
/ GENERAL INFORMATION:
/ APPLICANT: Stahl, Neil
/ APPLICANT: Yancopoulos, George D.
/ APPLICANT: Karow, Margaret
/ APPLICANT: Smith, Eric
/ TITLE OF INVENTION: HIGH AFFINITY FUSION PROTEINS AND THERAPEUTIC AND DIAGNOSTIC MET
/ FILE REFERENCE: REG 20352
/ CURRENT APPLICATION NUMBER: US/10/879,994
/ CURRENT FILING DATE: 2004-06-29
/ PRIOR APPLICATION NUMBER: 10/610,452
/ PRIOR FILING DATE: 2003-06-30
/ NUMBER OF SEQ ID NOS: 112
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 59
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: mus musculus
/ US-10-879-994-59
```

```
Query Match      25.2%; Score 29; DB 5; Length 11;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 75
US-10-411-869A-36
/ Sequence 36, Application US/10411869A
/ Publication No. US20030228605A1
/ GENERAL INFORMATION:
/ APPLICANT: Slocatara, Jelle Mouter
/ APPLICANT: Puijk, Mouter Cornelis
/ APPLICANT: Melsen, Robert Hane
/ APPLICANT: van Dijken, Pieter
/ APPLICANT: van Dijken, Pieter
/ TITLE OF INVENTION: IDENTIFICATION OF PROTEIN BINDING SITES
/ FILE REFERENCE: 2183-5921US (SVD/P54407US00)
/ CURRENT APPLICATION NUMBER: US/10/411,869A
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: PCT/NL01/00744
/ PRIOR FILING DATE: 2001-10-10
/ PRIOR APPLICATION NUMBER: EP 00203518.6
/ PRIOR FILING DATE: 2000-10-11
/ NUMBER OF SEQ ID NOS: 65
/ SOFTWARE: Patentin version 3.2
/ SEQ ID NO 36
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: LCDRI of 1fd1.pdb
/ US-10-411-869A-36
```

```
Query Match      25.2%; Score 29; DB 4; Length 12;
Best Local Similarity 83.3%; Pred. No. 1.6e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 NIHKYL 12
        |||||
Db      5 NIHNVL 10
```

```
RESULT 76
US-10-283-940-59
/ Sequence 59, Application US/10283940
/ Publication No. US20030220394A1
/ GENERAL INFORMATION:
/ APPLICANT: Danisco A/S
```

```
/ APPLICANT: Morgan, Andrew J
/ APPLICANT: Yu, Shukun
/ APPLICANT: Weiergang, Inge
/ APPLICANT: Pedersen, Hans C
/ TITLE OF INVENTION: Sequences
/ FILE REFERENCE: 674509-2041.1
/ CURRENT APPLICATION NUMBER: US/10/283,940
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: PCT/GB02/04916
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: GB 0126164.3
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: US 60/343,485
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 59
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Phanerochaete chrysosporium
/ US-10-283-940-59
```

```
Query Match      25.2%; Score 29; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
```

```
QY      4 HPTNHIKYLVC 14
      |||:||||
Db      6 HP--VMSYLVLC 14
```

```
RESULT 77
US-11-022-454-59
/ Sequence 59, Application US/11022454
/ Publication No. US20050164259A1
/ GENERAL INFORMATION:
/ APPLICANT: Morgan, Andrew John      Pedersen, Hans Christian
/ APPLICANT: Weiergang, Inge
/ APPLICANT: Yu, Shukun
/ TITLE OF INVENTION: Sequences
/ FILE REFERENCE: 674509-2041.2
/ CURRENT APPLICATION NUMBER: US/11/022,454
/ PRIOR FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: US 10/283,940
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: PCT/GB02/04916
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: GB 0126164.3
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: US 60/343,485
/ PRIOR FILING DATE: 2001-12-21
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 59
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Phanerochaete chrysosporium
/ US-11-022-454-59
```

```
Query Match      25.2%; Score 29; DB 6; Length 15;
Best Local Similarity 54.5%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 2; Gaps 1;
```

```
QY      4 HPTNHIKYLVC 14
      |||:||||
Db      6 HP--VMSYLVLC 14
```

```
RESULT 78
US-10-219-834-123
/ Sequence 123, Application US/10219834
/ Publication No. US20030096751A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: G-PROTEIN COUPLED RECEPTOR POLYNUCLEOTIDES AND METHODS OF USE TH
/ FILE REFERENCE: D0191 NP
/ CURRENT APPLICATION NUMBER: US/10/219,834
/ PRIOR FILING DATE: 2002-08-15
/ PRIOR APPLICATION NUMBER: US 60/313,658
/ PRIOR FILING DATE: 2001-08-20
/ PRIOR APPLICATION NUMBER: US 60/340,703
/ PRIOR FILING DATE: 2001-10-30
/ PRIOR APPLICATION NUMBER: US 60/318,675
/ PRIOR FILING DATE: 2001-09-12
/ PRIOR APPLICATION NUMBER: US 60/355,596
/ PRIOR FILING DATE: 2002-02-06
/ PRIOR APPLICATION NUMBER: US 60/333,417
/ PRIOR FILING DATE: 2001-11-26
/ PRIOR APPLICATION NUMBER: US 60/338,367
/ PRIOR FILING DATE: 2001-12-06
/ NUMBER OF SEQ ID NOS: 192
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 123
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ US-10-219-834-123
```

```
Query Match      25.2%; Score 29; DB 4; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      12 LVCSVNGG 20
      |||:||||
Db      7 LVCSAVHTG 15
```

```
RESULT 79
US-10-244-151-15
/ Sequence 15, Application US/10244151
/ Publication No. US2004005371A1
/ GENERAL INFORMATION:
/ APPLICANT: Grace Mareah and Alan Snow
/ TITLE OF INVENTION: Therapeutic and Diagnostic Applications
/ of Perlecan Domain I Splice Variants
/ NUMBER OF SEQUENCES: 20
/ CORRESPONDENCE ADDRESSES:
/ ADDRESS: Patrick M. Dwyer
/ STREET: 1818 Westlake Avenue N, Suite 114
/ CITY: Seattle
/ STATE: WA (Washington)
/ COUNTRY: United States of America
/ ZIP: 98109
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette - 3.50 inch, 1.44 Mb storage
/ COMPUTER: IBM PC
/ OPERATING SYSTEM: PC-DOS (Windows NT '95)
/ SOFTWARE: WordPerfect 9
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/10/244,151
/ FILING DATE: 13-Sep-2002
/ CLASSIFICATION: Unknown
/ PRIOR APPLICATION DATA:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Dwyer, Patrick M.
/ REGISTRATION NUMBER: 32,411
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (206) 343-7074
/ TELEFAX: (206) 343-7085
/ INFORMATION FOR SEQ ID NO: 15
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 17 AMINO ACIDS
/ TYPE: AMINO ACID
/ STRANDEDNESS: SINGLE
/ TOPOLOGY: LINEAR
```

```

/ MOLECULE TYPE: PROTEIN
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-10-244-151-15

Query Match      25.2%; Score 29; DB 4; Length 17;
Best Local Similarity 43.8%; Pred. No. 2.3e+03;
Matches 7; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY      5 PTNHHKLVCSVNGG 20
DB      1 PTPGSAVPKSLHGG 16

RESULT 80
US-09-988-493-136
/ Sequence 136, Application US/09988493
/ Publication No. US20030064419A1
/ GENERAL INFORMATION:
/ APPLICANT: Herath, Herath Mudiyanselage Athula Chandrasiri
/ APPLICANT: O'Hare, Michael John
/ APPLICANT: Page, Martin John
/ APPLICANT: Parekh, Rajesh Bhikhu
/ APPLICANT: Waterfield, Michael Derek
/ TITLE OF INVENTION: Proteins, Genes, and Their Use for
/ FILE REFERENCE: 2543-1-024
/ CURRENT APPLICATION NUMBER: US/09/988,493
/ PRIOR FILING DATE: 2002-05-21
/ PRIOR APPLICATION NUMBER: PCT/GB01/01219
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: GB 0006695.1
/ PRIOR FILING DATE: 2000-03-20
/ PRIOR APPLICATION NUMBER: GB 0007265.2
/ PRIOR FILING DATE: 2000-02-24
/ NUMBER OF SEQ ID NOS: 308
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 136
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapien
US-09-988-493-136

Query Match      25.2%; Score 29; DB 3; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      11 YLVCSVNGG 20
DB      4 PLVTEVNGG 13

RESULT 81
US-10-481-180-280
/ Sequence 280, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacks, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ PRIOR FILING DATE: 2001-06-19

```

```

/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 280
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-280

Query Match      25.2%; Score 29; DB 4; Length 19;
Best Local Similarity 28.6%; Pred. No. 2.6e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 DIPPTNHHKYLVC 14
DB      6 ELFNDKTHCYVAC 19

RESULT 82
US-09-466-035-84
/ Sequence 84, Application US/09466035
/ Patent No. US20020165172A1
/ GENERAL INFORMATION:
/ APPLICANT: SALBERG, MATTI
/ APPLICANT: MILICH, DAVID R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING
/ INTRACELLULAR DISEASES
/ NUMBER OF SEQUENCES: 86
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Robine & Pasternak LLP
/ STREET: 545 Middlefield Road, Suite 180
/ CITY: Menlo Park
/ STATE: California
/ COUNTRY: U.S.
/ ZIP: 94025
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patentin Releasee #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/466,035
/ FILING DATE: 17-Dec-1999
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pasternak, Dana S.
/ REGISTRATION NUMBER: 41,411
/ REFERENCE/DOCKET NUMBER: 2300-1231.01
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-325-7812
/ TELEFAX: 650-325-7823
/ TELEX: <Unknown>
/ INFORMATION FOR SEQ ID NO: 84:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 20 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: <Unknown>
/ TOPOLOGY: linear
/ SEQUENCE DESCRIPTION: SEQ ID NO: 84:
US-09-466-035-84

Query Match      25.2%; Score 29; DB 3; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHPTNHHKYLVC 14
DB      1 PPHPTNHHKYLVC 12

```

RESULT 83
US-10-103-395-195
; Sequence 195, Application US/10103395
; Publication No. US20020160019A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE, Inc.
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
; TITLE OF INVENTION: RESTRICTED EPITOPES
; FILE REFERENCE: 3963-20016.01
; CURRENT APPLICATION NUMBER: US/10/103,395
; CURRENT FILING DATE: 2003-01-03
; PRIOR APPLICATION NUMBER: US 09/009,953
; PRIOR FILING DATE: 1998-01-21
; PRIOR APPLICATION NUMBER: PCT/US98/01373
; PRIOR FILING DATE: 1998-01-23
; PRIOR APPLICATION NUMBER: US 60/036,713
; PRIOR FILING DATE: 1997-01-23
; PRIOR APPLICATION NUMBER: US 60/037,432
; PRIOR FILING DATE: 1997-02-07
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 195
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-103-395-195

Query Match 25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLC 14
| | | : : :
DB 1 PHHTALRQAILC 12

RESULT 84
US-10-225-567A-2221
; Sequence 2221, Application US/10225567A
; Publication No. US20030113798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenna C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1920-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2221
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-2221

Query Match 25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 35.3%; Pred. No. 2.8e+03;
Matches 6; Conservative 1; Mismatches 10; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLCVANG 19
| | | : : :
DB 2 PRSSGSHKAYSRPQG 18

RESULT 85
US-10-029-386-33390

; Sequence 33390, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
; FILE REFERENCE: A60MICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 33390
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC001237.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.9
US-10-029-386-33390

Query Match 25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | | : : :
DB 3 HATNVH 8

RESULT 86
US-10-371-525-150
; Sequence 150, Application US/10371525
; Publication No. US20030203869A1
; GENERAL INFORMATION:
; APPLICANT: Pike, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Ishioke, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: Expression Vectors for Stimulating an
; TITLE OF INVENTION: Immune Response and Methods of Using the Same
; FILE REFERENCE: 3963-20022.01
; CURRENT APPLICATION NUMBER: US/10/371,525
; CURRENT FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/311,784
; PRIOR FILING DATE: 1999-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; PRIOR FILING DATE: 1998-05-15
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-525-150

Query Match 25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLC 14
| | | : : :
DB 1 PHHTALRQAILC 12

```
RESULT 87
US-10-371-069-150
; Sequence 150, Application US/10371069
; Publication No. US20030216342A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Immune Response Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.10
; CURRENT APPLICATION NUMBER: US/10/371,069
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-069-150

Query Match          25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHEPTNKHXYLVC 14
      |||:|:|:|
      1 PHTTALRQAALIC 12

RESULT 88
US-10-371-645-150
; Sequence 150, Application US/10371645
; Publication No. US20030216343A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Immune Response Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.11
; CURRENT APPLICATION NUMBER: US/10/371,645
; PRIOR FILING DATE: 2003-06-20
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-645-150
```

```
Query Match          25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHEPTNKHXYLVC 14
      |||:|:|:|
      1 PHTTALRQAALIC 12

RESULT 89
US-10-371-260-150
; Sequence 150, Application US/10371260
; Publication No. US20030220285A1
; GENERAL INFORMATION:
; APPLICANT: EPIMUNE Inc.
; APPLICANT: Fikes, John D.
; APPLICANT: Hermanson, Gary G.
; APPLICANT: Sette, Alessandro
; APPLICANT: Iehloka, Glenn Y.
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert W.
; APPLICANT: Epimmune Inc.
; TITLE OF INVENTION: Immune Response Vectors for Stimulating an
; FILE REFERENCE: 39963-20022.13
; CURRENT APPLICATION NUMBER: US/10/371,260
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: US 09/078,904
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: US 60/085,751
; NUMBER OF SEQ ID NOS: 463
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 150
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBV CORE 50 (peptide 857.02)
US-10-371-260-150

Query Match          25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PHEPTNKHXYLVC 14
      |||:|:|:|
      1 PHTTALRQAALIC 12

RESULT 90
US-10-666-480-5
; Sequence 5, Application US/1066480
; Publication No. US20040121959A1
; GENERAL INFORMATION:
; APPLICANT: Boone, Thomas C
; APPLICANT: Wild, Kenneth D
; APPLICANT: Stiney, Karen C
; APPLICANT: Min, Hosing
; APPLICANT: Kimmel, Bruce
; TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
; FILE REFERENCE: A-82705
; CURRENT APPLICATION NUMBER: US/10/666,480
; PRIOR FILING DATE: 2003-09-18
; PRIOR APPLICATION NUMBER: 60/412,524
; PRIOR FILING DATE: 2002-09-19
; NUMBER OF SEQ ID NOS: 286
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 5
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
```

```
/ OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
/ OTHER INFORMATION: ly occurring sequence
US-10-666-480-5

Query Match      25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY      5 PPHNHNKYLIV 13
DB      10 PSNIDRYML 18

RESULT 91
US-10-732-862A-232
/ Sequence 232, Application US/10732862A
/ Publication No. US20040146524A1
/ GENERAL INFORMATION:
/ APPLICANT: ASHLEY, BIRKETT J.
/ APPLICANT: Lyons, Katelynne J.
/ APPLICANT: Jay, Haron J.
/ TITLE OF INVENTION: STABILIZED IMMUNOGENIC HBC CHIMER PARTICLES
/ FILE REFERENCE: ICC-136.0 (4564-88881)
/ CURRENT APPLICATION NUMBER: US/10/732,862A
/ PRIOR FILING DATE: 2003-12-10
/ PRIOR APPLICATION NUMBER: US 60/432,123
/ PRIOR FILING DATE: 2002-12-10
/ PRIOR APPLICATION NUMBER: US 10/274,616
/ PRIOR FILING DATE: 2002-10-21
/ PRIOR APPLICATION NUMBER: US 10/080,299
/ PRIOR FILING DATE: 2002-02-21
/ PRIOR APPLICATION NUMBER: US 10/082,014
/ PRIOR FILING DATE: 2002-02-22
/ NUMBER OF SEQ ID NOS: 455
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 232
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Hepatitis B virus
US-10-732-862A-232

Query Match      25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNHNKYLIV 14
DB      1 PHTALRAAILC 12

RESULT 92
US-10-481-180-283
/ Sequence 283, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamhawi, Shaden
/ APPLICANT: Sacke, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ PRIOR FILING DATE: 2001-06-19
/ NUMBER OF SEQ ID NOS: 884
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/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 283
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-283

Query Match      25.2%; Score 29; DB 4; Length 20;
Best Local Similarity 28.6%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 6; Indels 0; Gaps 0;

QY      1 DIPHTNHNKYLIV 14
DB      7 ELPNDEKTHCYKVC 20

RESULT 93
US-10-474-960A-403
/ Sequence 403, Application US/10474960A
/ Publication No. US20040248113A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Livingston, Brian
/ APPLICANT: Baker, Denise
/ APPLICANT: Newman, Mark
/ APPLICANT: Brown, David
/ TITLE OF INVENTION: Methods and System for Optimizing Multi-epitope Nucleic
/ TITLE OF INVENTION: Acid Constructors and Peptides Encoded Thereby
/ FILE REFERENCE: 2060.0320004
/ CURRENT APPLICATION NUMBER: US/10/474,960A
/ PRIOR FILING DATE: 2003-10-16
/ PRIOR APPLICATION NUMBER: PCT/US02/09877
/ PRIOR FILING DATE: 2002-03-28
/ PRIOR APPLICATION NUMBER: US 09/894,018
/ PRIOR FILING DATE: 2001-06-27
/ PRIOR APPLICATION NUMBER: US 60/284,221
/ PRIOR FILING DATE: 2001-04-16
/ NUMBER OF SEQ ID NOS: 419
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 403
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-474-960A-403

Query Match      25.2%; Score 29; DB 5; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY      3 PPHNHNKYLIV 14
DB      1 PHTALRAAILC 12

RESULT 94
US-10-654-601-2566
/ Sequence 2566, Application US/10654601
/ Publication No. US20050063983A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Vitiello, Maria A.
/ APPLICANT: Livingston, Brian D.
/ APPLICANT: Cells, Brehan
/ APPLICANT: Kubo, Ralph T.
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Epiimmune Inc.
```

/ TITLE OF INVENTION: Inducing Cellular Immune Responses to Hepatitis B Virus
/ TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.006007
/ CURRENT APPLICATION NUMBER: US/10/654,601
/ CURRENT FILING DATE: 2003-09-04
/ PRIOR APPLICATION NUMBER: US/09/239,043
/ PRIOR FILING DATE: 1999-01-27
/ PRIOR APPLICATION NUMBER: US 09/189,702
/ PRIOR FILING DATE: 1998-11-10
/ PRIOR APPLICATION NUMBER: US 08/978,291
/ PRIOR FILING DATE: 1997-11-25
/ PRIOR APPLICATION NUMBER: US 08/820,360
/ PRIOR FILING DATE: 1997-03-12
/ PRIOR APPLICATION NUMBER: US 60/013,363
/ PRIOR FILING DATE: 1996-03-13
/ PRIOR APPLICATION NUMBER: US 08/461,603
/ PRIOR FILING DATE: 1995-06-05
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ PRIOR APPLICATION NUMBER: US 08/344,824
/ PRIOR FILING DATE: 1994-11-23
/ PRIOR APPLICATION NUMBER: US 08/278,634
/ PRIOR FILING DATE: 1994-07-21
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 2579
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 2566
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Orthohepadnaviridae hepatitis B virus
US-10-654-601-2566

Query Match 25.2%; Score 29; DB 5; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

Qy 3 PHTNHIKIVC 14
Db 1 PHTALRQALIC 12

RESULT 95
US-11-127-702-5
/ Sequence 5, Application US/11127702
/ Publication No. US20050222035A1
/ GENERAL INFORMATION:
/ APPLICANT: Boone, Thomas C
/ APPLICANT: Wild, Kenneth D
/ APPLICANT: Stiney, Karen C
/ APPLICANT: Min, Hoesung
/ APPLICANT: Kimmel, Bruce
/ TITLE OF INVENTION: Peptides and Related Molecules That Modulate Nerve Growth Factor
/ FILE REFERENCE: A-827US
/ CURRENT APPLICATION NUMBER: US/11/127,702
/ CURRENT FILING DATE: 2005-05-11
/ PRIOR APPLICATION NUMBER: US/10/666,480
/ PRIOR FILING DATE: 2003-09-18
/ PRIOR APPLICATION NUMBER: 60/412,524
/ PRIOR FILING DATE: 2002-09-19
/ NUMBER OF SEQ ID NOS: 286
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 5
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Therapeutically active peptide of randomly generated, non-natural
US-11-127-702-5

Query Match 25.2%; Score 29; DB 6; Length 20;

Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

Qy 5 PTNHIKIVC 13
Db 10 PSNIDRYML 18

RESULT 96
US-10-469-304-106
/ Sequence 106, Application US/10469304
/ Publication No. US20040091974A1
/ GENERAL INFORMATION:
/ APPLICANT: KIRIN BEER KABUSHIKI KAISHA
/ TITLE OF INVENTION: Anti HLA-DR antibody
/ FILE REFERENCE: PH-1646-PCF
/ CURRENT APPLICATION NUMBER: US/10/469,304
/ CURRENT FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: JP2001/317054
/ PRIOR FILING DATE: 2001-10-15
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 106
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-106

Query Match 24.8%; Score 28.5; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 9 HKYLVCESYNG 19
Db 4 HNLIVC-SVSG 13

RESULT 97
US-10-469-304-107
/ Sequence 107, Application US/10469304
/ Publication No. US20040091974A1
/ GENERAL INFORMATION:
/ APPLICANT: KIRIN BEER KABUSHIKI KAISHA
/ TITLE OF INVENTION: Anti HLA-DR antibody
/ FILE REFERENCE: PH-1646-PCF
/ CURRENT APPLICATION NUMBER: US/10/469,304
/ CURRENT FILING DATE: 2003-08-29
/ PRIOR APPLICATION NUMBER: JP2001/317054
/ PRIOR FILING DATE: 2001-10-15
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 107
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence:peptide
US-10-469-304-107

Query Match 24.8%; Score 28.5; DB 4; Length 13;
Best Local Similarity 63.6%; Pred. No. 2.1e+03;
Matches 7; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

Qy 9 HKYLVCESYNG 19
Db 2 HNLIVC-SVSG 11

RESULT 98
US-10-133-210-83
/ Sequence 83, Application US/10133210

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; Publication No. US20030103964A1
; GENERAL INFORMATION:
; APPLICANT: Deliel, Charles
; APPLICANT: Berzofsky, Jay
; APPLICANT: Gulukota, Kamalakara
; APPLICANT: Vaccaro, Dennis
; APPLICANT: Weng, Zhiping
; APPLICANT: Zhang, Chao
; TITLE OF INVENTION: METHODS FOR DESIGNING MOLECULAR CONJUGATES AND
; TITLE OF INVENTION: COMPOSITIONS THEREOF
; FILE REFERENCE: BU-035AX
; CURRENT APPLICATION NUMBER: US/10/133,210
; CURRENT FILING DATE: 2002-04-26
; NUMBER OF SEQ ID NOS: 281
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 83
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-133-210-83

Query Match          24.3%; Score 28; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
   |||||
   :
Db 2 IPHPAGL 8

RESULT 99
US-10-442-909-4
; Sequence 4, Application US/10442909
; Publication No. US20040001845A1
; GENERAL INFORMATION:
; APPLICANT: Altfield, Marcus
; APPLICANT: Yu, Xu
; APPLICANT: Walker, Bruce
; APPLICANT: Adde, Marylyn
; TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of HIV-1 Virus
; FILE REFERENCE: 24028-010
; CURRENT APPLICATION NUMBER: US/10/442,909
; CURRENT FILING DATE: 2003-05-20
; PRIOR APPLICATION NUMBER: 60/382,120
; PRIOR FILING DATE: 2002-05-20
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Human immunodeficiency virus type 1
US-10-442-909-4

Query Match          24.3%; Score 28; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
   |||||
   :
Db 2 IPHPAGL 8

RESULT 100
US-10-182-252A-758
; Sequence 758, Application US/10182252A
; Publication No. US20040072162A1
; GENERAL INFORMATION:
; APPLICANT: FOMSGAARD, ANDERS
; APPLICANT: BRUNAK, SOREN
; APPLICANT: BUUS, SOREN
; APPLICANT: CORBERT, SYLVIE

```

```

; APPLICANT: LAUEMOLLER, SANNE LISE
; APPLICANT: HANSEN, JAN
; TITLE OF INVENTION: HIV PEPTIDE AND NUCLEIC ACIDS ENCODING THEM FOR DIAGNOSIS AND
; TITLE OF INVENTION: CONTROL OF HIV INFECTIONS
; FILE REFERENCE: 030307/0205
; CURRENT APPLICATION NUMBER: US/10/182,252A
; CURRENT FILING DATE: 2003-04-10
; PRIOR APPLICATION NUMBER: PCT/DK01/00059
; PRIOR FILING DATE: 2001-01-29
; PRIOR APPLICATION NUMBER: EP 00610017.6
; PRIOR FILING DATE: 2000-01-28
; PRIOR APPLICATION NUMBER: US 60/179,333
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 1388
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 758
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: HIV peptide
US-10-182-252A-758

Query Match          24.3%; Score 28; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
   |||||
   :
Db 3 IPHPAGL 9

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Search completed: January 20, 2006, 19:45:38
 UOB Time : 74.1154 Secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 20, 2006, 19:12:21 ; Search time 8.07692 Seconds
(without alignments)
25.093 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115
Sequence: 1 DIPHTNHRKYLVCESVNGG 20

Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database :

1: Published Applications AA.New:*
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4: /cgn2_6/prodata/1/pubppa/PC7_NEW_PUB.pep:*
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7: /cgn2_6/prodata/1/pubppa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	32	27.8	10	7	US-11-045-024-3294
2	32	27.8	10	7	US-11-045-024-10214
3	32	27.8	10	7	US-11-045-024-12085
4	32	27.8	11	7	US-11-045-024-3376
5	32	27.8	11	7	US-11-045-024-10191
6	32	27.8	11	7	US-11-045-024-10215
7	32	27.8	11	7	US-11-045-024-12063
8	32	27.8	11	7	US-11-045-024-12086
9	32	27.8	15	7	US-11-045-024-13140
10	31	27.0	16	7	US-11-038-980-3
11	31	27.0	17	7	US-11-038-980-4
12	31	27.0	20	7	US-11-038-980-9
13	29.5	25.7	9	6	US-10-859-643-123
14	29.5	25.7	9	7	US-11-097-864-123
15	29.5	25.7	9	7	US-11-097-864-123
16	29.5	25.7	10	6	US-10-859-643-123
17	29.5	25.7	10	7	US-11-097-864-164
18	29.5	25.7	10	7	US-11-097-864-164
19	29	25.2	13	6	US-10-966-483-17
20	29	25.2	13	6	US-10-966-483-17
21	28	24.3	8	7	US-11-045-024-1657
22	28	24.3	8	7	US-11-045-024-4340
23	28	24.3	9	7	US-11-045-024-3222
24	28	24.3	9	7	US-11-045-024-10229
25	28	24.3	9	7	US-11-045-024-12094

26	28	24.3	9	7	US-11-045-024-13796	Sequence 13796, A
27	28	24.3	10	7	US-11-045-024-2073	Sequence 2073, Ap
28	28	24.3	10	7	US-11-045-024-4608	Sequence 4608, Ap
29	28	24.3	10	7	US-11-045-024-10231	Sequence 10231, A
30	28	24.3	10	7	US-11-045-024-12095	Sequence 12095, A
31	28	24.3	11	7	US-11-045-024-2288	Sequence 2288, Ap
32	28	24.3	11	7	US-11-045-024-3375	Sequence 3375, Ap
33	28	24.3	11	7	US-11-045-024-10232	Sequence 10232, A
34	28	24.3	11	7	US-11-045-024-12096	Sequence 12096, A
35	28	24.3	15	7	US-11-045-024-13150	Sequence 13150, A
36	28	24.3	16	6	US-10-967-671-10	Sequence 10, Ap1
37	27	23.5	13	7	US-11-033-039-792	Sequence 792, App
38	27	23.5	19	6	US-10-880-238-115	Sequence 115, App
39	27	23.5	20	6	US-11-033-039-794	Sequence 794, App
40	27	23.5	19	6	US-10-467-657-9183	Sequence 9183, Ap
41	26.5	23.0	18	7	US-11-119-581-113	Sequence 55, Ap1
42	26	22.6	5	6	US-10-956-755A-55	Sequence 73, Ap1
43	26	22.6	5	6	US-10-956-755A-73	Sequence 91, Ap1
44	26	22.6	5	6	US-10-956-755A-91	Sequence 1626, Ap
45	26	22.6	8	7	US-11-045-024-1656	Sequence 10228, A
46	26	22.6	7	7	US-11-045-024-10228	Sequence 17, Ap1
47	26	22.6	9	6	US-10-859-643-17	Sequence 17, Ap1
48	26	22.6	9	7	US-11-097-864-117	Sequence 17, Ap1
49	26	22.6	9	7	US-11-097-912-117	Sequence 17, Ap1
50	26	22.6	9	7	US-11-045-024-1831	Sequence 1831, Ap
51	26	22.6	9	7	US-11-045-024-13806	Sequence 13806, A
52	26	22.6	10	6	US-11-041-893-64	Sequence 64, Ap1
53	26	22.6	10	6	US-10-859-643-53	Sequence 53, Ap1
54	26	22.6	10	7	US-11-097-864-53	Sequence 53, Ap1
55	26	22.6	10	7	US-11-097-912-53	Sequence 53, Ap1
56	26	22.6	10	7	US-11-045-024-2072	Sequence 2072, Ap
57	26	22.6	10	7	US-11-045-024-10220	Sequence 10220, A
58	26	22.6	10	7	US-11-033-039-381	Sequence 381, App
59	26	22.6	13	6	US-10-511-559-126	Sequence 126, App
60	26	22.6	13	6	US-10-511-559-127	Sequence 127, App
61	26	22.6	13	6	US-10-511-559-128	Sequence 128, App
62	26	22.6	13	6	US-10-511-559-129	Sequence 129, App
63	26	22.6	13	7	US-11-116-144-64	Sequence 64, Ap1
64	26	22.6	15	6	US-10-929-988-189	Sequence 189, App
65	26	22.6	15	7	US-11-045-024-13137	Sequence 13137, A
66	26	22.6	20	6	US-10-623-155-247	Sequence 247, App
67	25	21.7	7	7	US-11-084-717-55	Sequence 55, Ap1
68	25	21.7	9	7	US-11-010-7488-856	Sequence 856, App
69	25	21.7	9	7	US-11-010-7488-860	Sequence 860, App
70	25	21.7	9	7	US-11-010-7488-861	Sequence 861, App
71	25	21.7	9	7	US-11-010-7488-864	Sequence 864, App
72	25	21.7	9	7	US-11-010-7488-866	Sequence 866, App
73	25	21.7	9	7	US-11-010-7488-868	Sequence 868, App
74	25	21.7	12	6	US-10-829-988-163	Sequence 869, App
75	25	21.7	17	7	US-11-010-7488-855	Sequence 163, App
76	25	21.7	18	7	US-11-033-039-1223	Sequence 855, App
77	25	21.7	20	6	US-10-485-788A-580	Sequence 1223, Ap
78	25	21.7	20	7	US-11-022-562-142	Sequence 580, App
79	25	21.7	20	7	US-11-022-562-142	Sequence 141, App
80	25	21.7	8	7	US-11-064-416-4	Sequence 142, App
81	24	20.9	8	7	US-11-064-416-5	Sequence 4, Ap11
82	24	20.9	9	6	US-10-966-483-14	Sequence 14, Ap1
83	24	20.9	10	6	US-10-614-599-26	Sequence 26, Ap1
84	24	20.9	10	6	US-10-929-988-102	Sequence 102, App
85	24	20.9	12	6	US-10-966-371-7	Sequence 7, Ap11
86	24	20.9	12	6	US-11-180-997-5	Sequence 5, Ap11
87	24	20.9	12	7	US-11-180-997-5	Sequence 7, Ap11
88	24	20.9	12	7	US-10-939-890-44	Sequence 44, Ap1
89	24	20.9	16	7	US-11-033-039-1428	Sequence 1428, Ap
90	24	20.9	17	7	US-11-033-039-1427	Sequence 1427, Ap
91	24	20.9	17	7	US-11-041-893-132	Sequence 132, App
92	24	20.9	18	7	US-11-033-039-1426	Sequence 1426, Ap
93	24	20.9	19	7	US-10-623-155-514	Sequence 514, App
94	24	20.9	20	6	US-11-022-562-173	Sequence 173, App
95	24	20.9	20	7	US-11-033-039-1424	Sequence 1424, Ap
96	24	20.9	20	7	US-11-226-701-28	Sequence 28, Ap1
97	24	20.9	20	7		
98	23	20.0	7	7		

99 23 20.0 8 7 US-11-140-417-18
100 23 20.0 11 7 US-11-108-135-8

Sequence 18, Appl
Sequence 8, Appl

ALIGNMENTS

RESULT 1
US-11-045-024-3294

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/ Sequence 3294, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3294
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-3294
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Query Match 27.8%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTIRK 10
||| : |
Db 2 IPHPAGLRK 10

RESULT 2

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US-11-045-024-10214
/ Sequence 10214, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Bateban
/ APPLICANT: Kubo, Ralph
```

```
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10214
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-10214
```

Query Match 27.8%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 2 IPHPTIRK 10
||| : |
Db 2 IPHPAGLRK 10

RESULT 3

```
US-11-045-024-12085
/ Sequence 12085, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
```

```
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaSeq for Windows Version 4.0
/ SEQ ID NO 12085
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12085
```

```
Query Match 27.8%; Score 32; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 13;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 IHPPTNHHK 10
DB 2 IHPAGLKK 10
```

```
RESULT 4
US-11-045-024-3376
/ Sequence 3376, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteen
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaSeq for Windows Version 4.0
/ SEQ ID NO 3376
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3376
```

```
Query Match 27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 IHPPTNHHK 10
DB 2 IHPAGLKK 10
```

```
RESULT 5
US-11-045-024-10191
```

```
/ Sequence 10191, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteen
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
```

```
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaSeq for Windows Version 4.0
/ SEQ ID NO 10191
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10191
```

```
Query Match 27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 2 IHPPTNHHK 10
DB 2 IHPAGLKK 10
```

```
RESULT 6
US-11-045-024-10215
/ Sequence 10215, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteen
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
```

```
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10215
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10215
```

```
Query Match          27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 IPHPTNHHK 10
        ||||| : |
DB      3 IPHPAGLKK 11
```

```
RESULT 7
US-11-045-024-12063
/ Sequence 12063, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12063
/ LENGTH: 11
```

```
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12063
```

```
Query Match          27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 IPHPTNHHK 10
        ||||| : |
DB      3 IPHPAGLKK 11
```

```
RESULT 8
US-11-045-024-12086
/ Sequence 12086, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12086
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12086
```

```
Query Match          27.8%; Score 32; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 15;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 IPHPTNHHK 10
        ||||| : |
DB      3 IPHPAGLKK 11
```

```
RESULT 9
US-11-045-024-13140
/ Sequence 13140, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
```

```
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Ebediah
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Epiimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 13140
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
/ US-11-045-024-13140

Query Match      27.8%; Score 32; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. No. 20;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      2 IHPHTNIHK 10
Db      6 IHPHAGLKK 14

RESULT 10
/ US-11-038-980-3
/ Sequence 3, Application US/11038980
/ Publication No. US20060002893A1
/ GENERAL INFORMATION:
/ APPLICANT: Centellon SAS
/ APPLICANT: Emmanuelle Vigne
/ APPLICANT: Jean-Francois Dedieu
/ APPLICANT: Martine Latta
/ APPLICANT: Patrice Yeh
/ APPLICANT: Michel Perricaudet
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: P26,992-C USA
/ CURRENT APPLICATION NUMBER: US/11/038,980
/ PRIOR FILING DATE: 2005-01-20
/ PRIOR APPLICATION NUMBER: US 09/791,524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: US 60/098,028
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 3
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Adenovirus
```

```
US-11-038-980-3

Query Match      27.0%; Score 31; DB 7; Length 16;
Best Local Similarity 45.5%; Pred. No. 31;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPHTNIHKYL 12
Db      4 MPHSLNFSQYL 14

RESULT 11
/ US-11-038-980-4
/ Sequence 4, Application US/11038980
/ Publication No. US20060002893A1
/ GENERAL INFORMATION:
/ APPLICANT: Centellon SAS
/ APPLICANT: Emmanuelle Vigne
/ APPLICANT: Jean-Francois Dedieu
/ APPLICANT: Martine Latta
/ APPLICANT: Patrice Yeh
/ APPLICANT: Michel Perricaudet
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: P26,992-C USA
/ CURRENT APPLICATION NUMBER: US/11/038,980
/ PRIOR FILING DATE: 2005-01-20
/ PRIOR APPLICATION NUMBER: US 09/791,524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: US 60/098,028
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 4
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Adenovirus
/ US-11-038-980-4

Query Match      27.0%; Score 31; DB 7; Length 17;
Best Local Similarity 45.5%; Pred. No. 33;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      2 IHPHTNIHKYL 12
Db      4 MPHSLNFSQYL 14

RESULT 12
/ US-11-038-980-9
/ Sequence 9, Application US/11038980
/ Publication No. US20060002893A1
/ GENERAL INFORMATION:
/ APPLICANT: Centellon SAS
/ APPLICANT: Emmanuelle Vigne
/ APPLICANT: Jean-Francois Dedieu
/ APPLICANT: Martine Latta
/ APPLICANT: Patrice Yeh
/ APPLICANT: Michel Perricaudet
/ TITLE OF INVENTION: Targeted Adenovirus Vectors For Delivery Of Heterologous Genes
/ FILE REFERENCE: P26,992-C USA
/ CURRENT APPLICATION NUMBER: US/11/038,980
/ PRIOR FILING DATE: 2005-01-20
/ PRIOR APPLICATION NUMBER: US 09/791,524
/ PRIOR FILING DATE: 2001-02-22
/ PRIOR APPLICATION NUMBER: PCT/IB99/01524
/ PRIOR FILING DATE: 1999-08-27
/ PRIOR APPLICATION NUMBER: US 60/098,028
/ PRIOR FILING DATE: 1998-08-27
/ NUMBER OF SEQ ID NOS: 165
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
```

/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Adenovirus
US-11-038-980-9

Query Match 27.0% Score 31; DB 7; Length 20;
Best Local Similarity 45.5%; Pred. No. 39;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 IPHPTNHYKL 12
DB 6 MPHSLNFSQYL 16

RESULT 13
US-10-859-643-123
/ Sequence 123, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ PRIOR FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-123

Query Match 25.7% Score 29.5; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
DB 2 IPHRPTNV 9

RESULT 14
US-11-097-864-123
/ Sequence 123, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ PRIOR FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123

/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-123

Query Match 25.7% Score 29.5; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
DB 2 IPHRPTNV 9

RESULT 15
US-11-097-912-123
/ Sequence 123, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ PRIOR FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 123
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-123

Query Match 25.7% Score 29.5; DB 7; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 2 IPH-PTNI 8
DB 2 IPHRPTNV 9

RESULT 16
US-10-859-643-164
/ Sequence 164, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ PRIOR FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 164

/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-164

Query Match 25.7% Score 29.5; DB 6; Length 10;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 2 IPR-PTNI 8
Db 3 IPRPTNV 10

RESULT 17
US-11-097-864-164

/ Sequence 164, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Eld, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Parle, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 164
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-164

Query Match 25.7% Score 29.5; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 2 IPR-PTNI 8
Db 3 IPRPTNV 10

RESULT 18
US-11-097-912-164

/ Sequence 164, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Eld, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Kaitano, Arthur B.
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FASTSEQ for Windows Version 4.0

/ SEQ ID NO 164
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-164

Query Match 25.7% Score 29.5; DB 7; Length 10;
Best Local Similarity 75.0%; Pred. No. 33;
Matches 6; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

Qy 2 IPR-PTNI 8
Db 3 IPRPTNV 10

RESULT 19
US-10-966-483-17

/ Sequence 17, Application US/10966483
/ Publication No. US20050281783A1
/ GENERAL INFORMATION:
/ APPLICANT: Kinch, Michael S.
/ APPLICANT: Kleiner, Peter A.
/ APPLICANT: Bruchelmeier, Elizabeth
/ APPLICANT: Dubensky, Jr. Thomas W.
/ APPLICANT: Cook, David N.
/ TITLE OF INVENTION: LISTERIA-BASED BphA2 VACCINES
/ FILE REFERENCE: 10271-146
/ CURRENT APPLICATION NUMBER: US/10/966,483
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,919
/ PRIOR FILING DATE: 2003-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,719
/ PRIOR FILING DATE: 2003-10-15
/ PRIOR APPLICATION NUMBER: US 60/532,666
/ PRIOR FILING DATE: 2003-12-24
/ PRIOR APPLICATION NUMBER: US 60/556,631
/ PRIOR FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE: 2004-10-07
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 17
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-966-483-17

Query Match 25.2% Score 29; DB 6; Length 13;
Best Local Similarity 41.7%; Pred. No. 53;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 8 IHKLYCBESVNG 19
Db 2 IYMSVCNWSG 13

RESULT 20
US-10-723-207-71

/ Sequence 71, Application US/10723207
/ Publication No. US20050250934A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Chang Yi
/ APPLICANT: Walfield, Alan M.
/ TITLE OF INVENTION: PEPTIDE COMPOSITION AS IMMUNOGEN FOR THE TREATMENT OF
/ TITLE OF INVENTION: ALLERGY
/ FILE REFERENCE: 1151-4153US2
/ CURRENT APPLICATION NUMBER: US/10/723,207
/ CURRENT FILING DATE: 2003-11-24
/ PRIOR APPLICATION NUMBER: 09/701,623
/ PRIOR FILING DATE: 2000-12-01
/ PRIOR APPLICATION NUMBER: PCT/US99/13959

;; PRIOR FILING DATE: 1999-06-21
;; PRIOR APPLICATION NUMBER: 09/100,287
;; PRIOR FILING DATE: 1998-06-20
;; NUMBER OF SEQ ID NOS: 91
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO 71
;; LENGTH: 20
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide
;; OTHER INFORMATION: synthesized from amino acids with no genetic
US-10-723-207-71

Query Match 25.2%; Score 29; DB 6; Length 20;
Best Local Similarity 33.3%; Pred. No. 81;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 PPHPTNHKYLVC 14
DB 1 PPHPTALRQALIC 12

RESULT 21
US-11-045-024-1627
; Sequence 1627, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 1627
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1627

Query Match 24.3%; Score 28; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 IPHPTNI 8

DB 2 IPHPTNI 8

RESULT 22
US-11-045-024-4340
; Sequence 4340, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 4340
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4340

Query Match 24.3%; Score 28; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 IPHPTNI 8
DB 2 IPHPTNI 8

RESULT 23
US-11-045-024-3222
; Sequence 3222, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eplimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency


```
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ SEQUENCE ID NO 10229
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3222
```

```
Query Match      24.3% Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPTNI 8
DB      2 IPHPAGL 8
```

```
RESULT 24
US-11-045-024-10229
/ Sequence 10229, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ SEQUENCE ID NO 12094
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12094
```

```
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQUENCE ID NO 10229
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10229
```

```
Query Match      24.3% Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPTNI 8
DB      2 IPHPAGL 8
```

```
RESULT 25
US-11-045-024-12094
/ Sequence 12094, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ SEQUENCE ID NO 12094
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12094
```

```
Query Match      24.3% Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      2 IPHPTNI 8
DB      2 IPHPAGL 8
```

```
RESULT 26
US-11-045-024-13796
/ Sequence 13796, Application US/11045024
```

```
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13796
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13796

Query Match          24.3%; Score 28; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IPHPNTI 8
      |||| :
      3 IPHPAGL 9

Db

RESULT 27
US-11-045-024-2073
/ Sequence 2073, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
```

```
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2073
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2073

Query Match          24.3%; Score 28; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      2 IPHPNTI 8
      |||| :
      4 IPHPAGL 10

Db

RESULT 28
US-11-045-024-4608
/ Sequence 4608, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4608
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4608
```

```
Query Match      24.3%; Score 28; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IHPPTNI 8
      |||||
      :
Db      4 IHPAGL 10

RESULT 29
US-11-045-024-10231
/ Sequence 10231, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eplimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10231
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10231

Query Match      24.3%; Score 28; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IHPPTNI 8
      |||||
      :
Db      3 IHPAGL 9

RESULT 30
US-11-045-024-12095
/ Sequence 12095, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eplimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12095
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12095

Query Match      24.3%; Score 28; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 58;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 IHPPTNI 8
      |||||
      :
Db      3 IHPAGL 9

RESULT 31
US-11-045-024-2288
/ Sequence 2288, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Cheenut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bstedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eplimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
```

PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2288
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2288

Query Match 24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
|||||
DB 5 IPHPAGL 11

RESULT 32
US-11-045-024-3375
Sequence 3375, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Cheesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Bsteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Eplimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3375
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3375

Query Match 24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 2 IPHPTNI 8
|||||

DB 4 IPHPAGL 10

RESULT 33
US-11-045-024-10232
Sequence 10232, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Cheesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Bsteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Eplimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 10232
LENGTH: 11
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10232

Query Match 24.3% Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
|||||
DB 4 IPHPAGL 10

RESULT 34
US-11-045-024-12096
Sequence 12096, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Cheesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Bsteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Eplimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

```
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12096
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12096
```

```
Query Match          24.3%; Score 28; DB 7; Length 11;
Best Local Similarity 57.1%; Pred. No. 64;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 2 IHPPTNI 8
Db 4 IHPAGL 10
```

```
RESULT 35
US-11-045-024-13150
/ Sequence 13150, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045.024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 03/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13150
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13150
```

```
Query Match          24.3%; Score 28; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 88;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy 2 IHPPTNI 8
Db 8 IHPAGL 14
```

```
RESULT 36
US-10-967-671-10
/ Sequence 10, Application US/10967671
/ Publication No. US20050245728A1
/ GENERAL INFORMATION:
/ APPLICANT: EDWARDS, ALBD
/ APPLICANT: DHARAMSI, AKIL
/ APPLICANT: VEDADI, MASOUD
/ APPLICANT: KIMBER, MATTHEW
/ APPLICANT: VALLEE, FRANCOIS
/ TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM PSEUDOMONAS AERUGINOSA
/ FILE REFERENCE: IPT-261.01
/ CURRENT APPLICATION NUMBER: US/10/967,671
/ CURRENT FILING DATE: 2004-10-18
/ PRIOR APPLICATION NUMBER: PCT/CA03/00714
/ PRIOR FILING DATE: 2003-05-21
/ PRIOR APPLICATION NUMBER: 60/382,443
/ PRIOR FILING DATE: 2002-05-21
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 10
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Pseudomonas aeruginosa
US-10-967-671-10
```

```
Query Match          24.3%; Score 28; DB 6; Length 16;
Best Local Similarity 44.4%; Pred. No. 94;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 11 YLVCSGNG 19
Db 7 YACGALGG 15
```

```
RESULT 37
US-11-033-039-792
/ Sequence 792, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 792
/ LENGTH: 13
/ TYPE: PRT
```

```
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
US-11-033-039-792
```

```
Query Match          23.5%; Score 27; DB 7; Length 13;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY          10 KLYVCSVNG 19
           |||:::|
DB          4 KFLVSGTIG 13
```

```
RESULT 38
US-10-880-238-115
/ Sequence 115, Application US/10880238
/ Publication No. US20050287538A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Cheng, Ming-Tai
/ TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
/ TITLE OF INVENTION: IMMUNOGLOBULIN GENES RETRIEVAL AND ANTIBODY ENGINEERING
/ FILE REFERENCE: 17329-003001
/ CURRENT APPLICATION NUMBER: US/10/880,238
/ PRIOR FILING DATE: 2004-06-29
/ NUMBER OF SEQ ID NOS: 214
/ SOFTWARE: PsecSeq for windows Version 4.0
/ SEQ ID NO 115
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

```
/ OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-115
```

```
Query Match          23.5%; Score 27; DB 6; Length 19;
Best Local Similarity 36.8%; Pred. No. 1.6e+02;
Matches 7; Conservative 1; Mismatches 11; Indels 0; Gaps 0;
```

```
QY          1 DIPHTNHHKYLVCESVNG 19
           |||:::|
DB          1 EIRSKANMHTYVAESVKG 19
```

```
RESULT 39
US-11-033-039-794
/ Sequence 794, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: HUMPHREYS, ROBERT
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIPTOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ PRIOR FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 794
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
```

```
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-033-039-794
```

```
Query Match          23.5%; Score 27; DB 7; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY          10 KLYVCSVNG 19
           |||:::|
DB          4 KFLVSGTIG 13
```

```
RESULT 40
US-10-467-657-9183
/ Sequence 9183, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASNIGANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ PRIOR FILING DATE: 2003-08-11
/ CURRENT APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqMan99, version 1.04
/ SEQ ID NO 9183
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9183
```

```
Query Match          23.5%; Score 27; DB 6; Length 20;
Best Local Similarity 31.2%; Pred. No. 1.7e+02;
Matches 5; Conservative 2; Mismatches 9; Indels 0; Gaps 0;
```

```
QY          5 PTNHHKYLVCESVNG 20
           |||:::|
DB          1 PATISCKIYCVIRINNG 16
```

```
RESULT 41
US-11-119-581-113
```

```
/ Sequence 113, Application US/11119581
/ Publication No. US20050250695A1
/ GENERAL INFORMATION:
/ APPLICANT: Hogenhaug, Hans-Henrik Kristensen
/ APPLICANT: Myglind, Per Holse
/ APPLICANT: Segura, Dorotea Raventos
/ APPLICANT: Taboureau, Olivier
/ APPLICANT: Sonksen, Carsten Peter
/ TITLE OF INVENTION: Antimicrobial Peptides
/ FILE REFERENCE: 10646.200-US
/ CURRENT APPLICATION NUMBER: US/11/119,581
/ PRIOR FILING DATE: 2005-05-02
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 113
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
```

```
/ OTHER INFORMATION: Synthetic antimicrobial polypeptide
US-11-119-581-113
```

```
Query Match          23.0%; Score 26.5; DB 7; Length 18;
Best Local Similarity 25.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 7; Mismatches 1; Indels 1; Gaps 1;
```

```
QY          7 NHHKYLVCESVN 18
           ||:|::|
```

Db 2 NLHR-IICKGII 12

RESULT 42

US-10-956-755A-55
; Sequence 55, Application US/10956755A
; Publication No. US20050282747A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; TITLE OF INVENTION: Methods and Compositions for Wound Healing
; FILE REFERENCE: STONYB-09223
; CURRENT APPLICATION NUMBER: US/10/956,755A
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 55
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-755A-55

Query Match 22.6%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7
|||||
Db 1 HPTN 4

RESULT 43

US-10-956-755A-73
; Sequence 73, Application US/10956755A
; Publication No. US20050282747A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; TITLE OF INVENTION: Methods and Compositions for Wound Healing
; FILE REFERENCE: STONYB-09223
; CURRENT APPLICATION NUMBER: US/10/956,755A
; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 73
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-755A-73

Query Match 22.6%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7
|||||
Db 1 HPTN 4

RESULT 44

US-10-956-755A-91
; Sequence 91, Application US/10956755A
; Publication No. US20050282747A1
; GENERAL INFORMATION:
; APPLICANT: Clark, Richard A.
; APPLICANT: Prestwich, Glenn
; TITLE OF INVENTION: Methods and Compositions for Wound Healing
; FILE REFERENCE: STONYB-09223
; CURRENT APPLICATION NUMBER: US/10/956,755A

; CURRENT FILING DATE: 2004-10-01
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 91
; LENGTH: 5
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic
US-10-956-755A-91

Query Match 22.6%; Score 26; DB 6; Length 5;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7
|||||
Db 1 HPTN 4

RESULT 45

US-11-045-024-1626
; Sequence 1626, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Betteban
; APPLICANT: Kudo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Bpimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060, 0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1626
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1626

Query Match 22.6%; Score 26; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHPH 5
|||||
Db 4 IHPH 7

```
RESULT 46
US-11-045-024-10228
; Sequence 10228, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10228
; LENGTH: 8
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10228

Query Match          22.6%; Score 26; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-17

Query Match          22.6%; Score 26; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy      1 DIPHPN 7
|:|:|:
Db      3 DVPIPTH 9

RESULT 48
US-11-097-864-17
; Sequence 17, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2FI0B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 17
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-17

Query Match          22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 DIPHPN 7
|:|:|:
Db      3 DVPIPTH 9

RESULT 49
US-11-097-912-17
; Sequence 17, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raltano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2FI0B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
```



```
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 17
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-17
```

```
Query Match      22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      1 DHPPTN 7
        |||||
Db       3 DVPDPTH 9
```

```
RESULT 50
US-11-045-024-1831
/ Sequence 1831, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1831
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1831
```

```
Query Match      22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IPHP 5
        |||||
Db       5 IPHP 8
```

```
RESULT 51
US-11-045-024-13806
/ Sequence 13806, Application US/11045024
```

```
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13806
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13806
```

```
Query Match      22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      2 IPHP 5
        |||||
Db       5 IPHP 8
```

```
RESULT 52
US-11-041-893-64
/ Sequence 64, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahalir, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ CURRENT FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Bacterioides coli
US-11-041-893-64
```

Query Match 22.6%; Score 26; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 DIPHTN 8
|:|:|:
DB 2 PNPART 7

RESULT 53
US-10-859-643-53
; Sequence 53, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; TITLE OF INVENTION: Cancer
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-53

Query Match 22.6%; Score 26; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHTN 7
|:|:|:
DB 3 DVPIPTH 9

RESULT 54
US-11-097-864-53
; Sequence 53, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-53

Query Match 22.6%; Score 26; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHTN 7
|:|:|:
DB 3 DVPIPTH 9

RESULT 55
US-11-097-912-53
; Sequence 53, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:
; APPLICANT: Chailita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Farris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
; TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006204
; CURRENT APPLICATION NUMBER: US/11/097,912
; CURRENT FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 53
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-912-53

Query Match 22.6%; Score 26; DB 7; Length 10;
Best Local Similarity 57.1%; Pred. No. 1.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHTN 7
|:|:|:
DB 3 DVPIPTH 9

RESULT 56
US-11-045-024-2072
; Sequence 2072, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Eusebio
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Reducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396

/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaSeq for Windows Version 4.0
/ SEQ ID NO 2072
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2072

Query Match 22.6%; Score 26; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHPH 5
DB 6 IHPH 9

RESULT 57
US-11-045-024-10220
/ Sequence 10220, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteen
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060, 0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: PaSeq for Windows Version 4.0
/ SEQ ID NO 10220
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10220

Query Match 22.6%; Score 26; DB 7; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IHPH 5
DB 6 IHPH 9

RESULT 58
US-11-033-039-381
/ Sequence 381, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: RSH-201/US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ CURRENT FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 381
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-039-381

Query Match 22.6%; Score 26; DB 7; Length 10;
Best Local Similarity 30.0%; Pred. No. 1.2e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHLYV 13
DB 1 HPQKTKFMH 10

RESULT 59
US-10-511-559-126
/ Sequence 126, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: PaSeq for Windows Version 4.0
/ SEQ ID NO 126
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-126

Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNH 9

Db 8 HPVSLH 13

```
RESULT 60
US-10-511-559-127
; Sequence 127, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 127
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-127
```

Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | : : |
Db 6 HPVSLH 11

```
RESULT 61
US-10-511-559-128
; Sequence 128, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 128
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-128
```

Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | : : |
Db 2 HPVSLH 7

```
RESULT 62
US-10-511-559-129
; Sequence 129, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 129
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-129
```

Query Match 22.6%; Score 26; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | : : |
Db 1 HPVSLH 6

```
RESULT 63
US-11-116-144-64
; Sequence 64, Application US/11116144
; Publication No. US20050277181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVALL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA ILOP
; APPLICANT: OLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; FILE REFERENCE: INT-084
; CURRENT APPLICATION NUMBER: US/11/116,144
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 64
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Dengue virus 3
US-11-116-144-64
```

Query Match 22.6%; Score 26; DB 7; Length 13;
Best Local Similarity 33.3%; Pred. No. 1.6e+02;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 PHPTNIRKYLVC 14
 Db 2 PHTEVEDIDC 13

RESULT 64

US-10-929-988-189
 / Sequence 189, Application US/10929988
 / Publication No. US2005027588A1
 / GENERAL INFORMATION:
 / APPLICANT: CWTILA, STEVEN E.
 / APPLICANT: BALU, PALANI
 / APPLICANT: DUFFIN, DAVID J.
 / APPLICANT: PIPLANI, SUNILA
 / APPLICANT: MERRILL, BARBARA MCEOWEN
 / APPLICANT: SCHATZ, PETER JOSEPH
 / TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
 / TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
 / TITLE OF INVENTION: USES
 / FILE REFERENCE: 0300-0014
 / CURRENT APPLICATION NUMBER: US/10/929,988
 / CURRENT FILING DATE: 2004-08-30
 / PRIOR APPLICATION NUMBER: US/09/620,091
 / PRIOR FILING DATE: 2000-07-20
 / NUMBER OF SEQ ID NOS: 491
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 189
 / LENGTH: 15
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: peptide
 / US-10-929-988-189

Query Match 22.6%; Score 26; DB 6; Length 15;
 Best Local Similarity 62.5%; Pred. No. 1.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCESVNGG 20
 Db 3 LCESVGVG 10

RESULT 65
 US-11-045-024-13137
 / Sequence 13137, Application US/11045024
 / Publication No. US20050271676A1
 / GENERAL INFORMATION:
 / APPLICANT: Sette, Alessandro
 / APPLICANT: Sidney, John
 / APPLICANT: Southwood, Scott
 / APPLICANT: Livingston, Brian
 / APPLICANT: Chesnut, Robert
 / APPLICANT: Baker, Denise Marie
 / APPLICANT: Celis, Bettean
 / APPLICANT: Kubo, Ralph
 / APPLICANT: Grey, Howard M.
 / APPLICANT: EpiImmune Inc.
 / TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 / TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 / FILE REFERENCE: 2060.0040007
 / CURRENT APPLICATION NUMBER: US/11/045,024
 / CURRENT FILING DATE: 2005-01-28
 / PRIOR APPLICATION NUMBER: US 09/412,863
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: US 08/027,146
 / PRIOR FILING DATE: 1993-03-05
 / PRIOR APPLICATION NUMBER: US 08/073,205
 / PRIOR FILING DATE: 1993-06-04
 / PRIOR APPLICATION NUMBER: US 08/103,396
 / PRIOR FILING DATE: 1993-08-06
 / PRIOR APPLICATION NUMBER: US 08/159,184

/ PRIOR FILING DATE: 1993-11-29
 / PRIOR APPLICATION NUMBER: US 08/159,339
 / PRIOR FILING DATE: 1993-11-29
 / PRIOR APPLICATION NUMBER: US 08/205,713
 / PRIOR FILING DATE: 1994-03-04
 / PRIOR APPLICATION NUMBER: US 08/347,610
 / PRIOR FILING DATE: 1994-12-01
 / NUMBER OF SEQ ID NOS: 14528
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 13137
 / LENGTH: 15
 / TYPE: PRT
 / ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 / US-11-045-024-13137

Query Match 22.6%; Score 26; DB 7; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.9e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 IPRP 5
 Db 11 IPRP 14

RESULT 66
 US-10-623-155-247
 / Sequence 247, Application US/10623155
 / Publication No. US20050261166A1
 / GENERAL INFORMATION:
 / APPLICANT: Wang, Tonglong
 / APPLICANT: Reiter, Marc W.
 / APPLICANT: Fanger, Gary R.
 / TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
 / TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
 / FILE REFERENCE: 210121.455C20
 / CURRENT APPLICATION NUMBER: US/10/623,155
 / CURRENT FILING DATE: 2003-07-17
 / NUMBER OF SEQ ID NOS: 560
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 247
 / LENGTH: 20
 / TYPE: PRT
 / ORGANISM: Homo sapiens
 / US-10-623-155-247

Query Match 22.6%; Score 26; DB 6; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.5e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNIR 9
 Db 4 PHPMVLY 10

RESULT 67
 US-11-084-717-55
 / Sequence 55, Application US/11084717
 / Publication No. US20050260736A1
 / GENERAL INFORMATION:
 / APPLICANT: GEORGIU, GEORGE
 / APPLICANT: JEONG, KI-JUN
 / APPLICANT: HARVEY, BRENT R.
 / APPLICANT: IVERSON, BRENT L.
 / TITLE OF INVENTION: SELECTION OF BACTERIAL INNER-MEMBRANE ANCHOR POLYPEPTIDES
 / FILE REFERENCE: UTSB:723US
 / CURRENT APPLICATION NUMBER: US/11/084,717
 / CURRENT FILING DATE: 2005-03-18
 / PRIOR APPLICATION NUMBER: 60/554,324
 / PRIOR FILING DATE: 2004-03-18
 / PRIOR APPLICATION NUMBER: 10/620,278
 / PRIOR FILING DATE: 2003-07-15
 / PRIOR APPLICATION NUMBER: 60/396,058

/ PRIOR FILING DATE: 2002-07-15
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO: 55
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-11-084-717-55

Query Match 21.7% Score 25; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 CESVN 18
|||:
1 PTMLK 5

DB 1 CESLN 5

RESULT 68
US-11-010-748A-856
/ Sequence 856, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMAYER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHARM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 856
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-856

Query Match 21.7% Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNIHK 10
|||:
3 PTMLK 8

DB 3 PTMLK 8

RESULT 69
US-11-010-748A-860
/ Sequence 860, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMAYER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHARM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5

/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 860
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-860

Query Match 21.7% Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNIHK 10
|||:
1 PTMLK 6

DB 1 PTMLK 6

RESULT 70
US-11-010-748A-861
/ Sequence 861, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMAYER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHARM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 861
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-861

Query Match 21.7% Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNIHK 10
|||:
1 PTMLK 6

DB 1 PTMLK 6

RESULT 71
US-11-010-748A-864
/ Sequence 864, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMAYER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHARM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13

/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 864
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-864

Query Match 21.7%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHR 10
DB 4 PTMHR 9

RESULT 72

US-11-010-748A-866
/ Sequence 866, Application US/11010748A
/ Publication No. US2005024421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMATTER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHAM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 866
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-866

Query Match 21.7%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHR 10
DB 4 PTMHR 9

RESULT 73

US-11-010-748A-868
/ Sequence 868, Application US/11010748A
/ Publication No. US2005024421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMATTER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHAM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926

/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 868
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-868

Query Match 21.7%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHR 10
DB 3 PTMHR 8

RESULT 74

US-11-010-748A-869
/ Sequence 869, Application US/11010748A
/ Publication No. US2005024421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMATTER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHAM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 869
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 855
US-11-010-748A-869

Query Match 21.7%; Score 25; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTMHR 10
DB 2 PTMHR 7

RESULT 75

US-10-929-988-163
/ Sequence 163, Application US/10929988
/ Publication No. US2005027588A1
/ GENERAL INFORMATION:
/ APPLICANT: CWRILA, STEVEN B.
/ APPLICANT: BALU, PALANI
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: PIPLANI, SUNILA
/ APPLICANT: MERRILL, BARBARA MCBOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ PRIOR FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ PRIOR FILING DATE: 2000-07-20

/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: Patentin Ver. 2.1
/ SEQ ID NO: 163
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: peptide
US-10-929-988-163

Query Match 21.7%; Score 25; DB 6; Length 12;
Best Local Similarity 71.4%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNG 20
DB 1 CESVVG 7

RESULT 76
US-11-010-748A-855
/ Sequence 855, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMATER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHAM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ PRIOR FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 855
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: "Smcy" peptide fragment
US-11-010-748A-855

Query Match 21.7%; Score 25; DB 7; Length 17;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PNNHK 10
DB 8 PNNLHK 13

RESULT 77
US-11-033-039-1223
/ Sequence 1223, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ PRIOR FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14

/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: Patentin version 3.3
/ SEQ ID NO: 1223
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: hybrid peptide
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1223

Query Match 21.7%; Score 25; DB 7; Length 18;
Best Local Similarity 57.1%; Pred. No. 3.2e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTNI 8
DB 6 VHHPPNI 12

RESULT 78
US-10-485-788A-580
/ Sequence 580, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Schweitzer, Johannes
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Arbor Vita Corporation
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-003320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ PRIOR FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: Patentin version 3.1
/ SEQ ID NO: 580
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-485-788A-580

Query Match 21.7%; Score 25; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNI 8
DB 1 HPTDI 5

RESULT 79
US-11-022-562-141
/ Sequence 141, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
/ FILE REFERENCE: DFN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22


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; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 141
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-141

Query Match          21.7%; Score 25; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 LVCESVN 18
Db      12 LVCEQGN 18

RESULT 80
US-11-022-562-142
; Sequence 142, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Rudrecht, Ruth M.
; APPLICANT: Shisong, Jlang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; CURRENT FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 142
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-142

Query Match          21.7%; Score 25; DB 7; Length 20;
Best Local Similarity 71.4%; Pred. No. 3.6e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      12 LVCESVN 18
Db      2 LVCEQGN 8

RESULT 81
US-11-064-416-4
; Sequence 4, Application US/11064416
; Publication No. US20060008461A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Vatsin, Milton B
; APPLICANT: Stowell, Michael HB
; APPLICANT: Gillicchio, Vincent S
; APPLICANT: Meredith, Michael J
; TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING
; FILE REFERENCE: 899-71532
; CURRENT APPLICATION NUMBER: US/11/064,416
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 10/050,271
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/573,497
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 09/060,011
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; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 08/691,891
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/441,770
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: 08/246,941
; PRIOR FILING DATE: 1994-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 4
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide linker
US-11-064-416-4

Query Match          20.9%; Score 24; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 YLVC 14
Db      5 YLVC 8

RESULT 82
US-11-064-416-5
; Sequence 5, Application US/11064416
; Publication No. US20060008461A1
; GENERAL INFORMATION:
; APPLICANT: Oregon Health & Science University
; APPLICANT: Vatsin, Milton B
; APPLICANT: Stowell, Michael HB
; APPLICANT: Gillicchio, Vincent S
; APPLICANT: Meredith, Michael J
; TITLE OF INVENTION: MICROPARTICLE-DRUG CONJUGATES FOR BIOLOGICAL TARGETING
; FILE REFERENCE: 899-71532
; CURRENT APPLICATION NUMBER: US/11/064,416
; CURRENT FILING DATE: 2005-02-22
; PRIOR APPLICATION NUMBER: 10/050,271
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 09/573,497
; PRIOR FILING DATE: 2000-05-16
; PRIOR APPLICATION NUMBER: 09/060,011
; PRIOR FILING DATE: 1998-04-14
; PRIOR APPLICATION NUMBER: 08/691,891
; PRIOR FILING DATE: 1996-08-01
; PRIOR APPLICATION NUMBER: 08/441,770
; PRIOR FILING DATE: 1995-05-16
; PRIOR APPLICATION NUMBER: 08/246,941
; PRIOR FILING DATE: 1994-05-19
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 5
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: peptide linker
US-11-064-416-5

Query Match          20.9%; Score 24; DB 7; Length 8;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      11 YLVC 14
Db      4 YLVC 7

RESULT 83
US-10-966-483-14
```

/ Sequence 14, Application US/10966483
/ Publication No. US20050281783A1
/ GENERAL INFORMATION:
/ APPLICANT: Kirsch, Michael S.
/ APPLICANT: Kiemer, Peter A.
/ APPLICANT: Bruckheimer, Elizabeth
/ APPLICANT: Dubensky, Jr. Thomas W.
/ APPLICANT: Cook, David N.
/ TITLE OF INVENTION: LISTERIA-BASED BphA2 VACCINES
/ FILE REFERENCE: 10271-146
/ CURRENT APPLICATION NUMBER: US/10/966,483
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,919
/ PRIOR FILING DATE: 2003-10-15
/ PRIOR APPLICATION NUMBER: US 60/511,719
/ PRIOR FILING DATE: 2003-10-15
/ PRIOR APPLICATION NUMBER: US 60/532,666
/ PRIOR FILING DATE: 2003-12-24
/ PRIOR APPLICATION NUMBER: US 60/556,631
/ PRIOR FILING DATE: 2004-03-26
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE: 2004-10-01
/ PRIOR APPLICATION NUMBER:
/ PRIOR FILING DATE: 2004-10-07
/ NUMBER OF SEQ ID NOS: 72
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 14
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-966-483-14

Query Match 20.9%; Score 24; DB 6; Length 9;
Best Local Similarity 44.4%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 11 YVCSVNG 19
| | | | |
| : : : : |
Db 1 YSVCMVMSG 9

RESULT 84
US-10-614-599-26
/ Sequence 26, Application US/10614599
/ Publication No. US20050250178A1
/ GENERAL INFORMATION:
/ APPLICANT: ANDREW, DAVID P.
/ APPLICANT: LEWIN, DAVID A.
/ APPLICANT: PENNICA, DIANE
/ APPLICANT: RASTELLI, LUCA
/ APPLICANT: TALLON, BRUCE
/ TITLE OF INVENTION: WNT-REGULATED CYTOKINE-LIKE POLYPEPTIDE AND NUCLEIC
/ FILE REFERENCE: 09800080-0104
/ CURRENT APPLICATION NUMBER: US/10/614,599
/ CURRENT FILING DATE: 2003-07-07
/ PRIOR APPLICATION NUMBER: 09/715,747
/ PRIOR FILING DATE: 2000-11-17
/ PRIOR APPLICATION NUMBER: 09/715,418
/ PRIOR FILING DATE: 2000-11-16
/ PRIOR APPLICATION NUMBER: 60/166,177
/ PRIOR FILING DATE: 1999-11-18
/ NUMBER OF SEQ ID NOS: 48
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 26
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Unknown Organism
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Membrane attack
US-10-614-599-26

Query Match 20.9%; Score 24; DB 6; Length 10;
Best Local Similarity 57.1%; Pred. No. 2.6e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 NIKTLY 13
| | | | |
| : : : : |
Db 3 NFHQYSV 9

RESULT 85
US-10-929-988-102
/ Sequence 102, Application US/10929988
/ Publication No. US20050277588A1
/ GENERAL INFORMATION:
/ APPLICANT: CMIRLA, STEVEN E.
/ APPLICANT: BALU, PALANI
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: PIPLANI, SONILA
/ APPLICANT: MERRILL, BARBARA MCBOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ CURRENT FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 102
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-102

Query Match 20.9%; Score 24; DB 6; Length 11;
Best Local Similarity 57.1%; Pred. No. 2.8e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CESVNG 20
| | | | |
| : : : : |
Db 1 CEQSNMG 7

RESULT 86
US-10-966-371-7
/ Sequence 7, Application US/10966371
/ Publication No. US20050250692A1
/ GENERAL INFORMATION:
/ APPLICANT: Huang, Jung San
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING CELL PROLIFERATION
/ FILE REFERENCE: SLU 03-006 US
/ CURRENT APPLICATION NUMBER: US/10/966,371
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: US 60/512,516
/ PRIOR FILING DATE: 2003-10-17
/ NUMBER OF SEQ ID NOS: 23
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 7
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-966-371-7

Query Match 20.9%; Score 24; DB 6; Length 12;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIFHP 5

Db 7 DIEHP 11

RESULT 87

US-11-180-997-5
 / Sequence 5, Application US/11180997
 / Publication No. US20050250150A1
 / GENERAL INFORMATION:
 / APPLICANT: Akzo Nobel Patent Department
 / TITLE OF INVENTION: Lawsonia Intracellularis Vaccine
 / FILE REFERENCE: 2000.605
 / CURRENT APPLICATION NUMBER: US/11/180,997
 / CURRENT FILING DATE: 2005-07-13
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 5
 / LENGTH: 12
 / TYPE: PRT
 / ORGANISM: Lawsonia Intracellularis
 US-11-180-997-5

Query Match 20.9%; Score 24; DB 7; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 HKYLVCESVN 18
 : : : : :
 Db 3 YETLVMLGVN 12

RESULT 88

US-11-180-997-19
 / Sequence 19, Application US/11180997
 / Publication No. US20050250150A1
 / GENERAL INFORMATION:
 / APPLICANT: Akzo Nobel Patent Department
 / TITLE OF INVENTION: Lawsonia Intracellularis Vaccine
 / FILE REFERENCE: 2000.605
 / CURRENT APPLICATION NUMBER: US/11/180,997
 / CURRENT FILING DATE: 2005-07-13
 / NUMBER OF SEQ ID NOS: 32
 / SOFTWARE: PatentIn version 3.2
 / SEQ ID NO 19
 / LENGTH: 12
 / TYPE: PRT
 / ORGANISM: Lawsonia Intracellularis
 US-11-180-997-19

Query Match 20.9%; Score 24; DB 7; Length 12;
 Best Local Similarity 50.0%; Pred. No. 3.1e+02;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 9 HKYLVCESVN 18
 : : : : :
 Db 3 YETLVMLGVN 12

RESULT 89

US-10-939-890-44
 / Sequence 44, Application US/1093890
 / Publication No. US20050250700A1
 / GENERAL INFORMATION:
 / APPLICANT: Sato, Aaron K.
 / APPLICANT: Sexton, Daniel J.
 / APPLICANT: Dransfield, Daniel T.
 / APPLICANT: Ledner, Robert C.
 / APPLICANT: Arbogast, Christophe
 / APPLICANT: Bussac, Philippe
 / APPLICANT: Fan, Hong
 / APPLICANT: Khurana, Sucha
 / APPLICANT: Lindner, Karen B.
 / APPLICANT: Marinelli, Edmund R.

/ APPLICANT: Nanjappan, Palaniappa
 / APPLICANT: Nunn, Adrian D.
 / APPLICANT: Pillai, Radhakrishna
 / APPLICANT: Pochon, Sibylle
 / APPLICANT: Ramalingam, Kondaredidhar
 / APPLICANT: Shrivastava, Ajay
 / APPLICANT: Song, Bo
 / APPLICANT: Swenson, Rolf R.
 / APPLICANT: Von Wronski, Mathew A.

/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
 / FILE REFERENCE: D0617.70014US00
 / CURRENT APPLICATION NUMBER: US/10/939,890
 / CURRENT FILING DATE: 2004-09-13
 / PRIOR APPLICATION NUMBER: US 10/661,156
 / PRIOR FILING DATE: 2003-09-11
 / PRIOR APPLICATION NUMBER: US 10/382,082
 / PRIOR FILING DATE: 2003-03-03
 / PRIOR APPLICATION NUMBER: PCT/US03/06731
 / PRIOR FILING DATE: 2003-03-03
 / PRIOR APPLICATION NUMBER: US 60/440,411
 / PRIOR FILING DATE: 2003-01-15
 / PRIOR APPLICATION NUMBER: US 60/360,851
 / PRIOR FILING DATE: 2002-03-01
 / NUMBER OF SEQ ID NOS: 883
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 44
 / LENGTH: 14
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Library Isolate
 US-10-939-890-44

Query Match 20.9%; Score 24; DB 6; Length 14;
 Best Local Similarity 33.3%; Pred. No. 3.6e+02;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 11 YLVCESVNG 19
 : : : : :
 Db 1 WIGQNSITG 9

RESULT 90

US-11-033-039-1428
 / Sequence 1428, Application US/11033039
 / Publication No. US20060002947A1
 / GENERAL INFORMATION:
 / APPLICANT: HUMPHREYS, ROBERT
 / APPLICANT: XU, MINZHEN
 / TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIPTOPES HYBRID PEPTIDE VACCINES
 / FILE REFERENCE: REH-2017US01
 / CURRENT APPLICATION NUMBER: US/11/033,039
 / CURRENT FILING DATE: 2005-01-11
 / PRIOR APPLICATION NUMBER: 10/245,871
 / PRIOR FILING DATE: 2002-09-17
 / PRIOR APPLICATION NUMBER: 10/197,000
 / PRIOR FILING DATE: 2002-07-17
 / PRIOR APPLICATION NUMBER: 09/396,813
 / PRIOR FILING DATE: 1999-09-14
 / NUMBER OF SEQ ID NOS: 1452
 / SOFTWARE: PatentIn version 3.3
 / SEQ ID NO 1428
 / LENGTH: 16
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 / OTHER INFORMATION: hybrid peptide
 US-11-033-039-1428

Query Match 20.9%; Score 24; DB 7; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.2e+02;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14
|||
Db 5 YLVC 8

RESULT 91
US-11-033-039-1427
; Sequence 1427, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1427
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1427

Query Match 20.9%; Score 24; DB 7; Length 17;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14
|||
Db 6 YLVC 9

RESULT 92
US-11-041-893-132
; Sequence 132, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahaitas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PatSeq for Windows Version 4.0
; SEQ ID NO 132
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Epstein Barr virus
US-11-041-893-132

Query Match 20.9%; Score 24; DB 7; Length 17;
Best Local Similarity 75.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 2 LPH 5
|||
Db 12 LPH 15

RESULT 93
US-11-033-039-1426
; Sequence 1426, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1426
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (5)..(5)
; OTHER INFORMATION: Ava
US-11-033-039-1426

Query Match 20.9%; Score 24; DB 7; Length 18;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14
|||
Db 7 YLVC 10

RESULT 94
US-11-033-039-1425
; Sequence 1425, Application US/11033039
; Publication No. US20060002947A1
; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: REH-2017US01
; CURRENT APPLICATION NUMBER: US/11/033,039
; CURRENT FILING DATE: 2005-01-11
; PRIOR APPLICATION NUMBER: 10/245,871
; PRIOR FILING DATE: 2002-09-17
; PRIOR APPLICATION NUMBER: 10/197,000
; PRIOR FILING DATE: 2002-07-17
; PRIOR APPLICATION NUMBER: 09/396,813
; PRIOR FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 1452
; SOFTWARE: Patentin version 3.3
; SEQ ID NO 1425
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: hybrid peptide

Query Match 20.9%; Score 24; DB 7; Length 19;
Best Local Similarity 75.0%; Pred. No. 4.7e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)-(5)
OTHER INFORMATION: Ava
US-11-033-039-1423

Query Match 20.9%; Score 24; DB 7; Length 19;
Best Local Similarity 100.0%; Pred. No. 5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14
DB 8 YLVC 11

RESULT 95
US-10-623-155-514
Sequence 514, Application US/10623155
Publication No. US20050261166A1
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Beckham, David W.
APPLICANT: Reiter, Marc W.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C20
CURRENT APPLICATION NUMBER: US/10/623.155
CURRENT FILING DATE: 2003-07-17
NUMBER OF SEQ ID NOS: 560
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 514
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-623-155-514

Query Match 20.9%; Score 24; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVN 18
DB 11 CEQVN 15

RESULT 96
US-11-022-562-173
Sequence 173, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shiobong, Jiansg
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DPN-043CN
CURRENT APPLICATION NUMBER: US/11/022.562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 173
LENGTH: 20
TYPE: PRT
ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-173

Query Match 20.9%; Score 24; DB 7; Length 20;
Best Local Similarity 42.9%; Pred. No. 5.2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNHRX 11
DB 9 PTDVRY 15

RESULT 97
US-11-033-039-1424
Sequence 1424, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-201US01
CURRENT APPLICATION NUMBER: US/11/033.039
CURRENT FILING DATE: 2005-01-11
PRIOR APPLICATION NUMBER: 10/245.871
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/197.000
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396.813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1424
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: hybrid peptide
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (5)-(5)
OTHER INFORMATION: Ava
US-11-033-039-1424

Query Match 20.9%; Score 24; DB 7; Length 20;
Best Local Similarity 100.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14
DB 9 YLVC 12

RESULT 98
US-11-226-701-28
Sequence 28, Application US/11226701
Publication No. US20060009632A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Kaplaner-Libermann, Rosana
APPLICANT: Robison, Keith E.
APPLICANT: White, David
APPLICANT: Williamson, Mark W.
APPLICANT: Cook, William James
APPLICANT: Meyers, Rachel E.
APPLICANT: Macbeth, Kyle J.
APPLICANT: Carroll, Joseph M.
APPLICANT: Chun, Miyoung
TITLE OF INVENTION: NOVEL 27875, 22025, 27420, 17906, 16319,
TITLE OF INVENTION: 55092 AND 10218 MOLECULES AND USES THEREFOR
FILE REFERENCE: MP103-0210NMIM
CURRENT APPLICATION NUMBER: US/11/226.701
CURRENT FILING DATE: 2005-09-14
PRIOR APPLICATION NUMBER: US/10/386.414
PRIOR FILING DATE: 2003-03-11
PRIOR APPLICATION NUMBER: 09/426.282
PRIOR FILING DATE: 1999-10-25
PRIOR APPLICATION NUMBER: 09/668.266
PRIOR FILING DATE: 2000-09-22

```
/ PRIOR APPLICATION NUMBER: 09/330,970
/ PRIOR FILING DATE: 1999-06-11
/ PRIOR APPLICATION NUMBER: 09/724,599
/ PRIOR FILING DATE: 2000-11-28
/ PRIOR APPLICATION NUMBER: 09/860,193
/ PRIOR FILING DATE: 2001-05-16
/ PRIOR APPLICATION NUMBER: 09/571,689
/ PRIOR FILING DATE: 2000-05-16
/ PRIOR APPLICATION NUMBER: 10/283,023
/ PRIOR FILING DATE: 2002-10-29
/ PRIOR APPLICATION NUMBER: 60/335,044
/ PRIOR FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 10/010,943
/ PRIOR FILING DATE: 2001-12-06
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 28
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 28
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Catalytic signature
US-11-226-701-28

Query Match          20.0%; Score 23; DB 7; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY 1 DHPHP 5
   |  |
Db 2 DVDHP 6

RESULT 99
US-11-140-417-18
/ Sequence 18, Application US/11140417
/ Publication No. US20050266515A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Brien, Deborah A
/ APPLICANT: Eddy, Edward M
/ TITLE OF INVENTION: GLYCERALDEHYDE 3-PHOSPHATE DEHYDROGENASE-S (GAPDS), A GLYCOLYTIC
/ TITLE OF INVENTION: ENZYME EXPRESSED ONLY IN MALE GERM CELLS, IS A TARGET FOR MALE
/ FILE REFERENCE: 421/76/2 PCT/CIP
/ CURRENT APPLICATION NUMBER: US/11/140,417
/ CURRENT FILING DATE: 2005-05-27
/ PRIOR APPLICATION NUMBER: US 60/429,638
/ PRIOR FILING DATE: 2002-11-27
/ PRIOR APPLICATION NUMBER: PCT/US2003/037800
/ PRIOR FILING DATE: 2003-11-26
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 18
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-140-417-18
```

```
Query Match          20.0%; Score 23; DB 7; Length 8;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 TNNHKY 11
   |  |
Db 2 TTVHSY 7
```

```
RESULT 100
US-11-108-135-8
/ Sequence 8, Application US/11108135
/ Publication No. US20050260213A1
/ GENERAL INFORMATION:
```

```
/ APPLICANT: Koenig, Scott
/ APPLICANT: Veri, Maria Concetta
/ APPLICANT: Thuillon, Nadine
/ APPLICANT: Bonvini, Ezio
/ APPLICANT: Stavenhagen, Jeffrey
/ APPLICANT: Rankin, Christopher
/ TITLE OF INVENTION: P $\gamma$ -gamma-RiIB-specific antibodies and methods of use thereof
/ FILE REFERENCE: 11183-014-999
/ CURRENT APPLICATION NUMBER: US/11/108,135
/ CURRENT FILING DATE: 2005-04-15
/ PRIOR APPLICATION NUMBER: US 60/562,804
/ PRIOR FILING DATE: 2004-04-16
/ PRIOR APPLICATION NUMBER: US 60/582,044
/ PRIOR FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: US 60/582,045
/ PRIOR FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: US 60/654,713
/ PRIOR FILING DATE: 2005-02-18
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 8
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: 286 Light chain variable region - CDRI
US-11-108-135-8

Query Match          20.0%; Score 23; DB 7; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 6 TNNH 9
   |  |
Db 8 TNNH 11
```

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Search completed: January 20, 2006, 19:46:29
Job time : 9.07692 secs
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 ; Search time 11.3462 Seconds
(without alignments)
169.602 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115
Sequence: 1 DHPPTNHHKYLVCBSVNGG 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: PIR 80: *
2: p1r1: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the target being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	38	33.0	15	2 A60929	dichloromethane de
2	38	33.0	15	2 B60929	dichloromethane de
3	27	23.5	11	2 S42587	cell protein - Esc
4	27	23.5	18	2 H64711	hypothetical prote
5	26	22.6	18	2 S65454	aspergillopepsin I
6	25.5	22.2	16	2 S55307	glutathione transf
7	25	21.7	19	2 PQ0548	capsid protein VP2
8	25	21.7	20	2 D84716	hypothetical prote
9	24	20.9	9	2 A60108	exotoxin A - Strept
10	24	20.9	9	2 S10920	venom protein HR-3
11	24	20.9	17	2 S15778	insulin chain B -
12	24	20.9	18	2 S29264	ovomethionin - d
13	24	20.9	18	2 PN0175	glutathione transf
14	24	20.9	19	2 I50153	alpha-actin - chic
15	24	20.9	20	2 A45655	Crotalus atrox ser
16	23	20.0	10	2 PH0925	T-cell receptor be
17	23	20.0	10	2 C60787	sperm-activating p
18	23	20.0	13	2 S38736	lipid transfer pro
19	23	20.0	13	2 A08416	isomaltase kinase
20	23	20.0	16	2 PH1604	Ig H chain V-D-J r
21	23	20.0	17	2 S15754	actin 6 - soybean
22	23	20.0	17	2 S63503	83K protein - Bub
23	23	20.0	18	2 A58589	alpha-conotoxin R1
24	22.5	19.6	20	2 A48394	major fec-globule
25	22	19.1	10	2 B59272	peptide-N4-(N-acet
26	22	19.1	10	2 B37196	bradykinin-potent
27	22	19.1	11	2 B60409	kassinin-like pept
28	22	19.1	11	2 D60409	kassinin-like pept
29	22	19.1	13	2 B47415	mannose-1-phosphat

30	22	19.1	13	2 PH0788	T-cell receptor al
31	22	19.1	15	2 S60007	glial hyaluronate-
32	22	19.1	15	2 B56046	urinary tract ston
33	22	19.1	16	2 S00123	dihydroilipamide S
34	22	19.1	16	2 A41170	photosystem II 6.1
35	22	19.1	16	2 A11488	taurocyamine kinase
36	22	19.1	17	2 S59512	probable integrin
37	22	19.1	18	2 B48839	T-cell receptor be
38	22	19.1	19	2 D44101	calmodulin, vasocac
39	22	19.1	20	2 A38566	GTP-binding protei
40	22	19.1	20	2 T50757	pufK protein [limp
41	21	18.3	9	2 A57444	neuropeptide Grb-A
42	21	18.3	11	2 PH0947	T-cell receptor be
43	21	18.3	12	2 A54315	entactin/nidogen -
44	21	18.3	12	2 B47171	chondroitin sulfat
45	21	18.3	13	2 A54326	glanular kallikre
46	21	18.3	14	2 S41601	interferon alpha r
47	21	18.3	15	2 PQ0232	cystatin Cr-4a - m
48	21	18.3	15	2 A56786	pimefolyl-CoA synth
49	21	18.3	15	2 PH0136	T-cell receptor be
50	21	18.3	16	2 C59045	alpha-conotoxin Au
51	21	18.3	17	2 S15064	T-cell receptor be
52	21	18.3	17	2 C49255	hypothetical prote
53	21	18.3	18	2 PQ0680	photosystem I 5.6k
54	21	18.3	18	2 S20322	gluten - wheat
55	21	18.3	20	2 A24589	photosystem II chl
56	21	18.3	20	2 A60100	limbal antigen C
57	21	18.3	20	2 S18582	hypothetical prote
58	21	18.3	20	2 C56894	intracrySTALLINE c
59	21	18.3	20	2 B56894	intracrySTALLINE c
60	21	18.3	20	2 S44465	pyrrolic acid - Py
61	21	18.3	20	2 AB0120	insertion element
62	21	17.4	10	2 PH0944	T-cell receptor be
63	20	17.4	10	2 G60527	sperm-activating p
64	20	17.4	11	2 PA0028	protein OA300042 -
65	20	17.4	11	2 PH1375	T antigen variant
66	20	17.4	11	2 PH1376	T antigen variant
67	20	17.4	12	1 LFRCP8	pyr leader peptid
68	20	17.4	13	2 S47383	T-cell antigen rec
69	20	17.4	14	2 S48685	extension protein
70	20	17.4	15	2 S08209	hypothetical prote
71	20	17.4	15	2 PH1610	Ig H chain V-D-J r
72	20	17.4	15	2 PH0779	T-cell receptor al
73	20	17.4	15	2 PT0096	pyruvate dehydroge
74	20	17.4	17	2 PH1789	T-cell receptor al
75	20	17.4	18	2 PL0025	T-cell surface gly
76	20	17.4	19	2 S29167	guinaldine oxidore
77	20	17.4	19	2 PT0332	Ig heavy chain CRD
78	20	17.4	19	2 PH1352	Ig heavy chain DJ
79	20	17.4	19	2 D49404	T-cell receptor be
80	20	17.4	19	2 PQ0409	RNA-directed RNA p
81	20	17.4	20	2 PX0042	venom B (EC 3.4
82	20	17.4	20	2 S68028	iodochronine 5'-mo
83	20	17.4	20	2 B38382	15K protein B - ra
84	20	17.4	20	2 S03954	acidic fibroblast
85	19.5	17.0	14	2 A58963	alpha-conotoxin Cn
86	19.5	17.0	19	2 C32735	chrysoglobulin - pi
87	19.5	17.0	19	2 B32735	chrysoglobulin - sh
88	19.5	17.0	19	2 A34233	trehalase inhibito
89	19	16.5	9	2 S55696	phosphoenolpyruvat
90	19	16.5	9	2 B57444	neuropeptide Grb-A
91	19	16.5	10	2 S77980	cytochrome-c oxida
92	19	16.5	10	2 C60527	sperm-activating p
93	19	16.5	10	2 S6527	sperm-activating p
94	19	16.5	10	2 C60788	sperm-activating p
95	19	16.5	10	2 A60527	sperm-activating p
96	19	16.5	10	2 A60787	sperm-activating p
97	19	16.5	11	2 B49164	chromogranin-B - r
98	19	16.5	11	2 A26930	ermg leader peptid
99	19	16.5	13	2 S15755	actin 7 - soybean
100	19	16.5	2	2 PT0290	Ig heavy chain CRD

ALIGNMENTS

RESULT 1

A60929

dichloromethane dehalogenase (EC 4.5.1.3) - *Hyphomicrobium* sp. (ATCC 43129) (fragment)
 C/Species: Hyphomicrobium sp.

C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004

C/Accession: A60929

R/Kohler-Staud, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.

J. Gen. Microbiol. 132, 2837-2843, 1986

A/Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic

A/Reference number: A60929

A/Accession: A60929

A/Molecule type: protein

A/Residues: 1-15 <KOH>

A/Cross-references: UNIPROT:Q7M134; UNIPARC:UPI000017A8F8

C/Keywords: carbon-halide lyase

Query Match

Best Local Similarity 33.0%; Score 38; DB 2; Length 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNTH 9
 |:|||||

DB 3 PHPTNTH 9

RESULT 2

B60929

dichloromethane dehalogenase (EC 4.5.1.3) - *Pseudomonas* sp. (fragment)
 C/Species: Pseudomonas sp.

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: B60929

R/Kohler-Staud, D.; Hartmann, S.; Gaelli, R.; Suter, F.; Leisinger, T.

J. Gen. Microbiol. 132, 2837-2843, 1986

A/Title: Evidence for identical dichloromethane dehalogenases in different methylotrophic

A/Reference number: A60929

A/Contents: DSM 1565

A/Accession: B60929

A/Molecule type: protein

A/Residues: 1-15 <KOH>

A/Cross-references: UNIPROT:Q7M126; UNIPARC:UPI000017A8F8

C/Keywords: carbon-halide lyase

Query Match

Best Local Similarity 33.0%; Score 38; DB 2; Length 15;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPTNTH 9
 |:|||||

DB 3 PHPTNTH 9

RESULT 3

S42587

celF protein - *Escherichia coli* (fragment)
 C/Species: Escherichia coli

C/Date: 25-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995

C/Accession: S42587

R/Guzzo, A.; Dubow, M.S.

Mol. Gen. Genet. 242, 455-460, 1994

A/Title: A luxAB transcriptional fusion to the cryptic celF gene of *Escherichia coli* dis

A/Reference number: S42587; MUID:94166755; PMID:8121401

A/Accession: S42587

A/Molecule type: DNA

A/Residues: 1-11 <GUZ>

A/Cross-references: UNIPARC:UPI000017AA33

C/Genetics: celF

Query Match

Best Local Similarity 23.5%; Score 27; DB 2; Length 11;
 Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 PHPTN 7
 |||||

DB 7 PHPRN 11

RESULT 4

H64711

hypothetical protein HP1536 - *Helicobacter pylori* (strain 26695)
 C/Species: Helicobacter pylori

C/Date: 09-Aug-1997 #sequence_revision 09-Aug-1997 #text_change 09-Jul-2004

C/Accession: H64711

R/Tomb, J.F.; White, O.; Kervaseg, A.R.; Clayton, R.A.; Sutton, G.G.; Fleischmann, R.D.

Peterson, S.; Loftus, B.; Richardson, D.; Dodson, R.; Khalak, H.G.; Glodek, A.; McKen

son, J.D.; Kelley, J.M.; Cotton, M.D.; Weidman, J.M.; Fujii, C.; Bowman, C.; Watney, L.

Nature 388, 539-547, 1997

A/Authors: Wallin, E.; Hayes, W.S.; Borodovsky, M.; Karpe, P.D.; Smith, H.O.; Fraser, C.

A/Title: The complete genome sequence of the gastric pathogen *Helicobacter pylori*.

A/Reference number: A64520; MUID:97394467; PMID:9252185

A/Accession: H64711

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-18 <TOM>

A/Cross-references: UNIPROT:026062; UNIPARC:UPI00000C07C3; GB:AE000651; GB:AE000511; NID

Query Match 23.5%; Score 27; DB 2; Length 18;
 Best Local Similarity 55.6%; Pred. No. 8.7e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNTHKL 12
 ||:||||

DB 10 HPSRNPRTL 18

RESULT 5

S65454

aspergillopepsin I (EC 3.4.23.18) - *Aspergillus niger* (fragments)
 N/Alternate names: aspergillopepsinogen I

C/Species: Aspergillus niger

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C/Accession: S65454

R/Linco, H.; Hayashi, T.; Huang, X.P.; Lu, J.F.; Athauda, S.B.P.; Kong, K.H.; Yamagata,

Eur. J. Biochem. 237, 719-725, 1996

A/Title: Heterologous expression and site-directed mutagenesis studies on the activator

A/Reference number: S65454; MUID:96235238; PMID:8647118

A/Accession: S65454

A/Molecule type: protein

A/Residues: 1-5;6-10;11-18 <TNO>

A/Cross-references: UNIPARC:UPI000017B3BC; UNIPARC:UPI000017B3BD; UNIPARC:UPI000017B3BE

A/Experimental source: strain var. macrosporus

C/Keywords: aspartic proteinase; hydrolase

Query Match 22.6%; Score 26; DB 2; Length 18;
 Best Local Similarity 44.4%; Pred. No. 1.2e+03;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 3 PHPTNTHK 11
 ||:||||

DB 2 PAPTSLAKF 10

RESULT 6

S55307

glutathione transferase 3-3 - rat (fragments)
 C/Species: Rattus norvegicus (Norway rat)

C/Date: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

C/Accession: S55307

R/Cooke, R.U.; Bjornestedt, R.; Douglas, K.T.; McKie, J.H.; King, M.D.; Coles, B.; Ket

Biochem. J. 302, 383-390, 1994

A/Title: Photoaffinity labelling of the active site of the rat glutathione transferases

A/Reference number: S55307; MUID:94379965; PMID:8092989

A/Accession: S55307

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <COO>
A/Cross-references: UNIPARC:UPI000017C91B

Query Match	22.2%	Score 25.5; DB 2;	length 16;
Best Local Similarity	42.9%	Pred. No. 1.3e+03	
Matches	6; Conservative	2; Mismatches	3; Indels 3; Gaps 1;
Qy	2 IHPHNT--HKYL 12		
	:		
Db	2 LHPSQIMRFEXYL 15		

RESULT 7
 PQ0548
 capsid protein VP26 - human herpesvirus 1 (fragment)
 C|Species: human herpesvirus 1
 C|Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C|Accession: PQ0548
 R|Davison, M.D., Rixon, F.J., Davison, A.J.
 J. Gen. Virol. 73, 2709-2713, 1992
 A|Title: Identification of genes encoding two capsid proteins (VP24 and VP26) of herpes
 A|Reference number: PQ0544; MUID:93019027; PMID:1328483
 A|Accession: PQ0548
 A|Molecule type: protein
 A|Residues: 1-19 <DAV>
 A|Cross-references: UNIPROT:Q7L2W5; UNIPARC:UPI000017A7C9
 A|Experimental source: strain 17
 C|Genetics:
 A|Gene: UL35
 C|Keywords: capsid protein

Query Match	21.7%	Score 25;	DB 2;	length 19;
Best Local Similarity	80.0%	Pred. No. 1.9e+03;		
Matches	4;	Conservative	0;	Mismatches 1;
				Indels 0;
				Gaps 0;
Qy	1	DHPH	5	
Db	11	DHPH	15	

RESULT 8
D84716
hypochemical protein At2g31090 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: D84716
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Bento, M.I.; Town, C.D.; Fujii, C.Y.;
Wu, J.; Koo, H.; Moffett, K.B.; Cronin, L.A.; Shen, M.; Vankken, S.B.; Umayam, L.; Tallon, L.
Eaus, D.; Niekman, W.C.; White, O.; Riesen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: AB4420; MUID:20083487; PMID:10617197
A:Accession: D84716
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-20 <STC>
A:Cross-references: UNIPROT:O82275; UNIPARC:UP1000017A6CB; GB:AE002093; NID:G3746066; PIR:
C:Genetics:
A:Gene: At2g31090
A:Map position: 2

Query Match	21.7%	Score 25;	DB 2;	Length 20;
Best Local Similarity	50.0%	Pred. No. 2e+03;		
Matches 4;	Conservative 2;	Mismatches 2;	Indels 0;	Gaps 0;

RESULT 9

A60108
exotoxin A - Streptococcus pyogenes (strain C203.S) (fragment)
N|Alternative names: blastogen A/ scarlet fever toxin
C|Species: Streptococcus pyogenes
C|date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 31-Dec-2004
R|Accession: A60108
R|Schlievert, P.M.; Gray, E.D.
Infect. Immun. 57, 1865-1867, 1989
A|Title: Group A streptococcal pyrogenic exotoxin (scarlet fever toxin) type A and blas
A|Reference number: A60108; MUID:89254013; PMID:2498210
A|Accession: A60108
A|Molecule type: protein
A|Molecular weight: 1-9 <SCH>
A|Cross-references: UNIPROT:Q54779; UNIPROT:P97163; UNIPROT:Q9R931; UNIPROT:Q57453; UNI
C|Superfamily: enterotoxin B
C|Keywords: exotoxin

Query Match	20.9%	Score 24;	DB 2;	Length 9;
Best Local Similarity	42.9%	Pred. No. 2.8e+05;		
Matches	3;	Conservative	2;	Mismatches 2;
				Indels 0;
				Gaps 0;
QY	3	PHPTNIH	9	
			:	
			:	
Db	3	PDPSQLH	9	

```

RESULT 10
S10920
venom protein HR-3 - oriental hornet (fragment)
C:Species: Vespa orientalis (oriental hornet)
C:Date: 29-Jan-1993 #sequence_revision 29-Jan-1993 #text_change 09-Jul-2004
C:Accession: S10920
R:Tutchaev, M.U.; Akhmedova, N.U.; Kazakov, I.; Korneev, A.S.; Gagel'gans, A.I.
Biochemistry (N.Y.) 53, 183-190, 1988
A:Title: Low-molecular-weight peptides of venom of the giant hornet Vespa orientalis. S
A:Reference number: S06445
A:Accession: S10920
A:Molecule type: protein
A:Residues: 1-9 <TUI>
A:Cross-references: UNIPROT:Q7M471; UNIPARC:UPI000017BF07
:Keywords: venom

```

Query Match	20.9%	Score 24	DB 24	Length 9
Best Local Similarity	42.9%	Pred. No. 2.8e+05		
Matches	3	Conservative	4	Mismatches 0
				Indels 0
				Gaps 0
Qy	7	NIKKIV	13	
	:	: : :		
	:	: : :		
db	2	SVHPELV	8	

```

RESULT 11
S15778
insulin chain B - bovine (fragments)
C|Species: Bos primigenius indicus x Bos primigenius taurus (cattle)
C|Date: 19-Mar-1997 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C|Accession: S15778; S15779
R|Bergman, T.; Agerberth, B.; Joernvall, H.
FEBS Lett. 283, 100-103, 1991
A|Title: Direct analysis of peptides and amino acids from capillary electrophoresis
A|Reference number: S15778; MUID:91243852; PMID:2037061
A|Accession: S15778
A|Status: preliminary
A|Molecule type: protein
A|Residues: 1-8 <FEB1>
A|Cross-references: UNIPARC:UPI000015BC0B
A|Accession: S15779
A|Status: preliminary
A|Molecule type: protein
A|Residues: 9-17 <FEB2>
A|Cross-references: UNIPARC:UPI000015BC0B
C|Superfamily: Insulin
C|Keywords: hormone; pancreas

```

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 100.0%; Pred. No. 2.4e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 YLVC 14
| | | |
DB 3 YLVC 6

RESULT 12

S29264

ovoheremerythrin - duck leech (fragment)

N/Alternate names: 14k yolk protein

C/Species: Theromyzon tessulatium (duck leech)

C/Date: 19-Mar-1997 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004

C/Accession: S29264

R/Baert, J.L.; Britel, M.; Sautiere, P.; Malecha, J.

Eur. J. Biochem. 209, 563-569, 1992

A/Title: Ovoheremerythrin, a major 14-kDa yolk protein distinct from vitellogenin in leech

A/Reference number: S29264; MUID:93049299; PMID:1425663

A/Accession: S29264

A/Molecule type: protein

A/Residues: 1-18 <BMR>

A/Cross-references: UNIPROT:P80155; UNIPARC:UPI000012C58F; PIDN:AAB23969.1; PID:9258980

C/Keyword: hemerythrin

C/Keyword: egg yolk; oxygen carrier

Query Match 20.9%; Score 24; DB 2; Length 18;
Best Local Similarity 80.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHP 5
| | | |
DB 2 DIPHP 6

RESULT 13

PNO175

glutathione transferase (EC 2.5.1.18) 1 - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 22-Dec-1995 #sequence_revision 08-Feb-1996 #text_change 23-Mar-2001

C/Accession: PNO175

R/Taugita, A.; Kamo, M.; Kawakami, M.; Ohki, Y.

submitted to JIPID, December 1995

A/Description: Two dimensional electrophoresis of plant proteins and standardization of

A/Reference number: PNO173

A/Accession: PNO175

A/Molecule type: protein

A/Residues: 1-18 <RSU>

A/Cross-references: UNIPARC:UPI000017AF59

A/Experimental source: leaf

C/Keyword: transferase

Query Match 20.9%; Score 24; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIPHPNI 8
| | | |
DB 5 DEGHADI 12

RESULT 14

I50153

alpha-actin - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 05-Oct-2004

C/Accession: I50153

R/Chang, K.

Mol. Cell. Biol. 4, 2498-2508, 1984

A/Title: Isolation and characterization of six different chicken actin genes.

A/Reference number: I50153; MUID:85085956; PMID:6513927

A/Accession: I50153

A/Status: preliminary; translated from GB/BMBJ/DBJ

A/Molecule type: DNA

A/Residues: 1-19 <CHA>

A/Cross-references: UNIPROT:Q9PSW6; UNIPARC:UPI00000FB20E; GB:K02258; NID:9211084; PIDN

C/Superfamily: Actin

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.7e+03;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCSVNG 19
| | | | |
DB 10 LVCSVNG 17

RESULT 15

A45655

Crotaus atrox serine proteinase (EC 3.4.21.-) - western diamondback rattlesnake (fragme

N/Alternate names: alpha-fibrinogenase; thrombin-like proteinase

C/Species: Crotaus atrox (western diamondback rattlesnake)

C/Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 09-Jul-2004

C/Accession: A45655

R/Chlou, S.H.; Hung, C.C.; Lin, C.W.

Biochem. Int. 26, 105-112, 1992

A/Title: Isolation of a crotales-like protease with alpha-fibrinogenase activity from c

A/Reference number: A45655; MUID:92313365; PMID:1616487

A/Accession: A45655

A/Molecule type: protein

A/Residues: 1-20 <CHI>

A/Cross-references: UNIPROT:Q9PS55; UNIPARC:UPI00000FB75C

A/Experimental source: venom

A/Note: sequence extracted from NCBI backbone (NCBIP:107297)

C/Superfamily: trypsin; trypsin homology

C/Keyword: hydrolase; serine proteinase; venom

Query Match 20.9%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKKLV 13
| | | | |
DB 10 NEHRFLV 16

RESULT 16

PH0925

T-cell receptor beta chain V-D-J region (isolate 11) - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C/Accession: PH0925

R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A/Reference number: PH0891; MUID:92078857; PMID:1836012

A/Accession: PH0925

A/Molecule type: mRNA

A/Residues: 1-10 <GOL>

A/Cross-references: UNIPARC:UPI000017C9F4

A/Experimental source: concanavalin A-activated lymphoblast

C/Keyword: T-cell receptor

Query Match 20.0%; Score 23; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 CSVANG 20
| | | | |
DB 1 CASSDGG 7

RESULT 17

C60787

sperm-activating peptide (Ser-3,10 speract) - sea urchin (*Hemicentrotus pulcherrimus*)
 C/Species: *Hemicentrotus pulcherrimus*
 C/Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 16-Aug-2004
 C/Accession: C60787
 R/Suzuki, N.; Kajitani, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A/Title: Some more perfect derivatives associated with eggs of sea urchins, *Pseudocentrotus*
 A/Reference number: A60787; MUID:88242184; PMID:3378407
 A/Accession: C60787
 A/Molecule type: Protein
 A/Residues: 1-10 <SD>
 A/Cross-references: UNIPROT:Q7M4D0; UNIPARC:UPI000017A4DC
 C/Comment: This oligopeptide from egg jelly is one of several from this species, all of
 at shows some, but not absolute, species restriction.

Query Match 20.0%; Score 23; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 16 SVNGG 20
 |||||
 3 SLNGG 7

RESULT 18
 S38736
 Lipid transfer protein a1 - *Arabidopsis thaliana* (fragment)
 C/Species: *Arabidopsis thaliana* (mouse-ear cress)
 C/Date: 19-May-1994 #sequence_revision 19-Jan-1996 #text_change 19-Jan-1996
 C/Accession: S38736
 R/Segura, A.; Moreno, M.; Garcia-Olmedo, F.
 FEBS Lett. 332, 243-246, 1993
 A/Title: Purification and antipathogenic activity of lipid transfer proteins (LTPs) from
 A/Reference number: S38736; MUID:94009709; PMID:8405465
 A/Accession: S38736
 A/Molecule type: Protein
 A/Residues: 1-13 <SRG>
 A/Cross-references: UNIPARC:UPI000017AFPC

Query Match 20.0%; Score 23; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 2.6e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 12 LVCSVN 18
 |||||
 2 LSCGSVN 8

RESULT 19
 A08416
 Lumbrikinase (EC 2.7.3.5) - earthworm (*Lumbricus terrestris*) (fragment)
 C/Species: *Lumbricus terrestris* (common earthworm)
 C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
 C/Accession: A08416
 R/der Terrosian, E.; Desverges, G.; Pradel, L.A.; Kasab, R.; van Thoi, N.
 Eur. J. Biochem. 22, 585-592, 1971
 A/Title: Comparative structural studies of the active site of ATP: guanidine phosphotran
 A/Reference number: A08416; MUID:7206544; PMID:5128744
 A/Accession: A08416
 A/Molecule type: Protein
 A/Residues: 1-15 <DBR>
 A/Cross-references: UNIPROT:P11918; UNIPARC:UPI000012DEER
 C/Keywords: phosphotransferase

Query Match 20.0%; Score 23; DB 2; Length 15;
 Best Local Similarity 40.0%; Pred. No. 3e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

OY 11 YLVCSVNGG 20
 |||||
 3 YVCPGSNLG 12

RESULT 20

PH1604
 Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)
 C/Species: *Mus musculus* (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1604
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less m/c
 A/Reference number: PH1580; MUID:93301609; PMID:8315387
 A/Accession: PH1604
 A/Molecule type: DNA
 A/Residues: 1-16 <LEV>
 A/Cross-references: UNIPARC:UPI000017C6C0
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 20.0%; Score 23; DB 2; Length 16;
 Best Local Similarity 44.4%; Pred. No. 3.2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 3 PHEPTNIXY 11
 |||||
 4 PHEWMLHY 12

RESULT 21
 S15754
 actin 6 - soybean (fragment)
 C/Species: *Glycine max* (soybean)
 C/Date: 04-Dec-1992 #sequence_revision 04-Dec-1992 #text_change 05-Oct-2004
 C/Accession: S15754; S08049
 R/Pearson, L.; Meagher, R.B.
 Plant Mol. Biol. 14, 513-526, 1990
 A/Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
 A/Reference number: S15754; MUID:91346640; PMID:2102831
 A/Accession: S15754
 A/Molecule type: DNA
 A/Residues: 1-17 <PBA>
 A/Cross-references: UNIPROT:P15986; UNIPARC:UPI0000125427; EMBL:X17119; NID:G18525; PID

C/Supersfamily: Actin
 C/Keywords: cytoskeleton

Query Match 20.0%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

OY 12 LVCSYNG 19
 |||||
 10 LVCDNGTG 17

RESULT 22
 S63503
 83K protein - *Escherichia acidaminophilum* (fragment)
 C/Species: *Escherichia acidaminophilum*
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C/Accession: S63503
 R/Meyer, M.; Granderath, K.; Andreessen, J.R.
 Eur. J. Biochem. 234, 184-191, 1995
 A/Title: Purification and characterization of protein (PB) of betaine reductase and its
 phylum.
 A/Reference number: S63502; MUID:96096737; PMID:8529639
 A/Accession: S63503
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-17 <MEY>
 A/Cross-references: UNIPARC:UPI000017AD3D

Query Match 20.0%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 3.4e+03;
 Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 7 NIHXYL 12
:::|:|
Db 2 DLHKL 7

RESULT 23

A58589
alpha-conotoxin EI - cone shell (Conus ermineus)
C/Species: Conus ermineus (ermine cone)
C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
C/Accession: A58589
R/Martinez, J.S.; Oliveira, B.M.; Gray, W.R.; Craig, A.G.; Groebe, D.R.; Abramson, S.N.;
Biochemistry 34, 14519-14526, 1995
A/Title: alpha-Conotoxin EI, a new nicotinic acetylcholine receptor antagonist with novel
A/Reference number: A58589; PMID:96062516; PMID:7578057
A/Accession: A58589
A/Molecule type: protein
A/Residues: 1-18 <MAR>
A/Cross-references: UNIPROT:P50982; UNIPARC:UPI00001287C0
A/Note: sequence confirmed by chemical synthesis
C/Comment: This alpha-conotoxin, as an acetylcholine receptor inhibitor, is a postsynaptic
C/Keyword: acetylcholine receptor inhibitor; amidated carboxyl end; hydroxyproline; pro
F/3/Modified site: 4-hydroxyproline (Pro) #status experimental
F/4-10,5-18/Disulfide bonds: #status experimental
F/18/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 19.6%; Score 22.5; DB 1; Length 18;
Best Local Similarity 41.7%; Pred. No. 4.3e+03;
Matches 5; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

RESULT 24

A48394
major fat-globule membrane protein/MGF-R8 homolog - guinea pig (fragment)
C/Species: Cavia porcellus (guinea pig)
C/Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C/Accession: A48394
R/Mather, I.H.; Banghart, L.R.; Lane, W.S.
Biochem. Mol. Biol. Int. 29, 545-554, 1993
A/Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig
11-like sequences.
A/Reference number: A48394; PMID:93250576; PMID:8485470
A/Accession: A48394
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <MAT>
A/Cross-references: UNIPARC:UPI0000177AF
A/Experimental source: milk
A/Note: sequence extracted from NCBI backbone (NCBI:P131440)
C/Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homolo

Query Match 19.6%; Score 22.5; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 3; Gaps 1;

RESULT 25

B59272
peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase (EC 3.5.1.52) A, small chain -
N/Alternate names: peptide N-glycosidase
C/Species: Prunus dulcis var. sativa (sweet almond)
C/Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C/Accession: B59272
R/Altman, F.; Paschinger, K.; Dalik, T.; Vorauer, K.

Eur. J. Biochem. 252, 118-123, 1998
A/Title: Characterisation of peptide-N4-(N-acetyl-beta-glucosaminyl)asparagine amidase A
A/Reference number: B59272; PMID:98181894; PMID:9523720
A/Accession: B59272
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <ALT>
A/Cross-references: UNIPROT:P81898; UNIPARC:UPI00000ABBC4
C/Keywords: hydrolase

Query Match 19.1%; Score 22; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 2.8e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 26

B37196
bradykinin-potentiating peptide 2 - island jararaca
C/Species: Bothrops insularis (island jararaca)
C/Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C/Accession: B37196
R/Cintra, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A/Title: Primary structure and biological activity of bradykinin potentiating peptides f
A/Reference number: A37196; PMID:90351557; PMID:2386615
A/Accession: B37196
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <CIN>
A/Cross-references: UNIPROT:P30422; UNIPARC:UPI0000126A8F
C/Keywords: pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 19.1%; Score 22; DB 2; Length 10;
Best Local Similarity 100.0%; Pred. No. 2.8e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 27

B60409
kassinin-like peptide K-1 - frog (Pseudophryne guentheri)
C/Species: Pseudophryne guentheri
C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C/Accession: B60409
R/Stimaco, M.; Severini, C.; De Blase, D.; Barra, D.; Bosse, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A/Reference number: A60409; PMID:90287814; PMID:2356157
A/Accession: B60409
A/Molecule type: protein
A/Residues: 1-11 <SIM>
A/Cross-references: UNIPROT:P42986; UNIPARC:UPI0000136FCD
A/Note: this peptide was also found in a deamidated form
C/Keywords: amidated carboxyl end; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

Query Match 19.1%; Score 22; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 3.1e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 28

B60409
kassinin-like peptide K-1 - frog (Pseudophryne guentheri)
C/Species: Pseudophryne guentheri
C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004
C/Accession: B60409
R/Stimaco, M.; Severini, C.; De Blase, D.; Barra, D.; Bosse, F.; Roberts, J.D.; Melchior
Peptides 11, 299-304, 1990
A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro
A/Reference number: A60409; PMID:90287814; PMID:2356157
A/Accession: B60409
A/Molecule type: protein
A/Residues: 1-11 <SIM>
A/Cross-references: UNIPROT:P42986; UNIPARC:UPI0000136FCD
A/Note: this peptide was also found in a deamidated form
C/Keywords: amidated carboxyl end; pyroglutamic acid
F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental
F/11/Modified site: amidated carboxyl end (Met) (partial) #status experimental

RESULT 28

D60409

Kasein-1-like peptide K-III - frog (Pseudophryne guentheri)

C/Species: Pseudophryne guentheri

C/Date: 30-Jan-1993 #sequence_revision 30-Jan-1993 #text_change 16-Aug-2004

C/Accession: D60409

R/Simanco, M.; Severini, C.; De Blase, D.; Barra, D.; Bosca, F.; Roberts, J.D.; Melchior

Peptides 11, 299-304, 1990

A/Title: Six novel tachykinin- and bombesin-related peptides from the skin of the Austro

A/Reference number: A60409; PMID:90287814; PMID:2356157

A/Accession: D60409

A/Molecule type: protein

A/Residues: 1-11 <SIM>

A/Cross-references: UNIPROT:P42988; UNIPARC:UPI0000136FD7

C/Keywords: amidated carboxyl end; pyroglutamic acid

P/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

P/11/Modified site: amidated carboxyl end (Met) #status experimental

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 11;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5

Db 2 PHP 4

RESULT 29

B47415

mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43k alpha chain - pig (fragment)

N/Alternate names: GDP-mannose pyrophosphorylase 43k alpha chain

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996

C/Accession: B47415

R/Szumilo, T.; Drake, R.R.; York, J.L.; Elbelin, A.D.

J. Biol. Chem. 268, 17943-17950, 1993

A/Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and uti

A/Reference number: A47415; PMID:93352609; PMID:7688733

A/Accession: B47415

A/Molecule type: protein

A/Residues: 1-13 <82U>

A/Cross-references: UNIPARC:UPI000017C470

A/Experimental source: liver

C/Complex: The enzyme appears to be a heterodimer of alpha and beta chains.

C/Function: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP

A/Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac

C/Keywords: blocked amino end; nucleotidyltransferase

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 13;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHP 5

Db 8 PHP 10

RESULT 30

PH0788

T-cell receptor alpha chain (E22 V-alpha-8.F3.4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0788

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor gene in a series of class I major histocompatibility complex-2

allelic exclusion and antigen-specific repertoire.

C/Accession: PH0788

A/Reference number: PH0746; PMID:9207846; PMID:1836010

A/Molecule type: mRNA

A/Residues: 1-13 <CAS>

A/Cross-references: UNIPARC:UPI000017C76A; EMBL:X60893

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match 19.1%; Score 22; DB 2; Length 13;

Best Local Similarity 57.1%; Pred. No. 3.7e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CBSVNG 20

Db 1 CALVNG 7

RESULT 31

S60007

glial hyaluronate-binding protein - human (fragments)

C/Species: Homo sapiens (man)

C/Date: 23-Aug-1996 #sequence_revision 13-Mar-1997 #text_change 07-May-1999

C/Accession: S60007

R/Perides, G.; Asher, R.A.; Lark, M.W.; Lane, W.S.; Robinson, R.A.; Bignami, A.

Biochem. J. 312, 377-384, 1995

A/Title: Glial hyaluronate-binding protein: a product of metalloproteinase digestion of

A/Reference number: S60007; PMID:96103171; PMID:8526845

A/Accession: S60007

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 <PER>

A/Cross-references: UNIPARC:UPI000017C138

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 15;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CBSVNG 19

Db 7 CLDVNG 12

RESULT 32

B56046

urinary tract stone matrix protein 2, 21K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995

C/Accession: B56046

R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995

A/Description: Isolation, characterization and sequence of stone proteins.

A/Reference number: A56046

A/Accession: B56046

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 <BIN>

A/Cross-references: UNIPARC:UPI000017C408

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 15;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNG 20

Db 1 YVLQGVAPG 10

RESULT 33

S00123

dihydrolypamide S-nuccinyltransferase (EC 2.3.1.61) - bovine (fragment)

N/Alternate names: 2-oxoglutarate dehydrogenase complex chain E2; transsuccinylase

C/Species: Bos primigenius taurus (cattle)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: S00123

R/Bradford, A.P.; Aitken, A.; Beg, F.; Cook, K.G.; Yeaman, S.J.

FEBS Lett. 222, 211-214, 1987

A/Title: Amino acid sequence surrounding the lipic acid cofactor of bovine kidney 2-ox

A:Reference number: S00123; MUID:88005143; PMID:3115829

A:Accession: S00123

A:Molecule type: protein

A:Residues: 1-16

A:Cross-references: UNIPROT:P11179; UNIPARC:UPI0000130BDF

C:Superfamily: dihydrolipoamide acetyltransferase; lipoyl/biotin-binding homology

C:Keywords: acyltransferase; coenzyme A; lipamide; mitochondrion; oxidoreductase; trica

F:1-16/Domain: lipoyl/biotin-binding homology (fragment) <LPB>

F:5/Binding site: lipamide (lys) (covalent) #status experimental

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 16;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTN 7

DB 10 VPSPAN 15

RESULT 34

A41170

photoystem II 6.1k protein - Chlamydomonas reinhardtii (fragment)

C:Species: Chlamydomonas reinhardtii

C>Date: 05-Jun-1992 #sequence_revision 05-Jun-1992 #text_change 09-Jul-2004

C:Accession: A41170

R:de Vltty, C.; Diner, B.A.; Popot, J.L.

J. Biol. Chem. 266, 16614-16621, 1991

A>Title: Photosystem II particles from Chlamydomonas reinhardtii. Purification, molecule

A:Reference number: A41170; MUID:91358452; PMID:1885590

A:Accession: A41170

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-16 <DB>

A:Cross-references: UNIPROT:Q7M14; UNIPARC:UPI000017AF05

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 16;

Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCEVNG 19

DB 1 LVDERNMG 8

RESULT 35

A11488

taurocyamine kinase (EC 2.7.3.4) - lugworm (fragment)

C:Species: Arenicola marina (lugworm, rock worm)

C>Date: 05-Jun-1987 #sequence_revision 05-Jun-1987 #text_change 09-Jul-2004

C:Accession: A11488

R:Brevet, A.; Zeitoun, Y.; Pradel, L.A.

Biochim. Biophys. Acta 393, 1-9, 1975

A>Title: Comparative structural studies of the active site of ATP-guanidine phosphotrans

A:Reference number: A11488; MUID:75184095; PMID:166684

A:Accession: A11488

A:Molecule type: protein

A:Residues: 1-16

A:Cross-references: UNIPROT:P11917; UNIPARC:UPI000012E121

C:Keywords: phosphotransferase

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 16;

Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PTNI 8

DB 8 PTNI 11

RESULT 36

S59512

probable integrin alpha3 beta1 - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C:Accession: S59512

R:McCormick, J.I.; Johnstone, R.M.

Biochem. J. 311, 743-751, 1995

A>Title: Identification of the integrin alpha(3)beta(1) as a component of a partially pu

A:Reference number: S59512; MUID:96067588; PMID:7487928

A:Accession: S59512

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-17 <MC>

A:Cross-references: UNIPROT:Q7MOD8; UNIPARC:UPI00000353C9

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 17;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 12 LVCEVNG 20

DB 9 VVKEAVNPG 17

RESULT 37

B48839

T-cell receptor beta chain V-N-J region - mouse (fragment)

C:Species: Mus musculus (house mouse)

C>Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997

C:Accession: B48839

R:Katz, J.D.; Wang, B.; Hawkins, K.; Benoist, C.; Mathis, D.

Cell 74, 1089-1100, 1993

A>Title: Following a diabetogenic T cell from genesis through pathogenesis.

A:Reference number: A48839; MUID:94006520; PMID:8402882

A:Accession: B48839

A>Status: preliminary; not compared with conceptual translation

A:Molecule type: nucleic acid

A:Residues: 1-18 <RAT>

A:Cross-references: UNIPARC:UPI000017C857

A:Experimental source: NOD, transgenic, diabetogenic T cell clone BDC2.5

A>Note: sequence extracted from NCBI backbone (NCBIP:138473)

C:Keywords: T-cell receptor

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 18;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CESVNG 20

DB 1 CASSQGG 7

RESULT 38

D44101

calmodulin, vasoreactive intestinal peptide-binding protein, VIP binding protein, p18 - gu

C:Species: Cavia porcellus (guinea pig)

C>Date: 27-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 07-Feb-1997

C:Accession: D44101

R:Stallwood, D.; Brugger, C.H.; Baggenstoss, B.A.; Stemmer, P.M.; Shitraga, H.; Landers,

J. Biol. Chem. 267, 19617-19621, 1992

A>Title: Identity of a membrane-bound vasoreactive intestinal peptide-binding protein with

A:Reference number: A44101; MUID:92406918; PMID:1527080

A:Accession: D44101

A>Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <STA>

A:Cross-references: UNIPARC:UPI000017CA29

A:Experimental source: lung membranes

A>Note: sequence extracted from NCBI Backbone (NCBIP:114113)

C:Keywords: intestine

Query Match

Best Local Similarity 19.1%; Score 22; DB 2; Length 19;

Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 6 TIIHKYLVCEVNG 18

R/Shinomura, T.; Mashida, Y.; Ito, K.; Kimata, K.
 J. Biol. Chem. 268, 14461-14469, 1993
 A>Title: cDNA cloning of PG-M, a large chondroitin sulfate proteoglycan expressed during

A/Reference number: A47171; MUID:93300846; PMID:8314802
 A/Accession: B47171
 A/Status: preliminary
 A/Molecule type: nucleic acid
 A/Residues: 1-12 <SH1>
 A/Cross-references: UNIPARC:UPI000017BFR2
 A/Experimental source: CBF, embryo fibroblasts
 A/Note: sequence extracted from NCBI backbone (NCBIN:134459, NCBI:134462)

Query Match 18.3%; Score 21; DB 2; Length 12;
 Best Local Similarity 75.0%; Pred. No. 4.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 HPTN 7
 |||
 DB 8 HPVN 11

RESULT 45
 A54326
 glandular kallikrein-1 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 29-Aug-1994 #sequence_revision 18-Nov-1994 #text_change 23-Mar-1995
 C/Accession: A54326
 R/Riegman, P.H.; Vlietstra, R.J.; van der Korput, H.A.; Romijn, J.C.; Trapman, J.
 Mol. Cell. Endocrinol. 76, 181-190, 1991
 A>Title: Identification and androgen-regulated expression of two major human glandular K
 A/Reference number: A54326; MUID:92324494; PMID:1726490
 A/Accession: A54326
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid
 A/Residues: 1-13 <R1E>
 A/Cross-references: UNIPARC:UPI000035475
 A/Experimental source: prostate
 A/Note: sequence extracted from NCBI backbone (NCBI:108060)

Query Match 18.3%; Score 21; DB 2; Length 13;
 Best Local Similarity 37.5%; Pred. No. 5.2e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNH 9
 : ||| :
 DB 1 VSHPSQH 8

RESULT 46
 S41601
 interferon alpha receptor 1 - human (fragments)
 C/Species: Homo sapiens (man)
 C/Date: 25-Dec-1994 #sequence_revision 01-Dec-1995 #text_change 30-May-1997
 C/Accession: S41601
 R/Abzymovitch, C.; Ratovitski, E.; Lundgren, E.; Revel, M.
 FEBS Lett. 338, 295-300, 1994
 A>Title: Identification of mRNAs encoding two different soluble forms of the human inter
 A/Reference number: S41601; MUID:94139943; PMID:8307198
 A/Accession: S41601
 A/Molecule type: mRNA
 A/Residues: 1-14 <ABR>
 A/Cross-references: UNIPARC:UPI000017C27A
 C/Keywords: cytokine receptor

Query Match 18.3%; Score 21; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 5.6e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCESVN 18
 |||||
 DB 3 VCECEN 8

RESULT 47
 PQ0232
 cystatin CI-4a - maize (fragment)
 N/Alternate names: cysteine proteinase inhibitor
 C/Species: Zea mays (maize)
 C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 09-Jul-2004
 C/Accession: PQ0232
 R/Abbe, M.; Arai, S.
 Agric. Biol. Chem. 55, 2417-2418, 1991
 A>Title: Some properties of a cysteine proteinase inhibitor from corn endosperm.
 A/Reference number: PQ0232; MUID:92118331; PMID:1368742
 A/Accession: PQ0232
 A/Molecule type: protein
 A/Residues: 1-15 <ABR>
 A/Cross-references: UNIPROT:Q9S918, UNIPARC:UPI00009FDBE
 C/Superfamily: cystatin, cystatin homology

Query Match 18.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 33.3%; Pred. No. 6.1e+03;
 Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 PPHNIHKLYCESV 17
 ||| : |||
 DB 1 PHQELGMAVTEHV 15

RESULT 48
 A56786
 pmeIoyl-CoA synthase - Bacillus sphaericus (fragment)
 C/Species: Bacillus sphaericus
 C/Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 18-Aug-1995
 C/Accession: A56786
 R/Ploux, O.; Soularue, P.; Marquet, A.; Gloeckler, R.; Lemoine, Y.
 Biochem. J. 287, 685-690, 1992
 A>Title: Investigation of the first step of biotin biosynthesis in Bacillus sphaericus.
 A/Reference number: A56786; MUID:93075017; PMID:1445232
 A/Accession: A56786
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <PLO>
 A/Cross-references: UNIPARC:UPI000017ACAB
 A/Experimental source: Bacillus sphaericus protein overexpressed in Escherichia coli
 A/Note: sequence extracted from NCBI backbone (NCBI:117639)
 C/Genetics:
 A/Gene: bion
 C/Keywords: biotin biosynthesis; homodimer

Query Match 18.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 6.1e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCESV 17
 ||| :
 DB 2 LICYSI 7

RESULT 49
 PH0136
 T-cell receptor beta chain V-D-J region MS18 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 23-Nov-1991 #sequence_revision 23-Nov-1991 #text_change 30-May-1997
 C/Accession: PH0136
 R/Martin, R.; Howell, M.D.; Jarquemade, D.; Fletlage, M.; Richert, J.; Brostoff, S.; Le
 J. Exp. Med. 173, 19-24, 1991
 A>Title: A myelin basic protein peptide is recognized by cytotoxic T cells in the conte
 A/Reference number: PH0135; MUID:91086843; PMID:1702137
 A/Accession: PH0136
 A/Molecule type: mRNA
 A/Residues: 1-15 <MAR>
 A/Cross-references: UNIPARC:UPI000017C3AB
 C/Keywords: T-cell receptor

Query Match 18.3% Score 21; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 6.1e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCEBNG 19
 DB 1 YLVCEBNG 9

RESULT 50

CS9045

alpha-conotoxin AuiC - cone shell (Conus aulicus)

C/Species: Conus aulicus (cone shell)

C/Date: 23-Jul-1999 #sequence_rev1999 23-Jul-1999 #text_change 09-Jul-2004

C/Accession: CS9045

R/Luo, S.; Kulak, J.M.; Cartier, G.E.; Jacobsen, R.B.; Yoshikami, D.; Olivera, B.M.; McInt

J. Neurosci. 18, 8571-8579, 1998

A/Title: Alpha-conotoxin AuiB selectively blocks alpha3beta4 nicotinic acetylcholine rec

A/Reference number: A59045; PMID:9903392; PMID:9786965

A/Accession: CS9045

A/Status: preliminary

A/Molecule type: protein

A/Residues: 116 <LUD>

A/Cross-references: UNIPROT:P56641; UNIPARC:UPI00001287D0

C/Species: alpha-conotoxin

C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro

F/1-16/Product: alpha-conotoxin AuiC #status experimental <MT>

F/2-8.3-16/Diastylide bonds: #status experimental

F/6/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 18.3% Score 21; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 6.5e+03;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 11 YLVCEBNG 20
 DB 5 YLVCEBNG 14

RESULT 51

C49255

T-cell receptor beta chain V-D-J-C region (V beta 9, J beta 2.7) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 21-Jan-1994 #sequence_rev1999 18-Nov-1994 #text_change 30-May-1997

C/Accession: C49255

R/Rosenberg, W.M.; Mober, P.A.; Bell, J.I.

Eur. J. Immunol. 22, 541-549, 1992

A/Title: Variation in human T cell receptor V beta and J beta repertoire: analysis using

A/Reference number: A49039; PMID:92164737; PMID:1311263

A/Accession: C49255

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-17 <ROS>

A/Cross-references: UNIPARC:UPI000017C3BB

A/Note: sequence extracted from NCBI backbone (NCBIP:90724)

Query Match 18.3% Score 21; DB 2; Length 17;
 Best Local Similarity 33.3%; Pred. No. 6.9e+03;
 Matches 3; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 PHPTNHY 11
 DB 7 PABSTYEQ 15

RESULT 52

S15064

hypothetical protein A - Trypanosoma brucei (fragment)

C/Species: Trypanosoma brucei

C/Date: 31-Dec-1993 #sequence_rev1999 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: S15064; S12677

R/Clayton, C.E.

submitted to the EMBL Data Library, April 1990
 A/Reference number: S15063

A/Accession: S15064

A/Molecule type: DNA

A/Residues: 1-17 <CLA>

A/Cross-references: UNIPROT:P17961; UNIPARC:UPI000013A111; EMBL:X52586; NID:G10397; PID

R/Vijayarath, S.; Ernest, I.; Itzhaki, J.E.; Sherman, D.; Mowatt, M.R.; Michels, P.A.

Nucleic Acids Res. 18, 2967-2975, 1990

A/Title: The genes encoding fructose biphosphate aldolase in Trypanosoma brucei are in

A/Reference number: S12673; PMID:90272402; PMID:2349093

A/Accession: S12677

A/Molecule type: DNA

A/Residues: 1-9 <VID>

A/Cross-references: UNIPARC:UPI000017B597; EMBL:X52586

Query Match 18.3% Score 21; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IPHPT 6
 DB 12 LPRPT 16

RESULT 53

PQ0680

photosystem I 5.6K K chain - common tobacco (fragment)

C/Species: Nicotiana tabacum (common tobacco)

C/Date: 19-May-1994 #sequence_rev1999 19-May-1994 #text_change 09-Jul-2004

C/Accession: PQ0680

R/Obokata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.

Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I psad, psae, psaf, psah and psal are

A/Reference number: PQ0667; PMID:94105345; PMID:8278548

A/Accession: PQ0680

A/Molecule type: protein

A/Residues: 1-18 <OHO>

A/Cross-references: UNIPROT:Q9T2J5; UNIPARC:UPI0000097F66

C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 18.3% Score 21; DB 2; Length 18;
 Best Local Similarity 57.1%; Pred. No. 7.3e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 IPHPTI 8
 DB 3 ICSPTVL 9

RESULT 54

S20322

gluten - wheat

C/Species: Triticum aestivum (common wheat)

C/Date: 19-Mar-1997 #sequence_rev1999 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S20322

R/Fukudome, S.; Yoshikawa, M.

FEBS Lett. 296, 107-111, 1992

A/Title: Opioid peptides derived from wheat gluten: their isolation and characterization

A/Reference number: S20322; PMID:92111773; PMID:1309704

A/Accession: S20322

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 <FOK>

A/Cross-references: UNIPROT:Q7MIG0; UNIPARC:UPI000017B139

Query Match 18.3% Score 21; DB 2; Length 18;
 Best Local Similarity 37.5%; Pred. No. 7.3e+03;
 Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 4 IPHPTIHY 11
 DB 3 YPTGYVYP 10

RESULT 55

A24589

photosystem II chlorophyll a-binding protein psbB - barley chloroplast (fragment)

C/Species: chloroplast Hordeum vulgare (barley)

C/Date: 08-Aug-1987 #sequence_revision 08-Aug-1987 #text_change 09-Jul-2004

C/Accession: A24589

R/Hinz, U.G.

A/Reference number: A24589

A/Accession: A24589

A/Molecule type: protein

A/Residues: 1-20 <HIN>

A/Cross-references: UNIPROT:P10900; UNIPARC:UPI0000178147

C/Genetic:

A/Status: preliminary

A/Genome: chloroplast

A/Reference number: A56894; MUID:9240551; PMID:1526140

A/Keywords: chlorophyll; chloroplast; membrane protein; photosynthesis; photosystem II;

Query Match 18.3%; Score 21; DB 2; Length 20;

Best Local Similarity 42.9%; Pred. No. 8.2e+03;

Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTVNHY 11

DB 14 PATVKY 20

RESULT 56

A60100

fimbrial antigen CS4 - Escherichia coli (strain B8775) (fragment)

C/Species: Escherichia coli

C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004

C/Accession: A60100

R/Wolf, M.K.; Andrews, G.P.; Tall, B.D.; McConnell, M.M.; Levine, M.M.; Boedeker, E.C.

Infect. Immun. 57, 164-173, 1989

A/Title: Characterization of CS4 and CS6 antigenic components of PCF8775, a putative col

A/Reference number: A60100; MUID:89079281; PMID:2491834

A/Accession: A60100

A/Molecule type: protein

A/Status: preliminary

A/Reference number: A56894; MUID:9240551; PMID:1526140

A/Keywords: fimbria

Query Match 18.3%; Score 21; DB 2; Length 20;

Best Local Similarity 66.7%; Pred. No. 8.2e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 VCESVN 18

DB 7 VCASVD 12

RESULT 57

S18582

hypothetical protein K (puq3' region) - Rhodobacter sphaeroides

C/Species: Rhodobacter sphaeroides

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 03-May-1994

C/Accession: S18582; S32855

R/Hunter, C.N.; McGlynn, P.; Ashby, M.K.; Burgess, J.G.; Oleen, J.D.

Mol. Microbiol. 5, 2649-2661, 1991

A/Title: DNA sequencing and complementation/deletion analysis of the bchA-puf operon reg

A/Reference number: S18580; MUID:92140030; PMID:1779756

A/Accession: S18582

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-20 <HUN>

A/Cross-references: UNIPARC:UPI000017AB8B; EMBL:X68795

Query Match 18.3%; Score 21; DB 2; Length 20;

Best Local Similarity 21.1%; Pred. No. 8.2e+03;

Matches 4; Conservative 5; Mismatches 10; Indels 0; Gaps 0;

QY 2 IPHPTNIHKVCSVNG 20

DB 2 VPRNPRNHVASVIRSG 20

RESULT 58

C56894

intracrystalline chromoprotein 1 - Neochyris lenticularis (fragment)

C/Species: Neochyris lenticularis

C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 20-Jun-2000

C/Accession: C56894

R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.

Comp. Biochem. Physiol. B 102, 93-95, 1992

A/Title: An intracrystalline chromoprotein from red brachiopod shells: implications for

A/Reference number: A56894; MUID:9240551; PMID:1526140

A/Contents: Deshayes, red brachiopod shells

A/Accession: C56894

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <CUS>

A/Cross-references: UNIPARC:UPI000017CACA

A/Note: sequence extracted from NCBI backbone (NCBIP:114884)

A/Keywords: chromoprotein

Query Match 18.3%; Score 21; DB 2; Length 20;

Best Local Similarity 44.4%; Pred. No. 8.2e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10

DB 5 LPVATMISK 13

RESULT 59

B56894

intracrystalline chromoprotein 1 - Waltonia inconspicua (fragment)

C/Species: Waltonia inconspicua

C/Date: 05-Jan-1996 #sequence_revision 05-Jan-1996 #text_change 09-Jul-2004

C/Accession: B56894

R/Cusack, M.; Curry, G.; Clegg, H.; Abbott, G.

Comp. Biochem. Physiol. B 102, 93-95, 1992

A/Title: An intracrystalline chromoprotein from red brachiopod shells: implications for

A/Reference number: A56894; MUID:9240551; PMID:1526140

A/Contents: Sowerby, red brachiopod shells

A/Accession: B56894

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <CUS>

A/Cross-references: UNIPROT:Q7M466; UNIPARC:UPI000017CACC

A/Note: sequence extracted from NCBI backbone (NCBIP:114883)

A/Keywords: chromoprotein

Query Match 18.3%; Score 21; DB 2; Length 20;

Best Local Similarity 44.4%; Pred. No. 8.2e+03;

Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 2 IPHPTNIHK 10

DB 5 LPVATMISK 13

RESULT 60

S44465

pyrithocorcin - Pyrrhocoris apterus

C/Species: Pyrrhocoris apterus

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S44465

R/Coclanich, S.; Dupont, A.; Hegy, G.; Lanot, R.; Holdér, F.; Hetru, C.; Hoffmann, J.A.

Biochem. J. 300, 567-575, 1994

A/Title: Novel inducible antibacterial peptides from a hemipteran insect, the sep-eucki

A/Reference number: S44463; MUID:94271176; PMID:8002963

A/Accession: S44465
A/Molecule type: protein
A/Residues: 1-20 <COC>
A/Cross-references: UNIPROT:P37362; UNIPARC:UPI0000132B13
C/Function:
A/Description: antibacterial protein
A/Note: active against Gram-negative bacteria
C/Keywords: antibacterial; hemolymph; immune response

Query Match 18.3%; Score 21; DB 2; Length 20;
Best Local Similarity 60.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IPHT 6
DB 7 LPRPT 11

RESULT 61

AB0120
Insertion element protein (partial) [imported] - Yersinia pestis (strain CO92)
C/Species: Yersinia pestis
C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C/Accession: AB0120
R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Tibball, R.W.; Holden, M.T.G.; Prentice, M.B.
demo-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall,
Nature 411, 523-527, 2001
A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.
A/Reference number: AB0001; MUID:21470413; PMID:11586360
A/Accession: AB0120
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-20 <KOR>
A/Cross-references: UNIPROT:Q8ZHC1; UNIPARC:UPI00000CD77D; GB:AL590842; PIDN:CAC89824.1;
C/Genetics:
A/Genes: lnbB

Query Match 18.3%; Score 21; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 8.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVCE 15
DB 3 LICE 6

RESULT 62

PH0944
T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997
C/Accession: PH0944
R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenberg, A.A.; Wilson, D.B.
J. Exp. Med. 174, 1467-1476, 1991
A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy
A/Reference number: PH0941; MUID:92078857; PMID:1836012
A/Accession: PH0944
A/Molecule type: mRNA
A/Residues: 1-10 <GOL>
A/Cross-references: UNIPARC:UPI000017C9B1
A/Experimental source: complete Freund's adjuvant-immunized lymph node
A/Note: the authors translated the codon GAC for residue 9 as Glu
C/Keywords: T-cell receptor

Query Match 17.4%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 5.7e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CSVNGG 20
DB 1 CASSPGG 7

RESULT 63

G60527
Sperm-activating peptide (Br-Phe-2, Asn-3 SNA-1) - sea urchin (Tripneustes gratilla)
N/Alternate names: speract homolog TG-2; TG-10
N/Contains: sperm-activating peptide (Asn-3 SNA-1)
C/Species: Tripneustes gratilla
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C/Accession: G60527; B39572; A40051; B60527
R/Yoshino, K.I.; Takao, T.; Kajitani, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinometra machael and Heterocentrotus mammillatus.
A/Reference number: A60527
A/Accession: G60527
A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Cross-references: UNIPROT:Q7M3U0; UNIPARC:UPI000017A4E1

A/Note: this peptide was found both with both phenylalanine and bromophenylalanine
R/Yoshino, K.I.; Takao, T.; Suhara, M.; Kikui, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; S
Biochemistry 30, 6203-6209, 1991
A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated
A/Reference number: A39572; MUID:91283461; PMID:2059627
A/Accession: B39572

A/Molecule type: protein
A/Residues: 1-10 <Y02>
A/Cross-references: UNIPARC:UPI000017A4E1
C/Keywords: Bromine
F/2/Modified site: 2'-bromophenylalanine or 4'-bromophenylalanine (Phe) (partial) #acti

Query Match 17.4%; Score 20; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 5.7e+03;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVNGG 20
DB 3 NLNGG 7

RESULT 64

PA0028
protein QA300042 - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C/Accession: PA0028
R/Kamo, M.; Kawakami, T.; Miyake, N.; Tsugita, A.
submitted to JIPID, July 1994
A/Description: Separation and characterization of Arabidopsis proteins by two-dimension.
A/Reference number: PA0001
A/Accession: PA0028
A/Molecule type: protein
A/Residues: 1-11 <KAM>
A/Cross-references: UNIPARC:UPI000017APF9
A/Experimental source: seed
C/Keywords: seed

Query Match 17.4%; Score 20; DB 2; Length 11;
Best Local Similarity 42.9%; Pred. No. 6.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DIPHPN 7
DB 4 EAPFPNN 10

RESULT 65

PH1375
T antigen variant K-2 - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C/Accession: PH1375
R/Lill, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
J. Exp. Med. 176, 449-457, 1992

A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for tr
 A/Reference number: PH1373; MWID:92364547; PMID:1380062
 A/Accession: PH1375
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-11 <LIL>
 A/Cross-references: UNIPARC:UPI000017C758

Query Match 17.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVN 18
 | : |
 1 CKGVN 5

RESULT 66
 PH1376
 T antigen variant K-3 - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
 A/Accession: PH1376
 R/Lili, N.L.; Judith Tevethia, M.; Hendrickson, W.G.; Tevethia, S.S.
 J. Exp. Med. 176, 449-457, 1992
 A/Title: Cytotoxic T lymphocytes (CTL) against a transforming gene product select for tr
 A/Reference number: PH1373; MWID:92364547; PMID:1380062
 A/Accession: PH1376
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-11 <LIL>
 A/Cross-references: UNIPARC:UPI000017C759

Query Match 17.4%; Score 20; DB 2; Length 11;
 Best Local Similarity 60.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 14 CESVN 18
 | : |
 1 CKGVN 5

RESULT 67
 LFPCPR
 pyre leader peptide - Escherichia coli
 C/Species: Escherichia coli
 C/Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jul-2004
 A/Accession: A30400; A05110; Q00495
 R/Poulsen, P.; Bonekamp, F.; Jensen, K.F.
 EMBO J. 3, 1783-1790, 1984
 A/Title: Structure of the Escherichia coli pyre operon and control of pyre expression by
 A/Reference number: A30400; MWID:85003588; PMID:6207018
 A/Accession: A30400
 A/Molecule type: DNA
 A/Residues: 1-12 <POU1>
 A/Cross-references: UNIPROT:P17776; UNIPARC:UPI000013C281
 R.Poulsen, P.; Jensen, K.F.; Valentin-Hansen, P.; Carlsson, P.; Lundberg, L.G.
 Eur. J. Biochem. 135, 223-229, 1983
 A/Title: Nucleotide sequence of the Escherichia coli pyre gene and of the DNA in front o
 A/Reference number: A05110; MWID:83287414; PMID:6349999
 A/Accession: A05110
 A/Molecule type: DNA
 A/Residues: 1-12 <POU2>
 A/Cross-references: UNIPARC:UPI000013C281
 C/Genetics:
 A/Gene: PYRE-LP
 A/Map position: 82 min
 C/Superfamily: pyre leader peptide

Query Match 17.4%; Score 20; DB 1; Length 12;
 Best Local Similarity 42.9%; Pred. No. 6.3e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 11 YLVCSV 17
 : | |
 5 PFVCKRV 11

RESULT 68
 S47383
 T-cell antigen receptor V α junction beta chain - human
 C/Species: Homo sapiens (man)
 C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999
 A/Accession: S47383
 R/Lehner, P.J.
 submitted to the EMBL Data Library, August 1994
 A/Description: Human HLA-A*0201 restricted recognition of Influenza A is dominated by T c
 A/Reference number: S47355
 A/Accession: S47383
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-13 <LEH>
 A/Cross-references: UNIPARC:UPI000011668D; EMBL:Z35709; NID:9527513; PIDN:CAA84778.1; PI
 C/Keywords: T-cell receptor

Query Match 17.4%; Score 20; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 7.5e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 14 CESVNGG 20
 | | |
 1 CASSWGG 7

RESULT 69
 S48685
 extension protein - Streptomyces sp.
 C/Species: Streptomyces sp.
 C/Date: 28-Oct-1995 #sequence_revision 19-Apr-1996 #text_change 09-Jul-2004
 A/Accession: S48685
 R/Fanuel, L.; Granier, B.; Wilkin, J.M.; Bellefroid-Bouguignon, C.; Joris, B.; Knowles,
 FEBS Lett. 351, 49-52, 1994
 A/Title: The precursor of the Streptomyces R61 DP-peptidase containing a C-terminal exte
 A/Reference number: S48685; MWID:94357278; PMID:8076692
 A/Accession: S48685
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <FAN>
 A/Cross-references: UNIPROT:Q7MOK1; UNIPARC:UPI000017AB38
 A/Note: the source is designated as Streptomyces R61

Query Match 17.4%; Score 20; DB 2; Length 14;
 Best Local Similarity 60.0%; Pred. No. 8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIFHP 5
 | : |
 7 DLPAP 11

RESULT 70
 S08209
 hypothetical protein 2 - garden pea
 N/Alternate names: phytochrome
 C/Species: Pisum sativum (garden pea)
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Sep-1997
 A/Accession: S08209
 R/Sato, N.
 Plant Mol. Biol. 11, 697-710, 1988
 A/Title: Nucleotide sequence and expression of the phytochrome gene in Pisum sativum: di
 A/Reference number: S08856
 A/Accession: S08209
 A/Molecule type: DNA
 A/Residues: 1-15 <SAT>
 A/Cross-references: UNIPARC:UPI000011DF37; EMBL:X14077; NID:g20836; PID:g20838
 C/Genetics:

A:Gene: phy

Query Match 17.4%; Score 20; DB 2; Length 15;

Best Local Similarity 44.4%; Pred. No. 8.6e+03;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 12 LVCSVNG 20

Db 1 MVCMSPTNG 9

RESULT 71

PH1610

Ig H chain V-D-J region (wild-type clone 337) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1610

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1610

A/Molecule type: DNA

A/Residues: 1-15 <LEV>

A/Cross-references: UNIPARC:UPI000017C6C4

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: Immunoglobulin

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 15;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNG 19

Db 1 CARLNG 6

RESULT 72

PH0779

T-cell receptor alpha chain (B83) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PH0779

R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.

J. Exp. Med. 174, 1371-1383, 1991

A/Title: T cell receptor genes in a series of class I major histocompatibility complex-1

allelic exclusion and antigen-specific repertoire.

A/Reference number: PH0746; MUID:92078846; PMID:1836010

A/Accession: PH0779

A/Molecule type: mRNA

A/Residues: 1-15 <CNS>

A/Cross-references: UNIPARC:UPI000017C75B; EMBL:X60877

A/Experimental source: T lymphocyte

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 15;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVNG 20

Db 2 ALNG 6

RESULT 73

PT0096

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) beta chain - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004

C/Accession: PT0096

R/Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morinaga, T.; Tsugita, A.

submitted to JIPI, July 1998

A/Description: Proteome analysis of mouse brain.

A/Reference number: PT0091

A/Accession: PT0096

A/Molecule type: protein

A/Residues: 1-15 <KAW>

A/Cross-references: UNIPROT:Q9D051; UNIPARC:UPI000017C739

A/Experimental source: brain, striatum

C/Keywords: oxidoreductase

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 15;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 13 VCSVNG 20

Db 5 VRAHNG 12

RESULT 74

PH1789

T cell receptor alpha chain V region (clone 2PBL V alpha 24-5) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1789

R/Porcelll, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1789

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-17 <POR>

A/Cross-references: UNIPARC:UPI000017C378

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 17;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 11 YLVCSVNG 20

Db 1 YICVSPSG 10

RESULT 75

PL0025

T-cell surface glycoprotein Rta - rabbit (fragment)

N/Alternate names: thymocyte specific class I-like antigen, heavy chain

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: PL0025

R/Wang, C.R.; Chen, G.H.; Newkirk, M.; Capra, J.D.; Mandy, W.J.

Mol. Immunol. 25, 945-952, 1988

A/Title: Biochemical properties of a novel rabbit thymocyte specific class I-like anti

A/Reference number: PL0025; MUID:89096985; PMID:3264885

A/Accession: PL0025

A/Molecule type: protein

A/Residues: 1-18 <WAN>

A/Cross-references: UNIPROT:Q7M3P4; UNIPARC:UPI000017C5B9

A/Experimental source: thymus

C/Keywords: glycoprotein; surface antigen

Query Match

Best Local Similarity 17.4%; Score 20; DB 2; Length 18;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PTNH 9

Db 7 PTSYH 11

RESULT 76

S29167

guinaldine oxidoreductase (EC 1.5.99.-) gamma chain - Arthrobacter sp. (isolate Rue 61a)

C/Species: *Archrobacter* sp.
 A/Variety: isolate Rue 61a
 C/Date: 19-Mar-1997 #sequence_revision 11-Jun-1999 #text_change 11-Jun-1999
 C/Accession: S29167
 R/de Beyer, A.; Lingens, F.
 Biol. Chem. Hoppe-Seyler 374, 101-110, 1993
 A/Title: Microbial metabolism of quinaldine and related compounds. XVI. Quinaldine oxidoreductase.
 A/Reference number: S29165; PMID:93228843; PMID:8471177
 A/Accession: S29167
 A/Molecule type: protein
 A/Residues: 1-19 <BBY>
 A/Cross-references: UNIPARC:UPI00000B1AAD
 A/Experimental source: isolate Rue 61a
 C/Complex: heterohexamer; two alpha, two beta and two gamma chains
 C/Function: catalyzes the oxidation of quinaldine to 1H-4-oxoquinaldine
 A/Pathway: quinaldine degradation
 C/Keywords: FAD; flavoprotein; heterohexamer; molybdopterin; oxidoreductase

Query Match 17.4%; Score 20; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 16 SVNG 19
 ||||
 Db 7 SVNG 10

RESULT 77
 PT0332
 Ig heavy chain CDR3 region (clone J2-139) - human (fragment)
 C/Species: *Homo sapiens* (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0332
 R/Yamada, M.; Maeserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
 A/Reference number: PT0222; PMID:91108337; PMID:1899102
 A/Accession: PT0332
 A/Molecule type: DNA
 A/Residues: 1-19 <YAM>
 A/Cross-references: UNIPARC:UPI000017C21A
 A/Experimental source: B lymphocyte
 C/Keywords: heterotetramer; immunoglobulin

Query Match 17.4%; Score 20; DB 2; Length 19;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 SVNG 20
 ||||
 Db 15 SSNG 19

RESULT 78
 PH1352
 Ig heavy chain DJ region (clone CI00-115) - human (fragment)
 C/Species: *Homo sapiens* (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: PH1352
 R/Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A/Reference number: PH1302; PMID:93094761; PMID:1460419
 A/Accession: PH1352
 A/Molecule type: DNA
 A/Residues: 1-19 <MAS>
 A/Cross-references: UNIPARC:UPI000017C221
 A/Note: the authors translated the stop codon for residue 2 as X
 C/Keywords: heterotetramer; immunoglobulin

Query Match 17.4%; Score 20; DB 2; Length 19;

Best Local Similarity 60.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 IPHPT 6
 :|||
 Db 6 VPPPT 10

RESULT 79
 D49404
 T-cell receptor beta chain VDJ region - human (fragment)
 C/Species: *Homo sapiens* (man)
 C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999
 C/Accession: D49404
 R/Brooks, E.G.; Balk, S.P.; Aupel, K.; Colonna, M.; Strominger, J.L.; Groh-Spies, V.
 Proc. Natl. Acad. Sci. U.S.A. 90, 11787-11791, 1993
 A/Title: Human T-cell receptor (TCR) alpha/beta + CD4-CD8- T cells express oligoclonal T
 A/Reference number: D49404; PMID:94089717; PMID:7505446
 A/Accession: D49404
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-19 <BRO>
 A/Cross-references: UNIPARC:UPI000017C3BE; GB:S67402; NID:9455872; PIDN:AA29277.1; PID
 A/Experimental source: alpha/beta + CD4-CD8- T cells
 A/Note: sequence extracted from NCBI backbone (NCBIN:141028, NCBI:141029)
 C/Keywords: T-cell receptor

Query Match 17.4%; Score 20; DB 2; Length 19;
 Best Local Similarity 30.0%; Pred. No. 1.1e+04;
 Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 PHPTNHXYL 12
 ||::|
 Db 5 PTPARVYKYL 14

RESULT 80
 P00409
 RNA-directed RNA polymerase (EC 2.7.7.48) 2 - influenza A virus (strain A/Hobei/24/89 (I
 N/Alternate names: P3 protein; PB2 protein
 C/Species: *Influenza A virus*
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 31-Dec-2004
 C/Accession: P00409
 R/Li, X.S.; Zhao, C.Y.; Gao, H.M.; Zhang, Y.Q.; Ishida, M.; Kanegae, Y.; Endo, A.; Nerov
 J. Gen. Virol. 73, 1329-1337, 1992
 A/Title: Origin and evolutionary characteristics of antigenic reassortant influenza A (I
 A/Reference number: P00408; PMID:9230326; PMID:1607856
 A/Accession: P00409
 A/Molecule type: genomic RNA
 A/Residues: 1-19 <LIA>
 A/Cross-references: UNIPROT:Q67303; UNIPARC:UPI00001757E2
 C/Genetics:
 A/Map position: segment 1
 C/Keywords: nucleocidyltransferase

Query Match 17.4%; Score 20; DB 2; Length 19;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 IPHPTNHXYL 11
 :|||
 Db 7 VDHMAIRKXY 16

RESULT 81
 PX0042
 venomblin B (EC 3.4.21.-) - himenhabu (fragment)
 N/Alternate names: beta-fibrinogenase; okinaxobin I
 C/Species: *Trimerurus okinawensis* (himenhabu)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C/Accession: PX0042
 R/Iwaseki, A.; Shieh, T.C.; Shimohigashi, Y.; Waki, M.; Kihara, H.; Ohno, M.
 J. Biochem. 108, 822-828, 1990

A/Title: Purification and characterization of a coagulant enzyme, okinaxobin I, from the
 A/Reference number: PX0042; MUID:91185341; PMID:1964457
 A/Accession: PX0042
 A/Molecule type: protein
 A/Residues: 1-20 <IMA>
 A/Cross-references: UNIPROT:P20005; UNIPARC:UPI0000175C39
 C/Superfamily: trypsin; trypsin homology
 C/Keywords: hydrolase; serine proteinase; venom

Query Match 17.4%; Score 20; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKYL 12
 DB 10 NHRFL 15

RESULT 82
 S68028
 Iodochronine 5'-monodeiodinase - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C/Accession: S68028
 R/Zhou, L.X.; Dahal, S.S.; Kupfer, D.; Morrell, S.; McKenzie, B.A.; Eccleston Jr., B.D.;
 Arch. Biochem. Biophys. 322, 390-394, 1995
 A/Title: Cytochrome P450 catalyzed covalent binding of methoxychlor to rat hepatic, mch
 A/Reference number: S68028; MUID:96032659; PMID:7574712
 A/Accession: S68028
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <ZHO>
 A/Cross-references: UNIPARC:UPI00001761A4
 C/Superfamily: protein disulfide-isomerase; thioredoxin homology

Query Match 17.4%; Score 20; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 HKYLV 13
 DB 16 HNYVL 20

RESULT 83
 B38382
 15K protein B - rabbit (fragment)
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 28-Jun-1991 #sequence_revision 28-Jun-1991 #text_change 02-Sep-2000
 C/Accession: B38382
 R/Ooi, C.E.; Weiser, J.J.; Levy, O.; Elsbach, P.
 J. Biol. Chem. 265, 15956-15962, 1990
 A/Title: Isolation of two isoforms of a novel 15-kDa protein from rabbit polymorphonucle
 A/Reference number: A38382; MUID:90368617; PMID:2203792
 A/Accession: B38382
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <OOI>
 A/Cross-references: UNIPARC:UPI0000176378
 C/Superfamily: cathelin; cystatin homology

Query Match 17.4%; Score 20; DB 2; Length 20;
 Best Local Similarity 25.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 6; Mismatches 6; Indels 0; Gaps 0;

QY 2 IPHTNHYLVESV 17
 DB 1 IPHRLRYEVAQAL 16

RESULT 84
 S03954

acidic fibroblast growth factor - pig (fragment)
 N/Alternate names: alpha-endothelial cell growth factor
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004
 C/Accession: S03954
 R/Quinkler, W.; Maaberg, M.; Bernotat-Danilewski, S.; Luehe, N.; Sharma, H.S.; Schap
 Bur, J. Biochem. 181, 67-73, 1989
 A/Title: Isolation of heparin-binding growth factors from bovine, porcine and canine he
 A/Reference number: S03953; MUID:89231704; PMID:2714282
 A/Accession: S03954
 A/Molecule type: protein
 A/Residues: 1-20 <QUI>
 A/Cross-references: UNIPROT:P20002; UNIPARC:UPI000017C453
 C/Keywords: growth factor

Query Match 17.4%; Score 20; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 16 SYNGG 20
 DB 10 SSNGG 14

RESULT 85
 A58963
 alpha-conotoxin Cn1A - cone shell (Conus consors)
 N/Contains: alpha-conotoxin Cn1B
 C/Species: Conus consors
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
 C/Accession: A58963
 R/Favreau, P.; Krimm, I.; Le Gall, F.; Bobanliech, M.J.; Lamthanh, H.; Bouet, F.; Serve
 Biochemistry 38, 6317-6326, 1999
 A/Title: Biochemical characterization and nuclear magnetic resonance structure of novel
 A/Reference number: A58963; MUID:99255390; PMID:10320362
 A/Accession: A58963
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <FAV>
 A/Cross-references: UNIPROT:P56973; UNIPARC:UPI00001287B8
 C/Superfamily: alpha-conotoxin
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 F1-14/Product: alpha-conotoxin Cn1A #status experimental <MAT>
 F3-14/Product: alpha-conotoxin Cn1B #status experimental <MAT>
 F3-8, 4-14/Disulfide bonds: #status experimental
 F14/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 17.0%; Score 19.5; DB 2; Length 14;
 Best Local Similarity 45.5%; Pred. No. 9.6e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 1; Gaps 1;

QY 4 HPTNHYLVLC 14
 DB 5 HPA-CGKYSC 14

RESULT 86
 C32735
 thyroglobulin - pig (fragment)
 C/Species: Sus scrofa domestica (domestic pig)
 C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 09-Jul-2004
 C/Accession: C32735
 R/Rawitch, A.B.; Litwer, M.R.; Gregg, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.
 Biochem. Biophys. Res. Commun. 118, 423-429, 1984
 A/Title: The isolation of identical thyroxine containing amino acid sequences from bovin
 A/Reference number: A32735; MUID:84153804; PMID:6704086
 A/Accession: C32735
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-19 <RAW>
 A/Cross-references: UNIPROT:Q7M22; UNIPARC:UPI00001734C4
 C/Superfamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homo
 C/Keywords: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis

F/5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.0%; Score 19.5; DB 2; Length 19;
Best Local Similarity 37.5%; Pred. No. 1.3e+04;
Matches 6; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 7 NIHKYLV-----CE 15
||:|:|
1 NIFEYQVDAQPLRPCE 16

RESULT 87

B32735

thyroglobulin - sheep (fragment)

C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C/Date: 20-Jul-1990 #sequence_revision 20-Jul-1990 #text_change 03-Jul-2004

C/Accession: B32735

R/Rawitch, A.B.; Litwer, M.R.; Grege, J.; Turner, C.D.; Rouse, J.B.; Hamilton, J.W.

Biochem. Biophys. Res. Commun. 118, 423-429, 1984

A/Title: The isolation of identical thyroxine containing amino acid sequences from bovin

A/Reference number: A32735; MUID:84153804; PMID:6704086

A/Accession: B32735

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-19 <RAM>

A/Cross-references: UNIPROT:Q7M2Z1; UNIPARC:UPI00001734C4

C/Suprafamily: thyroglobulin; cholinesterase homology; thyroglobulin type I repeat homol

C/Keyword: dimer; glycoprotein; iodine; thyroid gland; thyroid hormone biosynthesis

F/5/Modified site: thyroxine (Tyr) #status predicted

Query Match 17.0%; Score 19.5; DB 2; Length 19;
Best Local Similarity 37.5%; Pred. No. 1.3e+04;
Matches 6; Conservative 1; Mismatches 2; Indels 7; Gaps 1;

QY 7 NIHKYLV-----CE 15
||:|:|
1 NIFEYQVDAQPLRPCE 16

RESULT 88

A34233

trehalase inhibitor - American cockroach (fragment)

C/Species: Periplaneta americana (American cockroach)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: A34233

R/Hayakawa, Y.; Jahagirdar, A.P.; Yaguchi, M.; Downer, R.G.H.

J. Biol. Chem. 264, 16165-16169, 1989

A/Title: Purification and characterization of trehalase inhibitor from hemolymph of the

A/Reference number: A34233; MUID:89380218; PMID:2777784

A/Accession: A34233

A/Molecule type: protein

A/Residues: 1-19 <RAY>

A/Cross-references: UNIPROT:P19986; UNIPARC:UPI000012DA2D

Query Match 17.0%; Score 19.5; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.3e+04;
Matches 6; Conservative 0; Mismatches 3; Indels 3; Gaps 1;

QY 2 IHPPTNIHKYLV 13
||:|:|
2 IFTP--HVKV 10

RESULT 89

S35696

phosphoenolpyruvate carboxykinase - Trypanosoma brucei

C/Species: Trypanosoma brucei

C/Date: 28-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 09-Jul-2004

C/Accession: S35696

R/Hunt, M.; Koehler, P.

Biochim. Biophys. Acta 1249, 15-22, 1995

A/Title: Purification and characterization of phosphoenolpyruvate carboxykinase from Try

panosoma brucei
A/Reference number: S35696; MUID:95284106; PMID:7766679

A/Accession: S35696

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <HUN>

A/Cross-references: UNIPROT:Q7M3S5; UNIPARC:UPI000017B599

Query Match 16.5%; Score 19; DB 2; Length 9;
Best Local Similarity 80.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYL 12
||:|:|
Db 4 IHKYL 8

RESULT 90

B57444

neuropeptide Grb-A27 B2 - two-spotted cricket

C/Species: Gryllus bimaculatus (two-spotted cricket)

C/Date: 26-Jan-1996 #sequence_revision 26-Jan-1996 #text_change 09-Jul-2004

C/Accession: B57444

R/Lorenz, M.W.; Kellner, R.; Hoffmann, K.H.

J. Biol. Chem. 270, 21103-21108, 1995

A/Title: A family of neuropeptides that inhibit juvenile hormone biosynthesis in the cri

A/Reference number: A57444; MUID:95403341; PMID:7673141

A/Accession: B57444

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <LOR>

A/Cross-references: UNIPROT:Q7M3N8; UNIPARC:UPI000017B818

Query Match 16.5%; Score 19; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VNGG 20
||:|:|
Db 5 VNGG 8

RESULT 91

S77980

cytochrome-c oxidase (EC 1.9.3.1) chain IV - bigeye tuna (fragment)

C/Species: Thunnus obesus (bigeye tuna)

C/Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004

C/Accession: S77980

R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottepeich, F.; Kadenbach, B.

submitted to the Protein Sequence Database, June 1997

A/Reference number: S77980

A/Accession: S77980

A/Molecule type: protein

A/Residues: 1-10 <ARN>

A/Cross-references: UNIPROT:P80971; UNIPARC:UPI000017BF70

A/Experimental source: heart; liver

A/Genome: nuclear

C/Function: oxidative phosphorylation; respiratory chain

A/Pathway: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 16.5%; Score 19; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 8.1e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 HKYLVCS 16
||:|:|
Db 3 HDHEVARS 10

RESULT 92

I60527

sperm-activating peptide (SAP-I) - sea urchin (Strongylocentrotus nudus)

N/Alternate names: spermact

C:\Species: Strongylocentrotus nudus
C:\Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:\Accession: I60527
R.Yoshihino, K.I., Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi Comp. Biochem. Physiol. B 94, 739-751, 1989
A>Title: A halogenated amino acid-containing sperm activating peptide and its related peccus nudus, Echinosmetra macthai and Heterocentrotus mammillatus.
A:\Reference number: A60527
A:\Accession: I60527
A:\Molecule type: protein
A:\Residues: 1-10 <YOS>
A:\Cross-references: UNIPROT:Q7M4B5, UNIPARC:UPI000003545B

Query Match 16.5% Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 17 VNGG 20
DB 4 LMGG 7

RESULT 93
C60527
Sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAR-I) - sea urchin (Tripneustes gratilla)
N:\Alternate names: speract homolog TG-4
C:\Species: tripneustes gratilla
C:\Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C:\Accession: C60527; D39572
R.Yoshihino, K.I., Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi Comp. Biochem. Physiol. B 94, 739-751, 1989
A>Title: A halogenated amino acid-containing sperm activating peptide and its related peccus nudus, Echinosmetra macthai and Heterocentrotus mammillatus.
A:\Reference number: A60527
A:\Accession: C60527
A:\Molecule type: protein
A:\Residues: 1-10 <YOS>
A:\Cross-references: UNIPROT:Q7M3T6, UNIPARC:UPI000017A4E5
A>Note: this peptide did not contain bromophenylalanine
R.Yoshihino, K.; Takao, T.; Suhara, M.; Kitai, T.; Horii, H.; Nomura, K.; Yamaguchi, M.; Sh Biochemistry 30, 6203-6209, 1991
A>Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated A:\Reference number: A39572; MUID:91283461; PMID:2055627
A:\Accession: D39572
A:\Molecule type: protein
A:\Residues: 1-10 <YO2>
A:\Cross-references: UNIPARC:UPI000017A4E5
C:\Keywords: bromine
F:\Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 16.5% Score 19; DB 2; Length 10;
Best Local Similarity 60.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 16 SVNGG 20
DB 3 SIGGG 7

RESULT 94
C60788
Sperm-activating peptide (Speract) - sea urchin (Pseudocentrotus depressus)
C:\Species: Pseudocentrotus depressus
C:\Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
C:\Accession: C60788
R.Suzuki, N.; Kajitara, H.; Nomura, K.; Garbers, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H Comp. Biochem. Physiol. B 89, 687-693, 1988
A>Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus A:\Reference number: A60787; MUID:88242184; PMID:3378407
A:\Accession: C60788
A:\Molecule type: protein
A:\Residues: 1-10 <SUZ>

Query Match 16.5% Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VNGG 20
: |||
Db 4 LINGG 7

RESULT 95
A60527
N:Alternate names: SAP-a; speract; TG-1; TG-9
C:Species: *Triplaneustes gratillia*
C>Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C:Accession: A60527; A39572; A60973; H60527; I39572
R:Yoshino, K.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamagu
Comp. Biochem. Physiol. B 94, 739-751, 1989
A>Title: A halogenated amino acid-containing sperm activating peptide and its related p
ocus nudus, *Echinometra mathaei* and *Heterocentrotus mamillatus*.
A:Reference number: A60527
A:Accession: A60527
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPARC:UPI000003545B
R:Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Horii, H.; Nomura, K.; Yamaguchi, M.; S
Biochemistry 30, 6203-6209, 1991
A>Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associat
A:Reference number: A39572; MUID:91283461; PMID:2059627
A:Accession: A39572
A:Molecule type: protein
A:Residues: 1-10 <YOS>
A:Cross-references: UNIPARC:UPI000003545B
R:Takao, T.; Yoshino, K.; Suzuki, N.; Shimomishi, Y.
Blomed. Environ. Mass Spectrom. 19, 705-712, 1990
A>Title: Analysis of post-translational modifications of proteins by accurate mass meas
A:Reference number: A60973; MUID:91167743; PMID:2076468
A:Accession: A60973
A:Molecule type: protein
A:Residues: 1-10 <TAK>
A:Cross-references: UNIPARC:UPI000003545B
C:Keywords: bromine
P:2/Modified site: 2-bromophenylalanine (Phe) (partial) #status experimental

Query Match 16.5% Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VNGG 20
: |||
Db 4 LINGG 7

RESULT 96
A60787
N:sperm-activating peptide (speract) - sea urchin (*Hemiacentrotus pulcherrimus*)
C:Species: *Hemiacentrotus pulcherrimus*
C>Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 05-Oct-2004
C:Accession: A60787
R:Suzuki, N.; Kajitani, H.; Nomura, K.; Garbars, D.L.; Yoshino, K.; Kurita, M.; Tanaka, I
Comp. Biochem. Physiol. B 69, 687-693, 1988
A>Title: Some more speract derivatives associated with eggs of sea urchins, *Pseudocentru
A:Reference number: A60787; MUID:88242184; PMID:3378407
A:Accession: A60787
A:Molecule type: protein
A:Residues: 1-10 <SUZ>
A:Cross-references: UNIPROT:Q25121; UNIPARC:UPI000003545B
C:Comment: This oligopeptide from egg jelly is one of several from this species, all of
ct shows some, but not absolute, species restriction.*

Query Match 16.5%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 8.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 17 VNGG 20
: |||
Db 4 LNGG 7

RESULT 97

B49164
chromogranin-B - rat (fragment)
C:Species: Rattus norvegicus (Norway rat)
C:Date: 19-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
C:Accession: B49164
R:Nielsen, E.; Wellinder, B.S.; Madsen, O.D.
Endocrinology 129, 3147-3156, 1991
A:Title: Chromogranin-B, a putative precursor of eight novel rat glucagonoma peptides th
A:Reference number: A49164; MUID:92063871; PMID:1954895
A:Accession: B49164
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-11 <NTE>
A:Cross-references: UNIPARC:UPI00000E7128
A>Note: sequence extracted from NCBI backbone (NCBIP:66370)
C:Superfamily: chromogranin B precursor

Query Match 16.5%; Score 19; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 8.9e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 15 ESYNG 20
: |||
Db 4 EDVNG 9

RESULT 98

A26930
ermg leader peptide 1 - Bacillus sphaericus
C:Species: Bacillus sphaericus
C:Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004
C:Accession: A26930
R:Monod, M.; Mohan, S.; Dubnau, D.
J. Bacteriol. 169, 340-350, 1987
A:Title: Cloning and analysis of ermG, a new macrolide-lincosamide-streptogramin B resis
A:Reference number: A91840; MUID:87083389; PMID:3025178
A:Accession: A26930
A:Molecule type: DNA
A:Residues: 1-11 <MON>
A:Cross-references: UNIPROT:P26840; UNIPARC:UPI00001E856; GB:M15332; NID:9142881; PIDN:

Query Match 16.5%; Score 19; DB 2; Length 11;
Best Local Similarity 27.3%; Pred. No. 8.9e+03;
Matches 3; Conservative 5; Mismatches 3; Indels 0; Gaps 0;

QY 8 IHKYLVCESVN 18
: |||
Db 1 MKYISKRDAIN 11

RESULT 99

S15755
actin 7 - soybean (fragment)
C:Species: Glycine max (soybean)
C:Date: 20-Feb-1995 #sequence_revision 29-May-1998 #text_change 05-Oct-2004
C:Accession: S15755
R:Pearson, L.; Meagher, R.B.
Plant Mol. Biol. 14, 513-526, 1990
A:Title: Diverse soybean actin transcripts contain a large intron in the 5' untranslated
A:Reference number: S15754; MUID:91346640; PMID:2102831
A:Accession: S15755
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-13 <PEA>
A:Cross-references: UNIPROT:P15987; UNIPARC:UPI000012542C; EMBL:X17120; NID:918527; PIDN:
C:Superfamily: Actin
C:Keywords: cytoskeleton; structural protein

Query Match 16.5%; Score 19; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 LVCE 15
: |||
Db 10 LVCD 13

RESULT 100

PT0290
Ig heavy chain CRD3 region (clone 4-115A) - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C:Accession: PT0290
R:Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A:Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A:Reference number: PT0222; MUID:91108337; PMID:1899102
A:Accession: PT0290
A:Molecule type: DNA
A:Residues: 1-13 <YAM>
A:Cross-references: UNIPARC:UPI000017C1FE
A:Experimental source: B lymphocyte
C:Keywords: heterotetramer; immunoglobulin

Query Match 16.5%; Score 19; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 1.1e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 10 KYLVC 14
: |||
Db 2 KYAVC 6

Search completed: January 20, 2006, 19:12:11
Job time : 12.3462 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 66.5385 Seconds
(without alignments)
212.066 Million cell updates/sec

Title: US-09-662-293-3

Perfect score: 115

Sequence: 1 DIHPPTNHHKYLVCESVNGS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: uniprot_05.80.*

2: uniprot_sprot.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Query length	DB ID	Description
1	38	33.0	15	2	Q7M126 PSEBSP
2	38	33.0	15	2	Q7M134 PRHIZ
3	37	32.2	13	2	Q00789_9DELA
4	37	32.2	13	2	Q76R60_9DELA
5	33	28.7	19	2	Q5C123 SCHUA
6	32	27.8	13	2	Q7S901 NEUCR
7	30	26.1	10	2	Q4X4H2 PLACH
8	30	26.1	18	2	Q16244_HUMAN
9	29	25.2	6	1	TWOF_SABBU
10	29	25.2	19	2	Q5EX89_9LAMI
11	28	24.3	19	2	Q5EX78_9LAMI
12	28	24.3	19	2	Q5EX77_9LAMI
13	28	24.3	19	2	Q5EX88_9LAMI
14	28	24.3	19	2	Q5EX90_9LAMI
15	28	24.3	19	2	Q5EX91_9LAMI
16	28	24.3	19	2	Q5EX92_9LAMI
17	28	24.3	19	2	Q5EX94_9LAMI
18	28	24.3	19	2	Q5EX95_9LAMI
19	28	24.3	19	2	Q5EX96_9LAMI
20	28	24.3	19	2	Q5EX97_9LAMI
21	28	24.3	19	2	Q5EX98_9LAMI
22	28	24.3	19	2	Q5EX99_9LAMI
23	28	24.3	19	2	Q5EXA1_9LAMI
24	28	24.3	19	2	Q5EXA2_9LAMI
25	28	24.3	19	2	Q5EXA3_9LAMI
26	28	24.3	19	2	Q5EXA4_9LAMI
27	28	24.3	19	2	Q5EXA5_9LAMI
28	28	24.3	19	2	Q5EXA6_9LAMI
29	28	24.3	19	2	Q5EXA7_9LAMI
30	28	24.3	19	2	Q5EXA8_9LAMI
31	28	24.3	19	2	Q5EXA9_9LAMI

32	28	24.3	19	2	Q5EXB0_9LAMI	O5exb0 saintpaulia
33	28	24.3	19	2	Q5EXB1_9LAMI	O5exb1 saintpaulia
34	28	24.3	20	2	Q4YMN1_PLABE	Q4ymn1 plasmodium
35	27	23.5	18	2	Q26062_HELPY	Q26062 helicobacte
36	27	23.5	19	2	Q4XJ38_PLACH	Q4xj38 plasmodium
37	27	23.5	19	2	Q4YK87_PLABE	Q4yk87 plasmodium
38	27	23.5	20	2	Q7RR59_PLAYO	Q7rr59 plasmodium
39	26	22.6	12	2	Q9UDR0_HUMAN	Q9umr0 homo sapien
40	26	22.6	17	2	Q4L0W0_BACTX	Q4l0w0 bacillus th
41	26	22.6	19	2	Q9XNQ7_BOONI	Q9xng7 boophilus m
42	26	22.6	19	2	Q5EX86_9LAMI	Q5ex86 streptocarp
43	26	22.6	20	1	PHYLA_PHYOR	P84569 phyllomedu
44	26	22.6	20	2	Q7RS12_PLAYO	Q7rs12 plasmodium
45	26	22.6	20	2	Q5K4V0_BOVIN	Q5k4v0 bos taurus
46	26	22.6	20	2	Q90X94_CHICK	Q90x94 gallus gall
47	25	21.7	11	2	Q8MM58_9NEOP	Q8mm58 heliconi
48	25	21.7	12	2	Q8MUN4_9NEOP	Q8mun4 heliconi
49	25	21.7	12	2	Q8MUN9_9NEOP	Q8mun9 heliconi
50	25	21.7	13	2	Q8MM57_9NEOP	Q8mm57 heliconi
51	25	21.7	14	2	Q8MUN8_9NEOP	Q8mun8 heliconi
52	25	21.7	14	2	Q8MUP0_9NEOP	Q8mup0 heliconi
53	25	21.7	15	2	Q9BZNO_HUMAN	Q9bzn0 homo sapien
54	25	21.7	15	2	Q8MUP2_9NEOP	Q8mup2 heliconi
55	25	21.7	16	2	Q8MM83_9NEOP	Q8mm83 heliconi
56	25	21.7	16	2	Q8MM84_9NEOP	Q8mm84 heliconi
57	25	21.7	16	2	Q8MM85_9NEOP	Q8mm85 heliconi
58	25	21.7	16	2	Q8MUN3_9NEOP	Q8mun3 heliconi
59	25	21.7	16	2	Q8MUN5_9NEOP	Q8mun5 heliconi
60	25	21.7	16	2	Q5G554_BALMU	Q5g554 balaenopte
61	25	21.7	17	2	Q9TW64_DICDI	Q9tw64 dicystostei
62	25	21.7	18	1	PHYI2_PHYRH	P84567 phyllomedu
63	25	21.7	18	2	Q6VYB3_9NEOP	Q6vyb3 heliconi
64	25	21.7	18	2	Q6VYD9_9NEOP	Q6vyd9 heliconi
65	25	21.7	18	2	Q6VYER_9NEOP	Q6vyer heliconi
66	25	21.7	18	2	Q4YEL0_PLABE	Q4yel0 plasmodium
67	25	21.7	18	2	Q28069_BOVIN	Q28069 bos taurus
68	25	21.7	19	2	Q6VYD8_9NEOP	Q6vyd8 heliconi
69	25	21.7	19	2	Q6VYEL_9NEOP	Q6vyel heliconi
70	25	21.7	19	2	Q7RG13_PLAYO	Q7rg13 plasmodium
71	25	21.7	19	2	Q7YK42_9FABA	Q7yk42 desmanthu
72	25	21.7	19	2	Q8CJ05_MESAU	Q8cj05 mesocricetu
73	25	21.7	19	2	Q7LZM5_HHVI	Q7lzm5 human herpe
74	25	21.7	20	1	APY3_PLECT	P83477 pleurotus c
75	25	21.7	20	1	APY3_PLECT	P83481 pleurotus c
76	25	21.7	20	2	Q64619_RAT	Q64619 rattus norv
77	25	21.7	20	2	Q9PRY1_TORCA	Q9pry1 torpedo cal
78	24.5	21.3	20	2	Q9R4Z4_PROMI	Q9r4z4 proteus mir
79	24	20.9	9	2	Q7M471_VESOR	Q7m471 vespa orien
80	24	20.9	15	2	Q9UCI7_HUMAN	Q9uci7 homo sapien
81	24	20.9	17	2	Q6R9U9_HUMAN	Q6r9u9 homo sapien
82	24	20.9	17	2	Q6R9P0_TRAFR	Q6r9p0 trachypithe
83	24	20.9	17	2	Q6R9P1_TRAFR	Q6r9p1 trachypithe
84	24	20.9	17	2	Q6R9P2_PYGNE	Q6r9p2 pygathrix n
85	24	20.9	17	2	Q6R9P3_PYGNI	Q6r9p3 pygathrix b
86	24	20.9	17	2	Q6R9P4_MACAU	Q6r9p4 macaca mula
87	24	20.9	17	2	Q6R9Q1_PONPY	Q6r9q1 ponpo pygma
88	24	20.9	17	2	Q6R9Q5_PPRIM	Q6r9q5 gorilla gor
89	24	20.9	18	1	Q6R9R4_PANTR	Q6r9r4 pan troglod
90	24	20.9	18	1	HEMTO_THERT	P80155 therozyon
91	24	20.9	18	2	Q9ZYV5_9HYME	Q9zyv5 opus kraus
92	24	20.9	18	2	Q4XS69_PLACH	Q4xs69 plasmodium
93	24	20.9	19	2	Q5CS28_SCHUA	Q5cs28 schistosoma
94	24	20.9	19	2	Q9ZYX3_9HYME	Q9zyx3 gnathopodon
95	24	20.9	19	2	Q9ZYX2_9HYME	Q9zyx2 centistes a
96	24	20.9	19	2	Q4Y3P1_PLACH	Q4y3p1 plasmodium
97	24	20.9	19	2	Q6R9P5_HYLLB	Q6r9p5 hylobates l
98	24	20.9	19	2	Q6R9P6_9PRIM	Q6r9p6 hylobathecu
99	24	20.9	19	2	Q6R9P7_MACAU	Q6r9p7 macaca mula
100	24	20.9	19	2	Q5EXA0_9LAMI	O5exa0 streptocarp

ALIGNMENTS

```

RESULT 1
Q7M126_PSESP PRELIMINARY; PRT; 15 AA.
AC Q7M126;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Pseudomonas sp.
OC Bacteria; Proteobacteria.
OX NCBI_TaxID=306;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staud D., Hartmann S., Gaelli R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
methylobacterial bacteria."
RL J. Gen. Microbiol. 132:2837-2843 (1986).
DR PIR; B60929; B60929.
DR GO; GO:0018834; P.dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match
Best Local Similarity 33.0%; Score 38; DB 2; Length 15;
Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPNTNH 9
DB 3 PNPNTNH 9

RESULT 2
Q7M134_9RHIZ PRELIMINARY; PRT; 15 AA.
AC Q7M134;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Dichloromethane dehalogenase (EC 4.5.1.3) (Fragment).
OS Hyphomicrobium sp.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Hyphomicrobiaceae; Hyphomicrobium.
OX NCBI_TaxID=82;
RN [1]
RP PROTEIN SEQUENCE.
RA Kohler-Staud D., Hartmann S., Gaelli R., Suter F., Leisinger T.;
RT "Evidence for identical dichloromethane dehalogenases in different
methylobacterial bacteria."
RL J. Gen. Microbiol. 132:2837-2843 (1986).
DR PIR; A60929; A60929.
DR GO; GO:0018834; P.dichloromethane dehalogenase activity; IEA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1667 MW; 05B170EF8B3721D9 CRC64;

Query Match
Best Local Similarity 33.0%; Score 38; DB 2; Length 15;
Pred. No. 68;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 PHPNTNH 9
DB 3 PNPNTNH 9

```

```

OS Human T-lymphotropic virus 1.
OC Viruses; Retroviruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; PubMed=3027244;
RA Hiramatsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
leukaemia virus type I: A new open reading frame in the gag-pol
region."
RL J. Gen. Virol. 68:213-218 (1987).
DR EMBL; D10033; BAA00925.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match
Best Local Similarity 32.2%; Score 37; DB 2; Length 13;
Pred. No. 84;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHPNTN 7
DB 1 DIPHPKN 7

RESULT 4
Q76R60_9DELA PRELIMINARY; PRT; 13 AA.
AC Q76R60;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Gag Protein (Fragment).
OS Human T-lymphotropic virus 1.
OC Viruses; Retroviruses; Retroviridae; Deltaretrovirus.
OX NCBI_TaxID=11908;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=87111460; PubMed=3027244;
RA Hiramatsu K., Nishida J., Naito A., Yoshikawa H.;
RT "Molecular cloning of the closed circular provirus of human T cell
leukaemia virus type I: A new open reading frame in the gag-pol
region."
RL J. Gen. Virol. 68:213-218 (1987).
DR EMBL; X04800; CAA28492.1; -; Genomic_DNA.
FT NON_TER 1
SQ SEQUENCE 13 AA; 1363 MW; 408035320911B443 CRC64;

Query Match
Best Local Similarity 32.2%; Score 37; DB 2; Length 13;
Pred. No. 84;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DIPHPNTN 7
DB 1 DIPHPKN 7

RESULT 5
Q5C123_SCHUA PRELIMINARY; PRT; 19 AA.
AC Q5C123;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiida;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RT Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY810763; AAX26652.1; -, mRNA.

```

KW Hypothetical protein.
SQ SEQUENCE 19 AA; 2259 MW; FE24492FB8464550 CRC64;

Query Match 28.7%; Score 33; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 5.6e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5 PTNHHKLV 13
| | | | |
DB 8 PMKHNYLV 16

RESULT 6

ID 07S901_NEUCR PRELIMINARY; PRT; 13 AA.

AC 07S901,
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Predicted protein.
GN Name=NCU05297.1;
OS Neurospora crassa.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
OX NCBI_TaxID=5141;
[1]
RP NUCLEOTIDE SEQUENCE.

RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
JAFFE D., Fitzhugh W., Ma L.-J., Smirnov S., Purcell S., Rehan B.,
RA Bikine T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
RA Qui D., Iankiev P., Pedersen D., Nelson M., Washburne M.,
RA Seltrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
RA Kothe G.O., Jedd K., Mewes W., Scaben C., Martote E., Greenberg D.,
RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Gierke S.,
RA Kamal M., Kamysheva M., Mauceli E., Bielke C., Rudd S., Frishman D.,
RA Kryazova S., Rasmussen C., Metzberg R.L., Perkins D.D., Kroken S.,
RA Cogoni C., Macino G., Carlsbeide D., Li W., Pratt R.J., Omani S.A.,
RA Desouza C.C., Glaser L., Orbach M.J., Berglund J., Voelker R.,
RA Yarden O., Plamann M., Selzer S., Dunlap J., Radford A., Atamayo R.,
RA Natvig D.O., Alex L.A., Manhaupt G., Ebbola D.J., Prellag M.,
RA Paulsen I., Sachs M.B., Lander B.S., Nussbaum C., Birren B.,
RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
RT Nature 0:0-0 (2003).
-1- CAUTION: The sequence shown here is derived from an
preliminary data.

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC EMBL/ABX01000220; EMBL2832.1; -; Genomic DNA.
SQ SEQUENCE 13 AA; 1543 MW; 091807018C8D404B CRC64;

Query Match 27.8%; Score 32; DB 2; Length 13;
Best Local Similarity 36.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 8 IHKYLVCESVN 18
: | | | | : | | | |
DB 3 VHTYINCTALN 13

RESULT 7

ID 04X4H2_PLACH PRELIMINARY; PRT; 10 AA.

AC 04X4H2,
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC400586.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
[1]
RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Plorens L., Jansen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Truman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses."
RT Science 307:82-86(2005).
-1- CAUTION: The sequence shown here is derived from an
preliminary data.

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC EMBL/CAJ010050; CAH8321.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1230 MW; 4C729FD7205059C3 CRC64;

Query Match 26.1%; Score 30; DB 2; Length 10;
Best Local Similarity 30.0%; Pred. No. 8.5e+02;
Matches 3; Conservative 6; Mismatches 1; Indels 0; Gaps 0;

QY 8 IHKYLVCESV 17
: | | | | : | | | |
DB 1 MHKFIILGSI 10

RESULT 8

ID 016244_HUMAN PRELIMINARY; PRT; 18 AA.

AC 016244,
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE SFS protein (Fragment).
GN Name=SFS;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
[1]
RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=95038775; PubMed=7951263;
RA Yen P.H., Ferrero G.B., Chinault A.C., Mohandas T., Ballabio A.,
RT "Characterization of the deletion breakpoints in a patient with
steroid sulfatase deficiency."
RT Hum. Mutat. 4:76-78(1994).
DR EMBL: S74383; AAD14153.1; -; Genomic DNA.
FT NON_TER 18 18

SQ SEQUENCE 18 AA; 1958 MW; 3B3072711330CCFA CRC64;

Query Match 26.1%; Score 30; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 1.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHEPTNHHKLVLC 14
| | | | |
DB 7 PCRVNHSYOLC 18

RESULT 9

ID TWOF_SARBU STANDARD; PRT; 6 AA.

AC P41495,
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Tryptin-modulating oostatic factor (TWOF).
OS Sarcophaga bullata (Grey flesh fly) (Neobellieria bullata).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachyera; Muscomorpha; Oestroidea;
OC Sarcophagidae; Sarcophaga; Neobellieria.
OX NCBI_TaxID=7385;

RN [1]
 RP PROTEIN SEQUENCE, AND SYNTHESIS.
 RC TISSUE=Ovary;
 RX MEDLINE=94211930; PubMed=8159807; DOI=10.1016/0167-0115(94)90192-9;
 RA Bylemans D., Borovsky D., Hunt D.F., Shabanowitz J., Grauwels L.,
 de Loof A.;
 RT "Sequencing and characterization of trypsin modulating oostatic factor
 (TMOF) from the ovaries of the grey fleshfly, Neobellieria
 (Sarcophaga) bullata.";
 RL Regul. Pept. 50:61-72(1994).
 CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
 in the midgut which indirectly reduces the vitellogenin
 concentration in the hemolymph resulting in inhibition of oocyte
 development.
 CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
 epithelium after a blood meal.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Direct protein sequencing; Hormone.
 SQ SEQUENCE 6 AA; 695 MW; 61B72451B7642000 CRC64;

Query Match 25.2%; Score 29; DB 1; Length 6;
 Best Local Similarity 66.7%; Pred. No. 2.2e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTNIN 9
 :|:|:|
 DB 1 NPTNLA 6

RESULT 10
 QSEX89_9LAMI PRELIMINARY; PRT; 19 AA.
 ID QSEX89_9LAMI
 AC QSEX89_9LAMI
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE STM2 protein (Fragment).
 OS Streptococcus venosus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
 OC Streptocarpus.
 OC NCBI_TaxID=301922;
 RX NCBI_TaxID=301922;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=B;
 RX PubMed=15659624; DOI=10.1105/lpc.104.028936;
 RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
 RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
 Streptocarpus.";
 RL Plant Cell 17:430-443(2005).
 DR EMBL; AY662115; AA033769.1; -; Genomic_DNA.
 DR InterPro; IPR001356; Homeobox.
 DR ProDom; PD000010; Homeobox; 1.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2057 MW; 1069FC9782AFD64A CRC64;

Query Match 25.2%; Score 29; DB 2; Length 19;
 Best Local Similarity 35.7%; Pred. No. 2.5e+03;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPTNINHKYLVCS 16
 :|:|:|:|
 DB 1 PYPSEXOKLALAS 14

RESULT 11
 QSEX77_9LAMI PRELIMINARY; PRT; 19 AA.
 ID QSEX77_9LAMI
 AC QSEX77_9LAMI
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE STM1 protein (Fragment).
 OS Streptocarpus thyanotus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
 OC Streptocarpus.
 OC NCBI_TaxID=167308;
 RX NCBI_TaxID=167308;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15659624; DOI=10.1105/lpc.104.028936;
 RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
 RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
 Streptocarpus.";
 RL Plant Cell 17:430-443(2005).
 DR EMBL; AY662127; AA033745.1; -; Genomic_DNA.
 DR InterPro; IPR001356; Homeobox.
 DR ProDom; PD000010; Homeobox; 1.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
 Best Local Similarity 35.7%; Pred. No. 3.6e+03;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPTNINHKYLVCS 16
 :|:|:|:|
 DB 1 PYPSEXOKLALAS 14

RESULT 12
 QSEX78_9LAMI PRELIMINARY; PRT; 19 AA.
 ID QSEX78_9LAMI
 AC QSEX78_9LAMI
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE STM1 protein (Fragment).
 OS Streptocarpus glandulosissimus.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
 OC Streptocarpus.
 OC NCBI_TaxID=167270;
 RX NCBI_TaxID=167270;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15659624; DOI=10.1105/lpc.104.028936;
 RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
 RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
 Streptocarpus.";
 RL Plant Cell 17:430-443(2005).
 DR EMBL; AY662126; AA033744.1; -; Genomic_DNA.
 DR InterPro; IPR001356; Homeobox.
 DR ProDom; PD000010; Homeobox; 1.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
 Best Local Similarity 35.7%; Pred. No. 3.6e+03;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PPTNINHKYLVCS 16
 :|:|:|:|
 DB 1 PYPSEXOKLALAS 14

```
RESULT 13
Q5EX88_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX88;
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptococcus beaumontensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=167246;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662116; AAW33770.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
FT SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNKHXYLVCS 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14

RESULT 14
Q5EX90_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX90;
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus venosus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=301922;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662114; AAW33768.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
FT SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNKHXYLVCS 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14
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DB 1 PYPSESQKLALAS 14

RESULT 15
Q5EX91_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX91;
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus thompsonii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=167307;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662113; AAW33767.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
FT SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNKHXYLVCS 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14

RESULT 16
Q5EX92_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EX92;
DT 10-MAY-2005 (TRENBLREL. 30, Created)
DT 10-MAY-2005 (TRENBLREL. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus primulifolius.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OX NCBI_TaxID=64018;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662112; AAW33766.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
FT SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNKHXYLVCS 16
|:|:|:|:|
DB 1 PYPSESQKLALAS 14
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Db 1 PYPSESQKLALES 14

RESULT 17
QSEX94_9LAMI PRELIMINARY; PRT; 19 AA.

AC QSEX94; 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus modestus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
NCBI_TaxId=167287;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A, and B;
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RT Plant Cell 17:430-443(2005).
RL EMBL; AY662111; AAW33765.1; -; Genomic_DNA.
DR EMBL; AY662110; AAW33764.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPNTNHYKLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 18
QSEX95_9LAMI PRELIMINARY; PRT; 19 AA.

AC QSEX95; 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus hirticarpa.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
NCBI_TaxId=167276;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RT Plant Cell 17:430-443(2005).
RL EMBL; AY662109; AAW33763.1; -; Genomic_DNA.
DR EMBL; AY662122; AAW33740.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;

Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPNTNHYKLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 19
QSEX96_9LAMI PRELIMINARY; PRT; 19 AA.

AC QSEX96; 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus burundianus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
NCBI_TaxId=167253;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RT Plant Cell 17:430-443(2005).
RL EMBL; AY662108; AAW33762.1; -; Genomic_DNA.
DR EMBL; AY662123; AAW33741.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPNTNHYKLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 20
QSEX97_9LAMI PRELIMINARY; PRT; 19 AA.

AC QSEX97; 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus witell.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianaceae; Cyrtandroideae; Didymocarpaceae;
OC Streptocarpus.
NCBI_TaxId=167311;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/ltpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
Streptocarpus.";
RT Plant Cell 17:430-443(2005).
RL EMBL; AY662107; AAW33761.1; -; Genomic_DNA.
DR EMBL; AY662123; AAW33741.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER 1 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%, Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
|:|:|:|:
Db 1 PYPSESQKALAES 14

RESULT 21

QSEX99_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEX98_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX98;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
OS STM2 protein (Fragment).
OC Streptococcus roxii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Geeneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=121488;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus".
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662106; AAW33760.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%, Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
|:|:|:|:
Db 1 PYPSESQKALAES 14

RESULT 22

QSEX99_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEX99_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEX99;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
OS STM2 protein (Fragment).
OC Streptocarpus wendlandii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Geeneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167310;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus".
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662105; AAW33759.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 19 19

SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%, Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
|:|:|:|:
Db 1 PYPSESQKALAES 14

RESULT 23

QSEXA1_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEXA1_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA1;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
OS STM2 protein (Fragment).
OC Streptocarpus dunali.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Geeneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=121487;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus".
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662103; AAW33757.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1 1
FT NON_TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%, Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PHPTNIHKYLVCS 16
|:~:~:~:~:
Db 1 PYPSESQKALAES 14

RESULT 24

QSEXA2_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEXA2_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA2;
DT 10-MAY-2005 (TREMBLrel. 30, Created)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
OS STM2 protein (STM1 protein) (Fragment).
OC Streptocarpus schlieffenii.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Geeneriaceae; Cyrtandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167302;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus".
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662102; AAW33756.1; -; Genomic_DNA.
DR EMBL; AY662124; AAW33742.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.

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FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHKYLVCES 16
Db 1 PYPSESQKLALAES 14

RESULT 25
QSEXA3_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEXA3_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus ibitiensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167279;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662101; AAW3375.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHKYLVCES 16
Db 1 PYPSESQKLALAES 14

RESULT 26
QSEXA4_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEXA4_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus ibitiensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167278;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=A, and B;
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662100; AAW33754.1; -; Genomic_DNA.
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DR EMBL; AY662120; AAW33738.1; -; Genomic_DNA.
DR EMBL; AY662121; AAW33739.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHKYLVCES 16
Db 1 PYPSESQKLALAES 14

RESULT 27
QSEXA5_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEXA5_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus papangae.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167293;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus.";
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662099; AAW33753.1; -; Genomic_DNA.
DR EMBL; AY662118; AAW33737.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON TER 1 1
FT NON TER 19 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHKYLVCES 16
Db 1 PYPSESQKLALAES 14

RESULT 28
QSEXA6_9LAMI PRELIMINARY; PRT; 19 AA.
ID QSEXA6_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus saxorum.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gesneriaceae; Cytrandroideae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=48776;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
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RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662098; AAW33752.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 29
QSEXA7_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA7;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (STM1 protein) (Fragment).
OS Streptocarpus pallidiflorus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Cytrandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=67292;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662097; AAW33751.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 30
QSEXA8_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA8;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Streptocarpus stomandrus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Cytrandroideae; Didymocarpeae;
OC Streptocarpus.
OC NCBI_TaxID=167305;
RN NUCLEOTIDE SEQUENCE.

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RC STRAIN=A;
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662096; AAW33750.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 31
QSEXA9_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXA9;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Saltpaulia velutina.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Cytrandroideae; Didymocarpeae;
OC Saltpaulia.
OC NCBI_TaxID=86150;
RN NUCLEOTIDE SEQUENCE.
RP PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662095; AAW33749.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR Prodom; PD000010; Homeobox; 1.
FT NON_TER 1
FT NON_TER 19
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match
Best Local Similarity 24.3%; Score 28; DB 2; Length 19;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNIHKYLVCS 16
Db 1 PYPSESQKLALES 14

RESULT 32
QSEXB0_9LAMI PRELIMINARY; PRT; 19 AA.
AC QSEXB0;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Saltpaulia ionantha.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Cytrandroideae; Didymocarpeae;
OC Saltpaulia.

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OX NCB1_TaxID=85262;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
  Streptocarpus.";
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662094; AAM33748.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHYKLVCS 16
Db 1 PYPSESQKLALAS 14

RESULT 33
O5EXB1_9LAMI PRELIMINARY; PRT; 19 AA.
ID O5EXB1_9LAMI
AC O5EXB1_9LAMI
DT 10-MAY-2005 (T-EMBLrel. 30, Created)
DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
DE STM2 protein (Fragment).
OS Sainpaulia longensis.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Gentianales; Gentianeaceae; Cyrtandroidae; Didymocarpaceae;
OC Sainpaulia.
OX NCB1_TaxID=86149;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=B, and A;
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
  Streptocarpus.";
RT Plant Cell 17:430-443(2005).
DR EMBL; AY662093; AAM33747.1; -; Genomic_DNA.
DR EMBL; AY662092; AAM33746.1; -; Genomic_DNA.
DR InterPro; IPR001356; Homeobox.
DR ProDom; PD000010; Homeobox; 1.
FT NON_TER
FT NON_TER
SQ SEQUENCE 19 AA; 2034 MW; 1069FC9782A6314A CRC64;

Query Match 24.3%; Score 28; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 3 PHPTNHYKLVCS 16
Db 1 PYPSESQKLALAS 14

RESULT 34
Q4YMN1_PLABE PRELIMINARY; PRT; 20 AA.
ID Q4YMN1_PLABE
AC Q4YMN1_PLABE
DT 13-SEP-2005 (T-EMBLrel. 31, Created)
DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (T-EMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
ORFNames=PB400077.00.0;
OS Plasmodium berghel.

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karris M., Raine J.D., Carlton J.M., Kool T.W.A.,
RA Berrieman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnuel D.J., Yates J.R., Kafatos F.C.,
RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
  transcriptomic, and proteomic analyses.";
RT Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
  EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
  preliminary data.
CC EMBL; CA01003517; CA0100729.1; -; Genomic_DNA.
DR Hypothetical protein.
FT NON_TER
FT NON_TER
SQ SEQUENCE 20 AA; 2221 MW; CB1EB3142E99E869 CRC64;

Query Match 24.3%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 KYLVCS 15
Db 12 KYLVCD 17

RESULT 35
O26062_HELPSY PRELIMINARY; PRT; 18 AA.
ID O26062_HELPSY
AC O26062_HELPSY
DT 01-JAN-1998 (T-EMBLrel. 05, Created)
DT 01-JAN-1998 (T-EMBLrel. 05, Last sequence update)
DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
DE Hypothetical protein HPI536.
GN OrderedCusNames=HPI536;
OS Helicobacter pylori (Campylobacter pylori).
OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;
OC Helicobacteraceae; Helicobacter.
OX NCB1_TaxID=210;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=26695 / ATCC 700392;
RX MEDLINE=979394467; PubMed=9252185; DOI=10.1038/41483;
RA Tomb J.-F., White O., Kerlavage A.R., Clayton R.A., Sutton G.G.,
RA Fleischmann R.D., Ketchum K.A., Klein H.-P., Gill S.R.,
RA Dougherty B.A., Nelson K.E., Quackenbush J., Zhou L., Kirkness B.F.,
RA Peterson S.N., Loftus B.J., Richardson D.L., Dodson R.J., Khalak H.G.,
RA Glodek A., McKenney K., Fitzgerald L.M., Lee N., Adams W.D.,
RA Hickey E.K., Berg D.B., Gocayne J.D., Uterback T.R., Peterson J.D.,
RA Wathey L., Wallin B., Hayes W.S., Borodovsky M., Karp P.D.,
RA Smith H.O., Fraser C.M., Venter J.C.;
RT "The complete genome sequence of the gastric pathogen Helicobacter
  pylori.";
RT Nature 388:539-547(1997).
DR EMBL; AE000651; AAD08578.1; -; Genomic_DNA.
DR PIR; H64711; H64711.
DR TIGR; HP1536; -.
KW Complete proteome; Hypothetical protein.
SQ SEQUENCE 18 AA; 2296 MW; AC0B5A3DPD9CD482 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 4.9e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 HPTNHYKLV 12
Db 10 HPSRNPXYL 18

```

RESULT 36

Q4XJ38_PLACH

ID Q4XJ38_PLACH PRELIMINARY; PRT; 19 AA.

AC Q4XJ38; DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DE Hypothetical protein.

GN ORFNames=PC400757.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=5825;

[1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

RT transcriptomic, and proteomic analyses."

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL/CAJ01005589; CAH83076.1; -; Genomic_DNA.

KM Hypothetical protein.

SQ SEQUENCE 19 AA; 2375 MW; 339771F259128CNC CRC64;

Query Match 23.5%; Score 27; DB 2; Length 19;

Best Local Similarity 55.6%; Pred. No. 5.2e+03;

Matches 5; Conservative 2; Mismatches 0; Indels 2; Gaps 1;

QY 8 IHK-YLVC 14

DB 3 VHKCTYIVC 11

RESULT 37

Q4YK87_PLABR

ID Q4YK87_PLABR PRELIMINARY; PRT; 19 AA.

AC Q4YK87; DT 13-SEP-2005 (TrEMBLrel. 31, Created)

DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

DE Hypothetical protein (Fragment).

GN ORFNames=PA401730.00.0;

OS Plasmodium berghei.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=5821;

[1]

RP NUCLEOTIDE SEQUENCE.

RA Hall N., Karras M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,

RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

RT transcriptomic, and proteomic analyses."

RL Science 307:82-86(2005).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL/CAJ01004271; CAI01575.1; -; Genomic_DNA.

KM Hypothetical protein.

SQ SEQUENCE 19 AA; 2230 MW; E9A5F910F35E0F35 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 19;

Best Local Similarity 55.6%; Pred. No. 5.2e+03;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 IHPHTNKH 10

DB 8 LPPRNIFK 16

RESULT 38

Q7RR59_PLAYO

ID Q7RR59_PLAYO PRELIMINARY; PRT; 20 AA.

AC Q7RR59; DT 01-MAR-2004 (TrEMBLrel. 26, Created)

DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

DE Hypothetical protein (Fragment).

GN Name=PY00877;

OS Plasmodium yoelii yoelii.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=73239;

[1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=17XN1;

RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;

RA Carlton J.M., Anguol S.V., Suh B.B., Kool J.T.W., Perica M.,

RA Silva J.C., Emolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,

RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,

RA Shalom S.J., van Aken S.B., Riedmiller S.B., Feldbylum T.V.,

RA Cho J.K., Quackenbush J., Sedegah M., Shoaihi A., Cummings L.M.,

RA Florens L., Yates J.R. III, Ratne J.D., Sinden R.E., Harris M.A.,

RA Cunningham D.A., Pfeiser P.R., Bergman L.W., Valdivia A.B.,

RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,

RA Carucci D.J.;

RT "Genome sequence and comparative analysis of the model rodent malaria

RT parasite Plasmodium yoelii yoelii."

RL Nature 419:512-519(2002).

CC -1- CAUTION: The sequence shown here is derived from an

CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

CC preliminary data.

CC EMBL/AAJ01000235; EAA19069.1; -; Genomic_DNA.

KM Hypothetical protein.

FT NON TER 20

SQ SEQUENCE 20 AA; 2509 MW; 85C3599786475AA6 CRC64;

Query Match 23.5%; Score 27; DB 2; Length 20;

Best Local Similarity 27.3%; Pred. No. 5.5e+03;

Matches 3; Conservative 6; Mismatches 2; Indels 0; Gaps 0;

QY 7 NIHKYLCBSV 17

DB 8 NIYVIMONI 18

RESULT 39

Q9UMR0_HUMAN

ID Q9UMR0_HUMAN PRELIMINARY; PRT; 12 AA.

AC Q9UMR0; DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).

GN Name=FBP2;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;

OC Homo.

NCBI_TaxID=9606;

[1]

RP NUCLEOTIDE SEQUENCE.

RA MEDLINE=20237676; PubMed=10773464; DOI=10.1016/S0378-1119(00)00079-2;

RA Tilmann H., Stein S., Ijeh T., Bechtich K.;

RT "Structure and chromosomal localization of the human and mouse muscle

fructose-1,6-bisphosphatase genes."

RL Gene 247:241-253(2000).
 DR EMBL; AJ238483; CAB53359.1; -; Genomic DNA.
 DR GO; GO:004132; F:fructose-bisphosphatase activity; IEA.
 DR GO; GO:0016787; F:hydrolase activity; IEA.
 KM Hydrolase.
 FT NON_TER 1 1
 SQ SEQUENCE 12 AA; 1382 MW; 4CEB259E57386403 CRC64;

Query Match
 Best Local Similarity 22.6%; Score 26; DB 2; Length 12;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 10 KYLVC 14
 Db 8 KYVVC 12

RESULT 40

Q4LOW0 BACTK
 ID Q4LOW0 BACTK PRELIMINARY; PRT; 17 AA.

AC Q4LOW0
 DT 13-SEP-2005 (TREMBLrel. 31, Created)
 DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
 DE Methyltransferase (Fragment).
 OS Bacillus thuringiensis (subsp. kurstaki).
 OC Bacteria; Firmicutes; Bacilliales; Bacillaceae; Bacillus;
 OC Bacillus cereus group.
 OK NCBI_TaxID=29339;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=8010;
 RA Huang T., Yu X., Guan X.;
 RT "Differential expression of genes at different growth phases in
 RT *Bacillus thuringiensis* strain 8010."
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY646411; AAV65152.1; -; mRNA.
 KM Methyltransferase; Transferase.
 FT NON_TER 1 1
 SQ SEQUENCE 17 AA; 2201 MW; 49C3D8C675DB667F CRC64;

Query Match
 Best Local Similarity 22.6%; Score 26; DB 2; Length 17;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 9 HKYLVCE 15
 Db 10 HRIPIICE 16

RESULT 41

Q9XN07 BOOMT
 ID Q9XN07 BOOMT PRELIMINARY; PRT; 19 AA.

AC Q9XN07
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Cytochrome b apoenzyme (Fragment).
 GN Name=Cyb;
 OS *Boophilus microplus* (Cattle tick).
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.
 OK NCBI_TaxID=6941;
 RN [1]

NUCLEOTIDE SEQUENCE.

RP STRAIN=N;
 RX MEDLINE=99297341; PubMed=10368952;

RA Campbell N.J.H., Barker S.C.;
 RT "The novel mitochondrial gene arrangement of the cattle tick,
 RT *Boophilus microplus*: fivefold tandem repetition of a coding region";
 RT Mol. Biol. Evol. 16:732-740(1999).

DR EMBL; AF110611; AAD28394.1; -; Genomic DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2144 MW; 07A018D65CEBD8D0 CRC64;

Query Match
 Best Local Similarity 22.6%; Score 26; DB 2; Length 19;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DHPPTNI 8
 Db 10 NLPPTNSI 17

RESULT 42

Q5EX86 GLAMI
 ID Q5EX86 GLAMI PRELIMINARY; PRT; 19 AA.

AC Q5EX86
 DT 10-MAY-2005 (TREMBLrel. 30, Created)
 DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
 DE STM2 protein (Fragment).
 OS Streptocarpus sp. JH-2004.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroidae; Didymocarpaceae;
 OC Streptocarpus.
 OK NCBI_TaxID=301924;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed=15659624; DOI=10.1105/epc.104.026936;
 RA Harrison J., Moller M., Langdale J., Cronk O., Hudson A.;
 RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
 RT *Streptocarpus*."
 RT Plant Cell 17:430-443(2005).
 DR EMBL; AY662118; AAW3772.1; -; Genomic DNA.
 DR InterPro: IPR001356; Homeobox.
 DR Prodom: PDD00010; Homeobox; 1.
 FT NON_TER 1 1
 FT NON_TER 19 19
 SQ SEQUENCE 19 AA; 2073 MW; 3D69FC9782A6315D CRC64;

Query Match
 Best Local Similarity 22.6%; Score 26; DB 2; Length 19;
 Matches 5; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

Qy 3 PPTNIHKYLVCS 16
 Db 1 PYPSESQKALXES 14

RESULT 43

PHYLA PHYOR
 ID PHYLA PHYOR STANDARD; PRT; 20 AA.

AC P84569
 DT 13-SEP-2005 (Rel. 48, Created)
 DT 13-SEP-2005 (Rel. 48, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Phylloleptin-4 (PS-4).
 OS *Phyllomedusa oreades* (Monkey frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Batrachia;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 OK NCBI_TaxID=239355;
 RN [1]

PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,

MASS SPECTROMETRY, AND AMIDATION.

RC TISSUE-Skin secretion;
 RX PubMed=15752569; DOI=10.1016/j.peptides.2004.11.002;
 RA Leite J.R.S.A., Silva L.P., Rodrigues M.I.S., Prates M.V., Brand G.D.,
 RA Lacerda B.M., Azevedo R.B., Bocca A.L., Albuquerque S., Bloch C. Jr.;
 RT "Phylloleptins: a novel class of anti-bacterial and anti-protozoan

RT peptides from the *Phyllomedusa genus*."
 RL Peptides 26:565-573(2005).
 CC -1- FUNCTION: Has antiprotozoal activity against *T. cruzi*.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
 CC -1- MASS SPECTROMETRY: MW=2112.18; METHOD=WALDI; RANGE=1-20;
 CC NOTE-Ref.1.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

CC Antidation: Amphibian defense peptide; Antimicrobial;
 KM Direct protein sequencing. Glycine amide.
 PT MOD RES 20 20 C648DIC5C8B91CFP CRC64;
 SQ SEQUENCE 20 AA; 2113 MW; 648DIC5C8B91CFP CRC64;

Query Match 22.6%; Score 26; DB 1; Length 20;
 Best Local Similarity 46.7%; Pred. No. 8e+03;
 Matches 7; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 2 IPRPTNHYKLVCS 16
 |||
 Db 5 IPRHNAVSTLVHNS 19

RESULT 44
 ID Q7RS12.PLAYO PRELIMINARY; PRT; 20 AA.
 AC Q7RS12;
 DT 01-MAR-2004 (T-EMBLrel. 26, Created)
 DT 01-MAR-2004 (T-EMBLrel. 26, Last sequence update)
 DE 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)
 GN Hypothetical protein.
 OS Name=PY00375;
 OS Plasmodium yoelii yoelii.
 OS Eukaryota, Alveolata, Apicomplexa, Haemosporida, Plasmodium.
 OC NCB1_TaxID=73259;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.

RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=1236865; DOI=10.1038/nature01099;
 RA Carlson J.M., Angluoli S.V., Sun B.B., Kooij T.W., Ferreira M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.D., Van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoabhi A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sindén R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA Van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RA "Genome sequence and comparative analysis of the model rodent malaria
 parasite *Plasmodium yoelii yoelii*."
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL: AABL0100104; EMBL337.1; -; Genomic_DNA.
 CC DR EMBL: AABL0100104; EMBL337.1; -; Genomic_DNA.
 CC KM Hypothetical protein.
 SQ SEQUENCE 20 AA; 2624 MW; 69E080147DF5DB06 CRC64;

Query Match 22.6%; Score 26; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 8e+03;
 Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 NHHKYVCSBV 17
 |||
 Db 6 NIPRYLFMDTI 16

RESULT 45
 ID OSK4V0.BOVIN PRELIMINARY; PRT; 20 AA.
 AC OSK4V0;
 DT 10-MAY-2005 (T-EMBLrel. 30, Created)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (T-EMBLrel. 30, Last annotation update)
 DE Zinc finger Y-chromosomal protein (Fragment).
 GN Name=ZFY;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 CC Pecora; Bovidae; Bovinae; Bos.
 OC NCB1_TaxID=9913;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.

RA Durstewitz G., Werner F.A.O., Bultkamp J., Thaller G., Kraemer W.,
 RA Kollers S., Brem G., Pfisterhammer J., Lips U., Borchers H.,
 RA Mosner J., Fries R.;
 RA "Discovery of SNPs for digital DNA signatures in cattle."
 RL Submitted (Aug-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A507102; CAD45343.1; -; Genomic_DNA.
 DR GO: GO:0005634; C:nucleus; IEA.
 DR GO: GO:0003676; F:nucleic acid binding; IEA.
 DR GO: GO:0008270; F:zinc ion binding; IEA.
 DR InterPro: IPR007087; Znf_C2H2.
 DR Pfam: PF00096; Zf_C2H2; 1.
 DR ProDom: PD000003; Znf_C2H2; 1.
 DR PROSITE: PSS0157; ZINC_FINGER_C2H2_2; 1.
 FT NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2320 MW; 931EC10F3FDDBE2F CRC64;

Query Match 22.6%; Score 26; DB 2; Length 20;
 Best Local Similarity 33.3%; Pred. No. 8e+03;
 Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNHYTL 12
 |||
 Db 7 HPSLKKHM 15

RESULT 46
 ID Q90X94.CHICK PRELIMINARY; PRT; 20 AA.
 AC Q90X94;
 DT 01-DEC-2001 (T-EMBLrel. 19, Created)
 DT 01-DEC-2001 (T-EMBLrel. 19, Last sequence update)
 DT 01-UTN-2002 (T-EMBLrel. 21, Last annotation update)
 DE Tyrosinase (Fragment).
 GN Name=TYR;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCB1_TaxID=9031;
 OX (1)
 RN NUCLEOTIDE SEQUENCE.

RA Deng X., Yang Y., Liu W.;
 RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AP416913; AML14559.1; -; Genomic_DNA.
 DR NON_TER 1 1
 FT NON_TER 20 20
 SQ SEQUENCE 20 AA; 2198 MW; 13282PB31CD17AA CRC64;

Query Match 22.6%; Score 26; DB 2; Length 20;
 Best Local Similarity 100.0%; Pred. No. 8e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 HPTN 7
 |||
 Db 17 HPTN 20

RESULT 47

Q8MM58_9NEOP PRELIMINARY; PRT; 11 AA.

AC Q8MM58; 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius cydno chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=171915;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
RL Mallet J.,
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516223; AAM61908.1; -; Genomic DNA.
DR EMBL; AF516223; AAM61909.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 11 AA; 1312 MW; 56A67DB31BD1EA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 11;
Best Local Similarity 66.7%; Pred. No. 6.1e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9
|||
Db 1 HPTKDH 6

RESULT 48

Q8MUN4_9NEOP PRELIMINARY; PRT; 12 AA.

AC Q8MUN4; 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius melpomene melpomene.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=171917;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
RL Mallet J.,
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516254; AAM61940.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1383 MW; 56A67DE318D1EA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9
|||
Db 2 HPTKDH 7

RESULT 49

Q8MUN9_9NEOP PRELIMINARY; PRT; 12 AA.

AC Q8MUN9; 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 29, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius melpomene rosiina.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=171916;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
RL Mallet J.,
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516231; AAM61917.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1383 MW; 56A67DE318D1EA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 6.7e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9
|||
Db 2 HPTKDH 7

RESULT 50

Q8MM57_9NEOP PRELIMINARY; PRT; 13 AA.

AC Q8MM57; 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
DE Mannose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius melpomene rosiina.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxID=171916;
RN [1]

RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
RL Mallet J.,
Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516233; AAM61919.1; -; Genomic DNA.
DR EMBL; AF516234; AAM61920.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 13 AA; 1512 MW; 56A67DE35C84EA3 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 7.3e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 HPTNTH 9
|||
Db 3 HPTKDH 8

RESULT 51

Q8MUN8_9NEOP PRELIMINARY; PRT; 14 AA.

AC OBMUN8;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN Name=Mpi;
 OS Heliconius melpomene rosina.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
 OX NCBI_TaxID=171916;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bull V., Beltiran M., Bermingham E., Jiggins C., McMillan O.,
 Mallet J.,
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516232; AAM61918.1; -; Genomic DNA.
 DR GO; GO:0016853; P:isomerase activity; IEA.
 KW Isomerase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 14 AA; 1625 MW; 56A67DE35CDECTA3 CRC64;
 QY Query Match 21.7%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 7.9e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 4 HPTNTH 9
 DB 4 HPTKDH 9

RESULT 52
 OBMUP2_9NEOP PRELIMINARY; PRT; 14 AA.
 ID OBMUP2_9NEOP PRELIMINARY; PRT; 14 AA.
 AC OBMUP2;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN Name=Mpi;
 OS Heliconius cydno chioneus.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
 OX NCBI_TaxID=171915;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bull V., Beltiran M., Bermingham E., Jiggins C., McMillan O.,
 Mallet J.,
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516221; AAM61907.1; -; Genomic DNA.
 DR GO; GO:0016853; P:isomerase activity; IEA.
 KW Isomerase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 14 AA; 1625 MW; 56A67DE35CDECTA3 CRC64;
 QY Query Match 21.7%; Score 25; DB 2; Length 14;
 Best Local Similarity 66.7%; Pred. No. 7.9e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 4 HPTNTH 9
 DB 4 HPTKDH 9

RESULT 53
 OQBZNO_HUMAN PRELIMINARY; PRT; 15 AA.
 ID OQBZNO_HUMAN PRELIMINARY; PRT; 15 AA.
 AC OQBZNO;
 DT 01-JUN-2001 (TReMBLrel. 17, Created)
 DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)

DT 01-JUN-2001 (TReMBLrel. 17, Last annotation update)
 DE CD36 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN=1955;
 RA Gelhaus A., Scheding A., Browne E., Burchard G.D., Horetman R.D.;
 RT "CD36 mutations in West Africa."
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF306531; AAC60630.1; -; Genomic DNA.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 15 AA; 1770 MW; EF2226C56D1B8E47 CRC64;
 QY Query Match 21.7%; Score 25; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 8.5e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 DB 14 CDSVNG 19
 DB 9 CDWING 14

RESULT 54
 OBMUP2_9NEOP PRELIMINARY; PRT; 15 AA.
 ID OBMUP2_9NEOP PRELIMINARY; PRT; 15 AA.
 AC OBMUP2;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN Name=Mpi;
 OS Heliconius cydno chioneus.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
 OX NCBI_TaxID=171915;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Bull V., Beltiran M., Bermingham E., Jiggins C., McMillan O.,
 Mallet J.,
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF516211; AAM61897.1; -; Genomic DNA.
 DR GO; GO:0016853; P:isomerase activity; IEA.
 KW Isomerase.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 15 AA; 1712 MW; 56A67DE35CDE817C CRC64;
 QY Query Match 21.7%; Score 25; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 8.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 DB 4 HPTNTH 9
 DB 5 HPTKDH 10

RESULT 55
 OBMW83_9NEOP PRELIMINARY; PRT; 16 AA.
 ID OBMW83_9NEOP PRELIMINARY; PRT; 16 AA.
 AC OBMW83;
 DT 01-OCT-2002 (TReMBLrel. 22, Created)
 DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
 DT 01-FEB-2005 (TReMBLrel. 29, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN Name=Mpi;
 OS Heliconius melpomene rosina.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

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OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=171916;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
  Mallet J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516224; AAM61910.1; -; Genomic DNA.
DR EMBL; AF516225; AAM61911.1; -; Genomic DNA.
DR EMBL; AF516226; AAM61912.1; -; Genomic DNA.
DR EMBL; AF516227; AAM61913.1; -; Genomic DNA.
DR EMBL; AF516228; AAM61914.1; -; Genomic DNA.
DR EMBL; AF516229; AAM61915.1; -; Genomic DNA.
DR EMBL; AF516230; AAM61916.1; -; Genomic DNA.
DR EMBL; AF516231; AAM61921.1; -; Genomic DNA.
DR EMBL; AF516236; AAM61922.1; -; Genomic DNA.
DR EMBL; AF516238; AAM61924.1; -; Genomic DNA.
DR EMBL; AF516239; AAM61925.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 16;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
   |||
Db 6 HPTKDH 11

RESULT 56
QBMM84_9NEOP PRELIMINARY; PRT; 16 AA.
ID QBMM84_9NEOP
AC QBMM84;
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-FEB-2003 (TReMBLrel. 29, Last annotation update)
DE Mammose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius melpomene melpomene.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=171917;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
  Mallet J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516240; AAM61926.1; -; Genomic DNA.
DR EMBL; AF516241; AAM61927.1; -; Genomic DNA.
DR EMBL; AF516242; AAM61928.1; -; Genomic DNA.
DR EMBL; AF516243; AAM61929.1; -; Genomic DNA.
DR EMBL; AF516244; AAM61930.1; -; Genomic DNA.
DR EMBL; AF516245; AAM61931.1; -; Genomic DNA.
DR EMBL; AF516246; AAM61932.1; -; Genomic DNA.
DR EMBL; AF516248; AAM61934.1; -; Genomic DNA.
DR EMBL; AF516249; AAM61935.1; -; Genomic DNA.
DR EMBL; AF516251; AAM61937.1; -; Genomic DNA.
DR EMBL; AF516253; AAM61939.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 16;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
   |||
Db 6 HPTKDH 11

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QY 4 HPTNTH 9
   |||
Db 6 HPTKDH 11

RESULT 57
QBMM85_9NEOP PRELIMINARY; PRT; 16 AA.
ID QBMM85_9NEOP
AC QBMM85;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-FEB-2003 (TReMBLrel. 29, Last sequence update)
DE Mammose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius cytho chioneus.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=171915;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
  Mallet J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516210; AAM61896.1; -; Genomic DNA.
DR EMBL; AF516212; AAM61898.1; -; Genomic DNA.
DR EMBL; AF516214; AAM61900.1; -; Genomic DNA.
DR EMBL; AF516215; AAM61901.1; -; Genomic DNA.
DR EMBL; AF516216; AAM61902.1; -; Genomic DNA.
DR EMBL; AF516217; AAM61903.1; -; Genomic DNA.
DR EMBL; AF516218; AAM61904.1; -; Genomic DNA.
DR EMBL; AF516219; AAM61905.1; -; Genomic DNA.
DR EMBL; AF516220; AAM61906.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 16;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
   |||
Db 6 HPTKDH 11

RESULT 58
QBMM83_9NEOP PRELIMINARY; PRT; 16 AA.
ID QBMM83_9NEOP
AC QBMM83;
DT 01-OCT-2002 (TReMBLrel. 22, Created)
DT 01-OCT-2002 (TReMBLrel. 22, Last sequence update)
DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
DE Mammose phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius numata.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=33419;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bull V., Beltran M., Bermingham E., Jiggins C., McMillan O.,
  Mallet J.;
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF516255; AAM61941.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
KW Isomerase.
FT NON_TER 1 1
SQ SEQUENCE 16 AA; 1825 MW; 1CE67DB35CDB8122 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 16;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
   |||
Db 6 HPTKDH 11

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SEQ SEQUENCE 16 AA; 1825 MW; 1CE67DE35CDE8122 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 9.1e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | | |
| | | |
Db 6 HPTKDH 11

RESULT 59

OBMUN5_9NEOP

ID OBMUN5_9NEOP PRELIMINARY; PRT; 16 AA.

AC OBMUN5_9NEOP PRELIMINARY; PRT; 16 AA.

DT 01-OCT-2002 (TREMBlrel. 22, Created)

DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)

DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)

DE Mannose phosphate isomerase (Fragment).

NCBI_TaxId=171917;

OS Helicobacter meliponensis meliponensis.

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyoptera;

OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.

NCBI_TaxId=171917;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Bill V., Beltrán M., Bermingham E., Jiggins C., McMillan O.,

RA Maillet J.,

RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF516252; AAM61938.1; -; Genomic DNA.

DR GO; GO:0016853; P:isomerase activity; IEA.

KM isomerase.

FT NON_TER 1 1

FT NON_TER 16 16

SEQ SEQUENCE 16 AA; 1811 MW; 1CE67DE35C62222 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 9.1e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNTH 9
| | | |
| | | |
Db 6 HPTKDH 11

RESULT 60

O5G554_BALMU

ID O5G554_BALMU PRELIMINARY; PRT; 16 AA.

AC O5G554_BALMU PRELIMINARY; PRT; 16 AA.

DT 10-MAY-2005 (TREMBlrel. 30, Created)

DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)

DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)

DE DNA polymerase beta (Fragment).

GN Name=POLB;

OS Balenoptera musculus (Blue whale).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Cetacea;

OC Mysticeti; Balenopteridae; Balenoptera.

NCBI_TaxId=9771;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RA Conway C.A., May B.P.,

RT "Global Population Structure of Blue Whales Balenoptera musculus ssp

Based on Nuclear Genetic Variation."

RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AV851160; AAM65802.1; -; Genomic DNA.

FT NON_TER 1 1

FT NON_TER 16 16

SEQ SEQUENCE 16 AA; 1732 MW; 06E7C60F3ACB84B0 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 16;

Best Local Similarity 66.7%; Pred. No. 9.1e+03;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ESYVNG 20
| | | | |
| | | | |
Db 3 ETLNGG 8

RESULT 61

O9TW4_DICDI

ID O9TW4_DICDI PRELIMINARY; PRT; 17 AA.

AC O9TW4_DICDI PRELIMINARY; PRT; 17 AA.

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)

DE V-ATPase 110 kDa subunit (Fragment).

OS Dictyostelium discoideum (Slime mold).

OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.

NCBI_TaxId=44689;

RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=96019266; PubMed=7593293;

RA Adesni C., Chapel A., Vincin M., Rabilloud T., Klein G., Saire M.,

RA Garin J.,

RT "Identification of major proteins associated with Dictyostelium

discoideum endocytic vesicles."

RL J. Cell Sci. 108:3331-3337(1995).

SEQ SEQUENCE 17 AA; 2075 MW; 89F1B1A959D61BB CRC64;

Query Match 21.7%; Score 25; DB 2; Length 17;

Best Local Similarity 42.9%; Pred. No. 9.7e+03;

Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 2 IHPHTNHYKLYCG 15
| | | | |
| | | | |
Db 3 IYHTXNLFGYDVG 16

RESULT 62

PHY12_PHYHY

ID PHY12_PHYHY STANDARD; PRT; 18 AA.

AC P84567;

DT 13-SEP-2005 (Rel. 48, Created)

DT 13-SEP-2005 (Rel. 48, Last sequence update)

DT 13-SEP-2005 (Rel. 48, Last annotation update)

DE Phyllosepelin-2 (PS-2).

OS Phyllomedusa hypochondrialis (Orange-legged leaf frog).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;

OC Phyllomedusinae; Phyllomedusa.

NCBI_TaxId=317381;

RN [1]

RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, TISSUE SPECIFICITY,

RP MASS SPECTROMETRY, AND AMIDATION.

RC TISSUE=Skin secretion.

RX PubMed=15752569; DOI=10.1016/j.peptides.2004.11.002;

RA Leite J.R.S.A., Silva L.P., Rodrigues M.T.S., Prates M.V., Brand G.D.,

RA Lacava B.M., Azevedo R.B., Bocca A.L., Albuquerque S., Bloch C. Jr.,

RT "Phyllosepelins: a novel class of anti-bacterial and anti-protozoan

peptides from the Phyllomedusa genus."

RL Peptides 26:565-573(2005).

CC -1- FUNCTION: Has antimicrobial activity. No hemolytic activity.

CC -1- SUBCELLULAR LOCATION: Secreted.

CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.

CC -1- MASS SPECTROMETRY: MW=2115.26; METHOD=MALDI; RANGE=1-18;

NOTE=Ref.1.

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC Amidation; Amphibian defense peptide; Antimicrobial;

```

KW Direct protein sequencing.
FT MOD_RES 18 18 Phenylalanine amide.
SQ SEQUENCE 18 AA; 2003 MW; 0B100A9F91CF9C CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 1; Length 18;
Pred. No. 1e+04;
Matches 6; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 2 IHPHTNHKIV 13
DB 4 IHPHAINAVSTLV 15

RESULT 63
Q6VYB3_9NEOP
ID Q6VYB3_9NEOP PRELIMINARY; PRT; 18 AA.
AC Q6VYB3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Mannoase phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius erato notabilis.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictysta;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=246613;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Planagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
RA Planas S., Linares M., Heckel D., McMillan W.O.;
RT "Historical demography of Mullerian mimicry in the neotropical
RT Heliconius butterflies."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
DR EMBL; AY319914; AA084670.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; A4942CE67DE35CDB CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9
DB 6 HPTKNH 11

RESULT 64
Q6VYD9_9NEOP
ID Q6VYD9_9NEOP PRELIMINARY; PRT; 18 AA.
AC Q6VYD9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Mannoase phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius erato erato.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictysta;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=64530;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Planagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
RA Planas S., Linares M., Heckel D., McMillan W.O.;
RT "Historical demography of Mullerian mimicry in the neotropical
RT Heliconius butterflies."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
DR EMBL; AY319914; AA084670.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2039 MW; A4942CE67DE35CDB CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9
DB 6 HPTKNH 11

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DR EMBL; AY319888; AA084644.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2088 MW; 2DEA7147E11DD6A6 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9
DB 2 HPTKNH 7

RESULT 65
Q6VYB7_9NEOP
ID Q6VYB7_9NEOP PRELIMINARY; PRT; 18 AA.
AC Q6VYB7;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DE Mannoase phosphate isomerase (Fragment).
GN Name=Mpi;
OS Heliconius erato hydara.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictysta;
OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
OX NCBI_TaxId=64529;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Planagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
RA Planas S., Linares M., Heckel D., McMillan W.O.;
RT "Historical demography of Mullerian mimicry in the neotropical
RT Heliconius butterflies."
RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
DR EMBL; AY319880; AA084636.1; -; Genomic DNA.
DR GO; GO:0016853; F:isomerase activity; IEA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 2088 MW; 2DEA7147E11DD6A6 CRC64;

Query Match
Best Local Similarity 21.7%; Score 25; DB 2; Length 18;
Pred. No. 1e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9
DB 2 HPTKNH 7

RESULT 66
Q4YEL0_PLABE
ID Q4YEL0_PLABE PRELIMINARY; PRT; 18 AA.
AC Q4YEL0;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Hypothetical protein.
GN ORFNames=PB405193.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15210977; DOI=10.1073/pnas.0306243101;
RA Hall N., Karras M., Raine J.D., Carlson J.M., Kooij T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carnuci D.J., Yates J.R., Kafatos F.C.,

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RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sindén R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RL transcriptomic, and proteomic analyses."
 Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, CA01005914; CA103559.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 18 AA; 2133 MW; 29C0F93F153D0E3D CRC64;

Query Match 21.7%; Score 25; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 1e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 9 HKTLV 13
 DB 9 HKYII 13

RESULT 67
 ID Q28069_BOVIN PRELIMINARY; PRT; 18 AA.
 AC Q28069;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-JUN-1999 (TrEMBLrel. 09, Last sequence update)
 DE 01-JUN-1999 (TrEMBLrel. 09, Last annotation update)
 DE Alpha-s1-casein (Fragment).
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 OC Pecora; Bovidae; Bovinae; Bos.
 OK NCBI_TaxID=9913;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Mammary gland;
 RA Maki M., Nagao M., Hirose M., Chiba H.;
 RT "Cloning of cDNA sequence coding for bovine alpha-s1-casein."
 RL Agric. Biol. Chem. 47:441-444(1983).
 DR EMBL, D00412; BAA00313.1; -; mRNA.
 FT NON_TER 1
 FT NON_TER 18
 SQ SEQUENCE 18 AA; 1880 MW; 8DEDCL740674108C CRC64;

Query Match 21.7%; Score 25; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 1e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPHP 5
 DB 12 DDPNP 16

RESULT 68
 ID Q6VYD8_9NEOP PRELIMINARY; PRT; 19 AA.
 AC Q6VYD8;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN Name=Mpi;
 OS Heliconius erato emma.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyssa;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
 OK NCBI_TaxID=246809;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15210977; DOI=10.1073/pnas.0306243101;
 RA Flanagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
 RA Planes S., Liner M., Heckel D., McMillan W.O.;
 RT "Historical demography of Mullerian mimicry in the neotropical

RT Heliconius butterflies."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
 DR EMBL, A319889; AA084645.1; -; Genomic_DNA.
 DR GO, GO:0016853; P:isomerase activity; IEA.
 KM Isomerase.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2186 MW; CE24942CE67DE35C CRC64;

Query Match 21.7%; Score 25; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9
 DB 6 HPTKNH 11

RESULT 69
 ID Q6VYB1_9NEOP PRELIMINARY; PRT; 19 AA.
 AC Q6VYB1;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Mannose phosphate isomerase (Fragment).
 GN Name=Mpi;
 OS Heliconius erato hydra.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Lepidoptera; Glossata; Dictyssa;
 OC Papilionoidea; Nymphalidae; Heliconiinae; Heliconiini; Heliconius.
 OK NCBI_TaxID=64529;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC PubMed=15210977; DOI=10.1073/pnas.0306243101;
 RA Flanagan N.S., Tobler A., Davison A., Pybus O.G., Kapan D.D.,
 RA Planes S., Liner M., Heckel D., McMillan W.O.;
 RT "Historical demography of Mullerian mimicry in the neotropical
 RT Heliconius butterflies."
 RL Proc. Natl. Acad. Sci. U.S.A. 101:9704-9709(2004).
 DR EMBL, AY319886; AA084642.1; -; Genomic_DNA.
 DR GO, GO:0016853; P:isomerase activity; IEA.
 KM Isomerase.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2216 MW; 2DEA1BF7911DD6A6 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 HPTNIH 9
 DB 3 HPTKNH 8

RESULT 70
 ID Q7RG13_PLAYO PRELIMINARY; PRT; 19 AA.
 AC Q7RG13;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN Name=PY04538;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OK NCBI_TaxID=73239;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XUL;
 RA MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguioni S.V., Suh B.B., Koel T.W., Petrea M.,

RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
 RA Shallow S.D., van Aken S.E., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shostak A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL: AABL01001387; EAA15415.1; -; Genomic_DNA.
 KM Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2346 MW; 5FAD63FC40D6B696 CRC64;
 QY
 Db 7 NIHKLVCESVN 18
 6 NFINILICNYIN 17

Query Match 21.7%; Score 25; DB 2; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.1e+04;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

RESULT 71
 ID Q7YK42_9FABA PRELIMINARY; PRT; 19 AA.
 AC Q7YK42;
 DT 01-OCT-2003 (TREMBlrel. 25, Created)
 DT 01-OCT-2003 (TREMBlrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Paba (Fragment).
 DE GN Name=paba;
 OS Desmanthus bicornutus.
 OS Chloropiast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Mimoidae; Mimoseae; Desmanthus.
 OC NCBI_TaxID=196645;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Miller J.T., Grimes J.W., Murphy D.J., Bayer R.J., Ladiges P.Y.;
 RT "A Phylogenetic Analysis of the Acaciae and Ingeae (Mimosoidae;
 RT Fabaceae) based on trnK, matK, psbA-trnH, and trnL/trnF Sequence
 RT Data.";
 RL Syst. Bot. 28:558-566(2003).
 DR EMBL: AF524960; AAP80478.1; -; Genomic_DNA.
 DR GO: 0009507; Chloropiast; IEA.
 KW Chloropiast.
 FT NON_TER
 SQ SEQUENCE 19 AA; 1964 MW; 4441E0C10D549D84 CRC64;
 QY
 Db 7 NIHKLVCESVN 19
 1 NAHKFPLDLAAVAPASING 19

Query Match 21.7%; Score 25; DB 2; Length 19;
 Best Local Similarity 31.6%; Pred. No. 1.1e+04;
 Matches 6; Conservative 3; Mismatches 4; Indels 6; Gaps 1;

RESULT 72
 ID Q8CJ05_MESAU PRELIMINARY; PRT; 19 AA.
 AC Q8CJ05;
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)

DB Cyclicin D1 (Fragment).
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Mesocricetus.
 OC NCBI_TaxID=10036;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22566058; PubMed=12569092; DOI=10.1074/jbc.M300412200;
 RA Hilton T.L., Wang E.H.;
 RT "Transcription factor IID recruitment and Sp1 activation. Dual
 RT function of TAF1 in cyclin D1 transcription.";
 RL J. Biol. Chem. 278:12992-13002(2003).
 DR EMBL: AF539477; AAN59789.1; -; Genomic_DNA.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2307 MW; 83E3J41F29C52279 CRC64;
 QY
 Db 9 HKYLVCE 15
 3 HQLLCCE 9

Query Match 21.7%; Score 25; DB 2; Length 19;
 Best Local Similarity 57.1%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

RESULT 73
 ID Q7LZM5_HHV1 PRELIMINARY; PRT; 19 AA.
 AC Q7LZM5;
 DT 01-MAR-2004 (TREMBlrel. 26, Created)
 DT 01-MAR-2004 (TREMBlrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Capsid protein VP26 (Fragment).
 OS Human herpesvirus 1 (HHV-1) (Human herpes simplex virus 1).
 OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
 OC Alphaherpesvirinae; Simplexvirus.
 OC NCBI_TaxID=10298;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Davidson M.D., Rixon F.J., Davidson A.J.;
 RT "Identification of genes encoding two capsid proteins (VP24 and VP26)
 RT of herpes simplex virus type 1.";
 RL J. Gen. Virol. 73:2709-2713(1992).
 RN [2]
 RP PROTEIN SEQUENCE.
 RX PubMed=1328483;
 RA Davidson M.D., Rixon F.J., Davidson A.J.;
 RT "Identification of genes encoding two capsid proteins (VP24 and VP26)
 RT of herpes simplex virus type 1.";
 RL J. Gen. Virol. 73 (Pt 10):2709-2713(1992).
 DR PIR: P00548; P00548.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2060 MW; BBE855419135AC5A CRC64;
 QY
 Db 1 DIFHP 5
 11 DNFHP 15

Query Match 21.7%; Score 25; DB 2; Length 19;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

RESULT 74
 ID APY3_PLECI STANDARD; PRT; 20 AA.
 AC P83477;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DR Antiviral protein Y3 (Fragment).

OS Pleurotus citrinopileatus (Golden oyster mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=98342;
RN
RP PROTEIN SEQUENCE.
RA Wu L.-P., Wu Z.-J., Lin Q.-Y., Xie L.-H.;
RL Submitted (OCT-2002) to Swiss-Prot.
CC
CC -1- MISCELLANEOUS: Has antiviral activity against Tobacco mosaic virus
and antitumor activity against stomach cancer cells in vitro.
CC
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC Antiviral protein; Direct protein sequencing.
KM
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2237 MW; 3D2B0A20A8BB1172 CRC64;

Query Match 21.7%; Score 25; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 YLVGESV 17
DB 14 YVACEAV 20

RESULT 75
APR3_PLECI STANDARD; PRT; 20 AA.
ID APR3_PLECI
AC P83481;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2003 (Rel. 48, Last annotation update)
DE Antiviral protein Yp3 (Fragment).
OS Pleurotus citrinopileatus (Golden oyster mushroom).
OC Eukaryota; Fungi; Basidiomycota; Hymenomycetes; Homobasidiomycetes;
OC Agaricales; Pleurotaceae; Pleurotus.
OX NCBI_TaxID=98342;
RN
RN [1]
RP PROTEIN SEQUENCE.
RA Wu L.-P., Wu Z.-J., Lin Q.-Y., Xie L.-H.;
RL Submitted (OCT-2002) to Swiss-Prot.
CC -1- FUNCTION: Unknown.
CC -1- MISCELLANEOUS: Has antiviral activity against Tobacco mosaic virus
and antitumor activity against stomach cancer cells in vitro.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC removed.
CC
CC Antiviral protein; Direct protein sequencing.
KM
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2237 MW; 3D2B0A20A8BB1172 CRC64;

Query Match 21.7%; Score 25; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 YLVGESV 17
DB 14 YVACEAV 20

RESULT 76

064619_RAT
ID 064619_RAT PRELIMINARY; PRT; 20 AA.
AC 064619;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Polymerase-beta (EC 2.7.7.7) (Fragment).
GN Namepold;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=87257910; PubMed=3600656;
RX Yamaguchi M., Hirose F., Hayashi Y., Nishimoto Y., Matsukage A.;
RT "Murine DNA polymerase beta gene: mapping of transcription initiation
RT sites and the nucleotide sequence of the putative promoter region.";
RL Mol. Cell. Biol. 7:2012-2018(1987).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA MEDLINE=88294046; PubMed=3042024;
RX Date T., Yamaguchi M., Hirose F., Nishimoto Y., Tanihara K.,
RA Matsukage A.;
RT "Expression of active rat DNA polymerase beta in Escherichia coli.";
RL Biochemistry 27:2983-2990(1988).
DR EMBL: M19679; AAA11902.1; -; Genomic_DNA.
DR HSSP: P06766; 1BNO.
DR GO: GO:0003887; F:DNA-directed DNA polymerase activity; IEA.
DR GO: GO:0016740; F:transferase activity; IEA.
KW Nucleotidyltransferase; Transferase.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 20 AA; 2190 MW; B7D8F9A3C5801825 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.2e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 15 ESYNGG 20
DB 9 ETLNGG 14

RESULT 77
O9PRY1_TORCA
ID O9PRY1_TORCA PRELIMINARY; PRT; 20 AA.
AC O9PRY1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AgRIN receptor 190 kDa SUBUNIT-ALPHA-dystroglycan homolog
(Fragment).
OS Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalia; Hypnosqualea; Pristigaster; Batoidae;
OC Torpediniformes; Torpedinoidei; Torpedinidae; Torpedo.
OX NCBI_TaxID=7787;
RN
RN [1]
RP PROTEIN SEQUENCE.
RA MEDLINE=94242436; PubMed=8185951; DOI=10.1016/0896-6273(94)90324-7;
RX Bowe M.A., Deyak K.A., Leszyk J.D., Fallon J.R.;
RT "Identification and purification of an agrin receptor from Torpedo
RT postmyotomal membranes: a heteromeric complex related to the
RT dystroglycans.";
RL Neuron 12:1173-1180(1994).
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2239 MW; 038622F02D189F90 CRC64;

Query Match 21.7%; Score 25; DB 2; Length 20;

Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 9 HKYLVCSYNG 20
DB 1 HEYFMHAXKGG 12

RESULT 78

Q9R4Z4_PROMI PRELIMINARY; PRT; 20 AA.
AC Q9R4Z4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE AMBIENT-temperature FIMBRIA; ATP (Fragment).
OS Proteus mirabilis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Proteus.
OX NCBI_TaxID=584;
RN [1]
RP PROTEIN SEQUENCE. PubMed=7909538;
RX MEDLINE=9422573; Mobley H.L.;
RA Massad G., Bahran P.K., Mobley H.L.;
RT "Proteus mirabilis fimbriae: identification, isolation, and
characterization of a new ambient-temperature fimbria.";
RL Infect. Immun. 62:1989-1994(1994).
FT NON_TER 1 1
PT NON_TER 20 20
SQ SEQUENCE 20 AA; 2017 MW; B2FC481003883AE2 CRC64;

Query Match 21.3%; Score 24.5; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 1.4e+04;
Matches 6; Conservative 3; Mismatches 2; Indels 7; Gaps 1;

QY 3 PPHNTHKYLVCESYNG 20
DB 6 PAPTEV-----TVDDGG 16

RESULT 79

Q7M471_VESOR PRELIMINARY; PRT; 9 AA.
AC Q7M471;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Venom protein HR-3 (Fragment).
OS Vespa orientalis (Oriental hornet).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespidae; Vespinae; Vespa.
OX NCBI_TaxID=7447;
RN [1]
RP PROTEIN SEQUENCE.
RA Tulichbaev M.U., Akhmedova N.U., Kazakov I., Korneev A.S.,
RA Gageg'gans A.I.;
RT "low-molecular-weight peptides of venom of the giant hornet Vespa
orientalis. Structure and function.";
RL Biochemistry 53:183-190(1988).
DR PIR; S10920; S10920.
FT NON_TER 1 1
FT NON_TER 9 9
SQ SEQUENCE 9 AA; 1029 MW; 9C27C729CB11P2D5 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.2e+06;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 7 NTHKYLTV 13
DB 2 SVHEFLV 8

RESULT 80

Q9UCI7_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q9UCI7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 38 kDa MYELOPEROXIDASE (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE. PubMed=1334087;
RX MEDLINE=93094240; Taylor K.L., Pohl J., Kinkade J.M.Jr.;
RT "Unique autolytic cleavage of human myeloperoxidase. Implications for
the involvement of active site MET409.";
RL J. Biol. Chem. 267:25282-25288(1992).
DR GO; GO:0004601; F:peroxidase activity; IEA.
DR InterPro; IPR02007; Anim_peroxidase.
DR PROSITE; PS50292; PEROXIDASE 3; 1.
SQ SEQUENCE 15 AA; 1791 MW; 8B76949B5D087321 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 15;
Best Local Similarity 38.5%; Pred. No. 1.2e+04;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 3 PPHNTHKYLVCESYNG 15
DB 1 PELTSMHTLLRE 13

RESULT 81

Q6R9U9_HUMAN PRELIMINARY; PRT; 17 AA.
AC Q6R9U9;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Microcephalin (Fragment).
RN Name=MCPH1;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
size.";
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RT Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506297; AAS88650.1; -; Genomic DNA.
DR EMBL; AY506293; AAS88656.1; -; Genomic DNA.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NTHKYLVCESYV 18
DB 1 SITQHKVCASBN 12


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RESULT 82
Q6R9P0 TRAPR
ID Q6R9P0 TRAPR PRELIMINARY; PRT; 17 AA.
AC Q6R9P0;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Trachypithecus francoisi (Francois' langur) (Indochinese langur).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Colobinae; Trachypithecus.
NCBI_TaxID=54180;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506356; AAS88719.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

RESULT 83
Q6R9P1 TRAPR PRELIMINARY; PRT; 17 AA.
ID Q6R9P1 TRAPR PRELIMINARY; PRT; 17 AA.
AC Q6R9P1;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Trachypithecus phayrei (Phayre's leaf monkey).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Colobinae; Trachypithecus.
NCBI_TaxID=61618;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506355; AAS88718.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

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DB 1 SITQHKVCASEN 12

RESULT 84
Q6R9P2 PYGBI
ID Q6R9P2 PYGBI PRELIMINARY; PRT; 17 AA.
AC Q6R9P2;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Pygathrix nemaeus (Dove langur) (Dove langur).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Colobinae; Pygathrix.
NCBI_TaxID=54133;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506354; AAS88717.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

RESULT 85
Q6R9P3 PYGBI
ID Q6R9P3 PYGBI PRELIMINARY; PRT; 17 AA.
AC Q6R9P3;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Pygathrix bieti (Black snub-nosed monkey) (Rhinopithecus bieti).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecoidea; Colobinae; Pygathrix.
NCBI_TaxID=61621;
RN [1];
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2];
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506353; AAS88716.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785E5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHKLVCESVN 18
DB 1 SITQHKVCASEN 12

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Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 NIHXYLVCSVN 18
:|::|||
Db 1 SITOHKVCASEN 12

RESULT 86
Q6R9P4_MACMU PRELIMINARY; PRT; 17 AA.

AC Q6R9P4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DB Microcephalin (Fragment).
GN Name=Mcpnl;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
ON NCB1_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506342; AAS88715.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1931 MW; DC663AF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 NIHXYLVCSVN 18
:|::|||
Db 1 SITOHKVCASEN 12

RESULT 87
Q6R9Q1_PONPY PRELIMINARY; PRT; 17 AA.

AC Q6R9Q1;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DE Microcephalin (Fragment).
GN Name=Mcpnl;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pongo.
ON NCB1_TaxID=9600;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506345; AAS88708.1; -; Genomic_DNA.
DR EMBL; AY506346; AAS88709.1; -; Genomic_DNA.
DR EMBL; AY506347; AAS88710.1; -; Genomic_DNA.

FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 NIHXYLVCSVN 18
:|::|||
Db 1 SITOHKVCASEN 12

RESULT 88
Q6R9Q5_9PRIM PRELIMINARY; PRT; 17 AA.

AC Q6R9Q5;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DB Microcephalin (Fragment).
GN Name=Mcpnl;
OS Gorilla gorilla (gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
ON NCB1_TaxID=9593;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506341; AAS88704.1; -; Genomic_DNA.
DR EMBL; AY506342; AAS88705.1; -; Genomic_DNA.
DR EMBL; AY506343; AAS88706.1; -; Genomic_DNA.
DR EMBL; AY506344; AAS88707.1; -; Genomic_DNA.
FT NON_TER 1 1
SQ SEQUENCE 17 AA; 1921 MW; DC64EAF1C7785B5B CRC64;

Query Match 20.9%; Score 24; DB 2; Length 17;
Best Local Similarity 41.7%; Pred. No. 1.4e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 7 NIHXYLVCSVN 18
:|::|||
Db 1 SITOHKVCASEN 12

RESULT 89
Q6R9R4_PANTR PRELIMINARY; PRT; 17 AA.

AC Q6R9R4;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TREMBLrel. 29, Last annotation update)
DB Microcephalin (Fragment).
GN Name=Mcpnl;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Pan.
ON NCB1_TaxID=9598;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain size."
RL Hum. Mol. Genet. 13:1131-1137(2004).

RL Hum. Mol. Genet. 13:1131-1137 (2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Wang Y., Su B.,
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY506332; AAS88695.1; -; Genomic DNA.
 DR EMBL; AY506333; AAS88696.1; -; Genomic DNA.
 DR EMBL; AY506334; AAS88697.1; -; Genomic DNA.
 DR EMBL; AY506335; AAS88698.1; -; Genomic DNA.
 DR EMBL; AY506336; AAS88699.1; -; Genomic DNA.
 DR EMBL; AY506337; AAS88700.1; -; Genomic DNA.
 DR EMBL; AY506338; AAS88701.1; -; Genomic DNA.
 DR EMBL; AY506339; AAS88702.1; -; Genomic DNA.
 DR EMBL; AY506340; AAS88703.1; -; Genomic DNA.
 FT NON TER 1
 SQ SEQUENCE 17 AA; 1921 MW; DC6EAF1C7785B5B CRC64;
 Query Match 20.9%; Score 24; DB 2; Length 17;
 Best Local Similarity 41.7%; Pred. No. 1.4e+04;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 7 NIHKYLVCSVN 18
 DB 1 SITQHKVCASEN 12
 RESULT 90
 HEMTO_THETS STANDARD; PRT; 18 AA.
 ID P80155;
 AC 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Ovoclemyrin (Yp14) (Fragment).
 OS Theromyzon tessulatum (Leech).
 OC Eukaryota; Metazoa; Annelida; Clitellata; Hirudinea; Hirudinea;
 OC Rhynchobdellida; Glossiphoniidae; Theromyzon.
 NC NCB1_Taxid=13286;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=Oocyte;
 RX MEDLINE=93049299; PubMed=1425663;
 RA Baert J.-L., Britel M., Sautiere P., Malecha J.;
 RT "Ovoclemyrin, a major 14-kDa yolk protein distinct from
 vitellogenin in leech.";
 RL Eur. J. Biochem. 209:563-569 (1992).
 CC -1- FUNCTION: Major yolk protein. This iron protein may play a role in
 the detoxification of free iron after a blood meal.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the hemerythrin family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR; S29264; S29264.
 DR HSSP; P0247; 2MR.
 DR InterPro; IPR002063; Hemerythrin.
 DR PROSITE; PS00550; HEMERYTHRINS; PARTIAL.
 KW Direct protein sequencing; Iron; Metal-binding; Oxygen transport;
 KW Transport.
 FT NON TER 18
 SQ SEQUENCE 18 AA; 2368 MW; 33397EEB57C81F1 CRC64;
 Query Match 20.9%; Score 24; DB 1; Length 18;
 Best Local Similarity 80.0%; Pred. No. 1.5e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DIPHP 5
 DB 2 DIPHP 6

RESULT 91
 Q92YV9_9HYME PRELIMINARY; PRT; 18 AA.
 ID Q92YV9;
 AC Q92YV9;
 DT 01-MAY-1999 (T-EMBLrel. 10, Created)
 DT 01-MAY-1999 (T-EMBLrel. 10, Last sequence update)
 DT 01-JUN-2003 (T-EMBLrel. 24, Last annotation update)
 DE Cytochrome oxidase II (Fragment).
 OS Opus krausii.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
 OC Braconidae; Opiinae; Opius.
 NC NCB1_Taxid=64839;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=99152621; PubMed=10028295;
 RA Dowton M., Austin A.D.;
 RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
 the Hymenoptera.";
 RL Mol. Biol. Evol. 16:298-309 (1999).
 DR EMBL; AF034602; AAC79750.1; -; Genomic DNA.
 DR GO; GO:0005739; Mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 SQ SEQUENCE 18 AA; 2245 MW; F834BD4587B14D66 CRC64;
 Query Match 20.9%; Score 24; DB 2; Length 18;
 Best Local Similarity 71.4%; Pred. No. 1.5e+04;
 Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 12 LVYCSVN 18
 DB 1 IYLVSVN 7
 RESULT 92
 Q4XS69_PLACH PRELIMINARY; PRT; 18 AA.
 ID Q4XS69;
 AC Q4XS69;
 DT 13-SEP-2005 (T-EMBLrel. 31, Created)
 DT 13-SEP-2005 (T-EMBLrel. 31, Last sequence update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC107016.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NC NCB1_Taxid=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Koof T.W.A.,
 RA Bertman M., Plorens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churche C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jansse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 transcriptomic, and proteomic analyses.";
 RL Science 307:82-86 (2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01003579; CAH80243.1; -; Genomic DNA.
 KW Hypothetical protein.
 FT NON TER 1
 SQ SEQUENCE 18 AA; 2271 MW; 6113B4C4387EB7B8 CRC64;
 Query Match 20.9%; Score 24; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1.5e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 NIKRYL 12
| | | |
DB 6 NIKRYI 11

RESULT 93
Q5C5Z8 SCHJA PRELIMINARY; PRT; 19 AA.
ID Q5C5Z8 SCHJA PRELIMINARY; PRT; 19 AA.
AC Q5C5Z8
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidae;
OC Schistosomatidae; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Han Z.;
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF030937; AX24926.1; -; mRNA.
KW Hypothetical protein.
SQ SEQUENCE 19 AA; 1908 MW; 442CDA5D856B3F21 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 1.6e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 CESVNG 19
| | | |
DB 3 CELANG 8

RESULT 94
Q9ZYX3_9HYME PRELIMINARY; PRT; 19 AA.
ID Q9ZYX3_9HYME PRELIMINARY; PRT; 19 AA.
AC Q9ZYX3;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Gnampodon pumilio.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Gnampodontinae; Gnampodon.
OX NCBI_TaxID=64833;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the Hymenoptera."
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF034598; AAC79746.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2290 MW; 77F1B7E7E787BCA CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 1.6e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCESVN 18
| | | |
DB 1 IYLESVN 7

RESULT 95
Q9ZYX2_9HYME PRELIMINARY; PRT; 19 AA.
ID Q9ZYX2_9HYME PRELIMINARY; PRT; 19 AA.

AC Q9ZYX2;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
DE Cytochrome oxidase II (Fragment).
OS Centistes sp.
OC Mitochondrion.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Ichneumonidae;
OC Braconidae; Euphorinae; Centistes.
OX NCBI_TaxID=64856;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA MEDLINE=99152621; PubMed=10028295;
RA Dowton M., Austin A.D.;
RT "Evolutionary dynamics of a mitochondrial rearrangement 'hot spot' in
RT the Hymenoptera."
RL Mol. Biol. Evol. 16:298-309(1999).
DR EMBL; AF034589; AAC79737.1; -; Genomic_DNA.
DR GO; GO:0005739; C:mitochondrion; IEA.
KW Mitochondrion.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2213 MW; 319C74242367B0FD CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 1.6e+04;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 LVCESVN 18
| | | |
DB 1 IYLESVN 7

RESULT 96
Q4Y3P1_PLACH PRELIMINARY; PRT; 19 AA.
ID Q4Y3P1_PLACH PRELIMINARY; PRT; 19 AA.
AC Q4Y3P1;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PC102236.00.0;
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Kairas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Berriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAJ01001297; CAH76219.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
SQ SEQUENCE 19 AA; 2341 MW; 215542A7D275C444 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 33.3%; Pred. No. 1.6e+04;
Matches 5; Conservative 2; Mismatches 2; Indels 6; Gaps 1;

QY 10 KYLVC-----ESVN 18
| | | |
DB 2 KYIACILKKGEIN 16

```
RESULT 97
Q6R9P5_HYLL6 PRELIMINARY; PRT; 19 AA.
ID Q6R9P5_HYLL6 PRELIMINARY; PRT; 19 AA.
AC Q6R9P5;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Hylobates leucogenys (White-cheeked gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Hylobatidae; Nomacae.
OX NCBI_TaxID=61853;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506351; AAS88714.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2216 MW; 099CEC663AFC1778 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18
: : : : :
Db 1 SITQHKVCASEN 12

RESULT 98
Q6R9P6_9PRIM PRELIMINARY; PRT; 19 AA.
ID Q6R9P6_9PRIM PRELIMINARY; PRT; 19 AA.
AC Q6R9P6;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Bunopithecus hollock (Hollock gibbon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Hylobatidae; Bunopithecus.
OX NCBI_TaxID=61851;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506350; AAS88713.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2216 MW; 099CEC663AFC1778 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18
: : : : :
Db 1 SITQHKVCASEN 12
```

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Db 1 SITQHKVCASEN 12

RESULT 99
Q6R9P7_MACMU PRELIMINARY; PRT; 19 AA.
ID Q6R9P7_MACMU PRELIMINARY; PRT; 19 AA.
AC Q6R9P7;
DT 05-JUL-2004 (TEMBLrel. 27, Created)
DT 05-JUL-2004 (TEMBLrel. 27, Last sequence update)
DE 05-JUL-2004 (TEMBLrel. 27, Last annotation update)
DE Microcephalin (Fragment).
GN Name=McpH1;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopithecidae; Cercopithecinae; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.Q., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size."
RL Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY506349; AAS88712.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 2169 MW; 09920C663AFC1778 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 41.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 7 NIHXYLVCSVN 18
: : : : :
Db 1 SITQHKVCASEN 12

RESULT 100
Q5EXA0_9LAMI PRELIMINARY; PRT; 19 AA.
ID Q5EXA0_9LAMI PRELIMINARY; PRT; 19 AA.
AC Q5EXA0;
DT 10-MAY-2005 (TEMBLrel. 30, Created)
DT 10-MAY-2005 (TEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TEMBLrel. 30, Last annotation update)
DE SPM2 protein (Fragment).
OS Streptocarpus pentherianus.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Lamiales; Gesneriaceae; Cyrtandroidae; Didymocarpaceae;
OC Streptocarpus.
OX NCBI_TaxID=167294;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15659624; DOI=10.1105/tpc.104.028936;
RA Harrison J., Moller M., Langdale J., Cronk Q., Hudson A.;
RT "The Role of KNOX Genes in the Evolution of Morphological Novelty in
RT Streptocarpus."
RL Plant Cell 17:430-443(2005).
DR EMBL; AY662104; AAW33758.1; -; Genomic_DNA.
FT NON TER 1 1
SQ SEQUENCE 19 AA; 1999 MW; 966867E782A63143 CRC64;

Query Match 20.9%; Score 24; DB 2; Length 19;
Best Local Similarity 35.7%; Pred. No. 1.6e+04;
Matches 5; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 3 PHTNIHKYLVCS 16
: : : : :
Db 1 SITQHKVCASEN 12
```

Db 1 PXPESQKLAES 14

Search completed: January 20, 2006, 19:11:05
Job time : 67.5385 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 : Search time 75.5769 Seconds
(without alignments)
116.273 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105

Sequence: 1 DPAKGMSPGFIVGSEGVLS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

A_Geneseq_21:*

- 1: geneseq219808:*
- 2: geneseq219809:*
- 3: geneseq220008:*
- 4: geneseq220018:*
- 5: geneseq220028:*
- 6: geneseq220038:*
- 7: geneseq220038:*
- 8: geneseq220048:*
- 9: geneseq220058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	3	AAVS2513
2	105	100.0	20	3	AAVS2522
3	105	100.0	20	5	AAU96317
4	105	100.0	20	5	AAU96326
5	36	34.3	16	8	ADR67576
6	35	33.3	9	5	AAE8728
7	35	33.3	10	5	AAE8728
8	35	33.3	20	7	ADC99464
9	34	32.4	8	2	AAW65590
10	34	32.4	8	4	AAW65590
11	34	32.4	8	4	AAW65590
12	34	32.4	8	6	ABU07632
13	34	32.4	11	8	ADRA3749
14	34	32.4	12	8	ADRA3750
15	34	32.4	13	8	ADRA3752
16	34	32.4	18	5	ABP48137
17	34	32.4	18	8	ADRA3748
18	34	32.4	19	8	ADRA3748
19	34	32.4	19	8	ADRA3748
20	33	31.4	15	2	AAW18175
21	33	31.4	15	2	AAW18175
22	33	31.4	15	6	ABU56381
23	33	31.4	15	7	AAE39326
24	33	31.4	15	7	ADP45168

25	33	31.4	15	8	AD036853	Ad036853 Majorly a
26	33	31.4	16	8	ADU64228	Adu64228 30 KD pro
27	33	31.4	16	8	AAU07809	AAU07809 Peptide e
28	33	31.4	20	5	ABP30905	Abp30905 Oe8 antib
29	33	31.4	20	7	ADA08550	Ada08550 Human Oe8
30	33	31.4	20	7	ADP09099	Adp09099 Secreted
31	33	31.4	20	7	ADP08893	Adp08893 Secreted
32	33	31.4	20	7	ADG46180	Adg46180 Oe8 antib
33	33	31.4	20	7	ADK40495	Adk40495 KDR & VEG
34	33	31.4	20	8	ADRA40713	Adra40713 KDR/ VEGF
35	33	31.4	20	9	ADX17776	Adx17776 Human ova
36	33	31.4	20	9	ADX17982	Adx17982 Human ova
37	32	30.5	10	5	AAO14949	AAO14949 Survivin-
38	32	30.5	15	7	ADG92606	Adg92606 Platelet
39	32	30.5	16	5	ADB49200	Adb49200 Biotinyl
40	32	30.5	16	5	AAU10333	AAU10333 Human PRO
41	32	30.5	16	6	ABP57840	Abp57840 A. margin
42	32	30.5	20	5	AAU71011	AAU71011 M. tuberc
43	32	30.5	20	7	ADK40519	Adk40519 KDR & VEG
44	32	30.5	20	8	ADRA40737	Adra40737 KDR/ VEGF
45	32	30.5	20	9	AAW49486	AAW49486 Human leu
46	31	29.5	9	8	AD068173	Ad068173 Human 213
47	31	29.5	9	8	AD068173	Ad068173 Human 213
48	31	29.5	9	8	AD068173	Ad068173 Human 213
49	31	29.5	9	8	AD068173	Ad068173 Human 213
50	31	29.5	9	8	AD068173	Ad068173 Human 213
51	31	29.5	9	8	AD068173	Ad068173 Human 213
52	31	29.5	9	8	AD068173	Ad068173 Human 213
53	31	29.5	9	8	AD068173	Ad068173 Human 213
54	31	29.5	9	8	AD068173	Ad068173 Human 213
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60	31	29.5	9	8	AD068173	Ad068173 Human 213
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70	31	29.5	10	8	AD067058	Ad067058 Human 213
71	31	29.5	10	8	AD067058	Ad067058 Human 213
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74	31	29.5	10	8	AD067058	Ad067058 Human 213
75	31	29.5	10	8	AD067058	Ad067058 Human 213
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86	31	29.5	10	8	AD067058	Ad067058 Human 213
87	31	29.5	10	8	AD067058	Ad067058 Human 213
88	31	29.5	10	8	AD067058	Ad067058 Human 213
89	31	29.5	10	8	AD067058	Ad067058 Human 213
90	31	29.5	10	8	AD067058	Ad067058 Human 213
91	31	29.5	10	8	AD067058	Ad067058 Human 213
92	31	29.5	10	8	AD067058	Ad067058 Human 213
93	31	29.5	10	8	AD067058	Ad067058 Human 213
94	31	29.5	10	8	AD067058	Ad067058 Human 213
95	31	29.5	10	8	AD067058	Ad067058 Human 213
96	31	29.5	10	8	AD067058	Ad067058 Human 213
97	31	29.5	10	8	AD067058	Ad067058 Human 213

98	31	29.5	15	8	AD076801	Human	213
99	31	29.5	15	8	AD077052	Human	213
100	31	29.5	15	8	AD076676	Human	213

ALIGNMENTS

RESULT 1

AAV52513

ID AAV52513 standard; peptide, 20 AA.

AC AAV52513;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(3).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

PN WO954349-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX PT used to modify an animals' hypersensitivity to mite allergens.

XX PS Claim 3; Page 69; 154pp; English.

CC Sequences AAV52510-Y52522 represent proteolytic fragments of

CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW

CC -map) composition. The HMW-map composition was isolated from a D. farinae

CC homogenate by gel filtration, with each fraction being analysed for the

CC presence of proteins that bound to IGE present in mite-allergic dog

CC antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

CC encoding them, may be used in therapeutic compositions to modify an

CC animal's hypersensitivity reaction to mite allergens. Animals that may be

CC treated include mammals and birds, especially felines, canines, equines,

CC humans, other pets, and work or domestic animals. The proteins or

CC fragments may also be used to diagnose allergies via a skin test. The

CC proteins and peptides can also be used to raise antibodies, which have a

CC variety of potential uses. For example, they can be used as vaccines to

CC passively immunise animals against dust mite hypersensitivity, as

CC positive controls in test kits and as tools to recover desired dust mite

CC allergens from a mixture of proteins

XX SQ Sequence 20 AA;

XX Query Match 100.0%; Score 105; DB 3; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 4,7e-09;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DPAKMSPPGFIVGEGVLS 20

XX DB 1 DPAKMSPPGFIVGEGVLS 20

RESULT 2

AAV52522

ID AAV52522 standard; peptide, 20 AA.

AC AAV52522;

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(12).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KW house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KW hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

PN WO954349-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX PT used to modify an animals' hypersensitivity to mite allergens.

XX PS Claim 3; Page 70; 154pp; English.

CC Sequences AAV52510-Y52522 represent proteolytic fragments of

CC Dermatophagoides farinae high molecular weight mite allergen protein (HMW

CC -map) composition. The HMW-map composition was isolated from a D. farinae

CC homogenate by gel filtration, with each fraction being analysed for the

CC presence of proteins that bound to IGE present in mite-allergic dog

CC antisera. The HMW-map composition comprises mapA (a 109 kD protein) and

CC mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

CC encoding them, may be used in therapeutic compositions to modify an

CC animal's hypersensitivity reaction to mite allergens. Animals that may be

CC treated include mammals and birds, especially felines, canines, equines,

CC humans, other pets, and work or domestic animals. The proteins or

CC fragments may also be used to diagnose allergies via a skin test. The

CC proteins and peptides can also be used to raise antibodies, which have a

CC variety of potential uses. For example, they can be used as vaccines to

CC passively immunise animals against dust mite hypersensitivity, as

CC positive controls in test kits and as tools to recover desired dust mite

CC allergens from a mixture of proteins

XX SQ Sequence 20 AA;

XX Query Match 100.0%; Score 105; DB 3; Length 20;

XX Best Local Similarity 100.0%; Pred. No. 4,7e-09;

XX Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX QY 1 DPAKMSPPGFIVGEGVLS 20

XX DB 1 DPAKMSPPGFIVGEGVLS 20

XX RESULT 3

XX AAU96317

XX ID AAU96317 standard; peptide, 20 AA.

AC	AAU96317;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Der HMW-map polypeptide #4.
XX	
KM	Der HMW-map; American house dust mite; antiallergic; mite; IgE; mice allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
KW	
XX	
OS	Dermatophagoides farinae.
XX	
PN	WO200222807-A2.
PD	
XX	21-MAR-2002.
PX	
PF	14-SEP-2001; 2001WO-US028730.
XX	
PR	14-SEP-2000; 2000US-00662293.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Mccall CA, Hunter SW, Weber ER;
XX	
DR	WPI, 2002-351888/38.
XX	
PT	New mite allergenic protein isolated from Dermatophagoides, designated Der HMW-map protein, useful as a vaccine for treating mite allergy.
PX	
PS	Claim 12; Page 70; 16pp; English.
XX	
CC	The invention relates to an isolated mite allergenic protein of Dermatophagoides, designated Der HMW-map protein, and its related nucleic acid. The Der HMW-map protein is useful for eliciting an immune response against Der HMW-map protein. The protein or a reagent comprising a non- proteinalcous epitope is useful for identifying an animal (e.g., dog, cat) susceptible to or having an allergic response to a mite. A therapeutic composition is useful for desensitizing a host animal to an allergic response to a mite. The DNA and protein can be used in the detection of anti-Der HMW-map antibodies in animal fluids, and inhibition of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a disease. Antibodies that bind to Der HMW-map are useful for inhibiting binding of proteins to IgE, to prevent immunocomplex formation, thus reducing hypersensitivity responses to mite allergens, and as vaccines against mite allergen hypersensitivity. Sequences AAU96314-AAU96342 represent Der HMW-map polypeptides of the invention
CC	
CC	
CC	
SO	Sequence 20 AA;
Query Match	100.0%; Score 105; DB 5; Length 20;
Best Local Similarity	100.0%; Pred. No. 4.7e-09;
Matches	20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy	1 DPAKGMSPPGPIVGBGVLS 20
Db	1 DPAKGMSPPGPIVGBGVLS 20
RESULT 4	
AAU96326	
ID	AAU96326 standard; peptide; 20 AA.
XX	
XX	AAU96326;
XX	
DT	15-JUL-2002 (first entry)
XX	
DE	Der HMW-map polypeptide #13.
XX	
KW	Der HMW-map; American house dust mite; antiallergic; mite; IgE; mite allergenic protein; immunoglobulin E; hypersensitivity; immunocomplex formation.
XX	
OS	Dermatophagoides farinae.

[illegible]

DR WPI; 2004-653416/63.
XX New modified nitrilase polypeptides, useful for preparing carboxylic
PT acids, preferably substituted chiral carboxylic acids.
XX
XX Discloure; Page 13; 96pp; English.
XX
CC The present invention relates to modified nitrilase proteins, which are
CC useful for preparing carboxylic acids, preferably substituted chiral
CC carboxylic acids. Nitrilases are enzymes which catalyse the hydrolysis of
CC nitriles into the corresponding carboxylic acids and ammonium ions. The
CC modified nitrilases of the invention have a modification at position 296
CC and exhibit a modulated acceptance in comparison to wild-type nitrilase.
CC The substitution of tyrosine at position 296 in wild-type Alcaligenes
CC faecalis nitrilase comprising a sequence of 356 amino acids (ADR67405)
CC was realized by site-directed mutagenesis utilizing overlap-extension
CC PCR. The present sequence is a fragment of a nitrilase used in a sequence
CC alignment to illustrate the invention.
XX
SQ Sequence 16 AA;

Query Match 34.3%; Score 36; DB 8; Length 16;
Best Local Similarity 58.3%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSPGPI 12
Db 1 DPAKHVSTPGFL 12

RESULT 6
AAE28728
ID AAE28728 standard; peptide; 9 AA.
XX
AC AAE28728;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human CASB88 antigenic epitope #19.
XX
XX CASB88 protein; Crohn's disease; Colitis ulcerosa; preneoplastic lesion;
KW colorectal cancer; Wilm's tumour; retinoblastoma; cancer; gene therapy;
KW rhabdomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human;
KW epitope.
XX
OS Homo sapiens.
XX
XX
XX WO200250103-A2.
XX
PD 27-JUN-2002.
XX
PF 18-SEP-2001; 2001WO-EP010980.
XX
XX 20-DEC-2000; 2000GB-00031095.
PR 27-MAR-2001; 2001GB-00007632.
PR 02-AUG-2001; 2001GB-00018926.
XX
PA (SMTK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Casbart J, Coche T, Gaulis SRJ, Ornroft T, Vinals Y De BassolsC;
XX
XX WPI; 2002-691493/74.
XX
PT Novel CASB88 polypeptide and polynucleotide useful for treating cancer,
PT Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and
PT preneoplastic lesions, Wilm's tumor, retinoblastoma and rhabdomyosarcoma.
XX
PS Claim 6; Page 77; 122pp; English.
XX
XX The invention relates to novel CASB88 polypeptides and polynucleotides.
CC Sequences of the invention are used for the treatment of diseases e.g.
CC Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and
CC preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell

CC cancer, Wilm's tumour, retinoblastoma, rhabdomyosarcoma, leiomyosarcoma
CC and synovial sarcoma. They are useful in gene therapy and as vaccines.
CC The present sequence is human CASB88 antigenic epitope
XX
SQ Sequence 9 AA;

Query Match 33.3%; Score 35; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMSPPG 10
Db 1 GMSPPG 6

RESULT 7
AAE28775
ID AAE28775 standard; peptide; 10 AA.
XX
AC AAE28775;
XX
DT 27-DEC-2002 (first entry)
XX
DE Human CASB88 antigenic epitope #66.
XX
XX CASB88 protein; Crohn's disease; Colitis ulcerosa; preneoplastic lesion;
KW colorectal cancer; Wilm's tumour; retinoblastoma; cancer; gene therapy;
KW rhabdomyosarcoma; leiomyosarcoma; synovial sarcoma; vaccine; human;
KW epitope.
XX
OS Homo sapiens.
XX
XX WO200250103-A2.
XX
PD 27-JUN-2002.
XX
PF 18-SEP-2001; 2001WO-EP010980.
XX
XX 20-DEC-2000; 2000GB-00031095.
PR 27-MAR-2001; 2001GB-00007632.
PR 02-AUG-2001; 2001GB-00018926.
XX
PA (SMTK) SMITHKLINE BEECHAM BIOLOGICALS.
XX
PI Casbart J, Coche T, Gaulis SRJ, Ornroft T, Vinals Y De BassolsC;
XX
XX WPI; 2002-691493/74.
XX
PT Novel CASB88 polypeptide and polynucleotide useful for treating cancer,
PT Crohn's disease, colitis ulcerosa, colorectal cancer, lung cancer and
PT preneoplastic lesions, Wilm's tumor, retinoblastoma and rhabdomyosarcoma.
XX
PS Claim 6; Page 81; 122pp; English.
XX
XX The invention relates to novel CASB88 polypeptides and polynucleotides.
CC Sequences of the invention are used for the treatment of diseases e.g.
CC Crohn's disease, Colitis ulcerosa, colorectal cancer, lung cancer and
CC preneoplastic lesions, breast, brain, uterus, muscle, eye and germ cell
CC cancer, Wilm's tumour, retinoblastoma, rhabdomyosarcoma, leiomyosarcoma
CC and synovial sarcoma. They are useful in gene therapy and as vaccines.
CC The present sequence is human CASB88 antigenic epitope
XX
SQ Sequence 10 AA;

Query Match 33.3%; Score 35; DB 5; Length 10;
Best Local Similarity 100.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMSPPG 10
Db 3 GMSPPG 8

RESULT 8
ADC99464
ID ADC99464 standard; peptide; 20 AA.
XX
AC ADC99464;
XX
DT 01-JAN-2004 (first entry)
XX
DE Cancer-related DGI-5-binder peptide - SEQ ID 302.
XX
KW Cytostatic; cancer; gene therapy; DGI-2; DGI-5; DGI-7; DGI-9; Hras;
KW IGF1R; VEGF; vascular endothelial growth factor receptor; VEGF-R1;
KW VEGF-R2; VEGF-R3; FLT1; FMS-related tyrosine kinase 1; Flk1; KDR;
KW kinase insert domain protein receptor; EGFR; epidermal growth factor;
KW FGFR1; fibroblast growth factor; Tie-1.
XX
OS unidentified.
XX
PN MO2003035839-A2.
XX
PD 01-MAY-2003.
XX
PF 24-OCT-2002; 2002MO-US034021.
XX
PR 24-OCT-2001; 2001US-0345471P.
XX
PA (DGI-5) DGI BIOTECHNOLOGIES INC.
XX
PI Piliutia RC, Brissette R, Spruyt M, Dedova O, Blume A;
PI Prendergast J, Goldstein N;
XX
DR WPI; 2003-457332/43.
XX
PT Selecting target and target binder pairs for preparing a composition for
PT treating cancer by mixing in a reaction vessel phase expressing
PT biological targets and phase expressing target binders.
XX
PS Claim 26; SEQ ID NO 302; 172pp; English.
XX
CC The invention relates to a novel method of selecting target and target
CC binder pairs comprising mixing in a reaction vessel phase expressing
CC biological targets and phase expressing target binders, each having
CC distinguishable selection markers and selecting target and target binder
CC pairs based on the selection markers. The molecules of the invention
CC demonstrate cytostatic activity whilst the method may be useful for
CC selecting target and target binder pairs for preparing a composition for
CC treating cancer. Furthermore, the method may be utilised during gene
CC therapy procedures. The current sequence is that of the cancer-related
CC DGI-5-binder peptide of the invention.
XX
SQ Sequence 20 AA;
XX
Query Match 33.3%; Score 35; DB 7; Length 20;
Best Local Similarity 53.3%; Pred. No. 3.4e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;
QY 5 GMSPEFTVGEBSGL 19
DB 2 GRLPFMGLVGRGGL 16

RESULT 9
AAW65590
ID AAW65590 standard; peptide; 8 AA.
XX
AC AAW65590;
XX
DT 15-OCT-1998 (first entry)
XX
DE Peptide #6.
XX
KW Epstein-Barr virus; diagnostic test; autoimmune disease; vaccine;
KW infection; antibody; screening; genetic marker.

XX
OS Synthetic.
XX
PN WO9830586-A2.
XX
PD 16-JUL-1998.
XX
PF 13-JAN-1998; 98MO-US000342.
XX
PR 13-JAN-1997; 97US-00781296.
XX
PA (OKLA-) OKLAHOMA MEDICAL RES FOUND.
XX
PI Harley JB, James JA;
XX
DR WPI; 1998-399062/34.
XX
PT Use of Epstein-Barr virus or component(s) - for developing product(s)
PT which can be used for preventing, diagnosing, treating or determining
PT risk of developing autoimmune disease.
XX
PS Disclosure; Page 54; 81pp; English.
XX
CC The invention relates to a vaccine for alleviating or preventing
CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV).
CC It comprises EBV or a component in a carrier for administration of the
CC virus or viral component to alleviate or prevent the autoimmune disorder.
CC Also claimed are: (1) a diagnostic test kit comprising: (a) reagents
CC which can be used to detect levels of antibodies to EBV, indicators of
CC EBV infection of cells, or levels of EBV DNA or protein in a patient; (b)
CC control samples from individuals not at risk of developing an autoimmune
CC disease; and (c) a device for determining the differences in levels of a
CC patient and control samples to distinguish individuals at higher risk of
CC developing an autoimmune disease from those at lower risk of developing
CC an autoimmune disease; and (2) a method for screening for genetic markers
CC or risk factors for development of autoimmune disorders induced by
CC infection with EBV comprising comparing the responses of different
CC strains of the same species of an animal vaccinated with EBV or a
CC component to induce an autoimmune response in at least one of the strains
CC and comparing the differences in the genetics of the different strains to
CC identify potential genetic markers or risk factors. The methods can be
CC used for the prevention, diagnosis, and treatment of autoimmune diseases
CC having EBV as an etiological agent. The autoimmune diseases may be e.g.
CC systemic lupus erythematosus, Sjogren's syndrome, rheumatoid arthritis,
CC juvenile onset diabetes mellitus, Wegener's granulomatosis, etc. The
CC present sequence is shown in the specification
XX
SQ Sequence 8 AA;
XX
Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 2e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 2 PAKGMP 9
DB 1 PAKGMP 8

RESULT 10
AAE09067
ID AAE09067 standard; peptide; 8 AA.
XX
AC AAE09067;
XX
DT 15-NOV-2001 (first entry)
XX
DE Human autoantigen Sm B/B' octapeptide #3 used in the invention.
XX
KW Vaccine; therapy; autoimmune disorder; Epstein-Barr virus; EBV; anaemia;
KW polymyositis; systemic lupus erythematosus; SLE; rheumatoid arthritis;
KW Sjogren's syndrome; diabetes mellitus; adrenalitis; multiple sclerosis;
KW demyelinating disease; Hashimoto's thyroiditis; autoimmune infertility;
KW hypoparathyroidism; primary biliary cirrhosis; ankylosing spondylitis;

KM inflammatory bowel disease; Addison's disease; thyroiditis; filariasis;
 KM Graves' disease; ulcerative colitis; dermatomyositis; myasthenia gravis;
 KM Crohn's disease; CREST syndrome; autoimmune cystitis; glomerulonephritis;
 KM polyarteritis nodosa; hepatitis; atopic rhinitis; Goodpasture's syndrome;
 KM sarcoidosis; rheumatic fever; anti-phospholipid syndrome; Farmer's lung;
 KM Cushing's syndrome; bird-fancier's lung; alveolitis; erythema nodosum;
 KM pyoderma gangrenosum; fibromyalgia; Kawasaki's disease; cardiomyopathy;
 KM Sampter's syndrome; asthma; polymyalgia rheumatica; psoriasis; arteritis;
 KM erythroblastosis foetalis; cystitis; IGA nephropathy; Hodgkin's lymphoma;
 KM renal cell carcinoma; eosinophilia; immunosuppressive; ophthalmological;
 KM thymometric; neuroprotective; cytostatic; nephrotoxic; antiallergic;
 KM dengue; antitumor; vasotropic; antipyretic; hepatotropic; human.
 OS Homo sapiens.
 XX
 XX MO200158481-A2.
 PN
 XX 16-AUG-2001.
 XX
 XX 09-FEB-2001; 2001WO-US004191.
 PF
 XX 09-FEB-2000; 2000US-00500904.
 PR
 XX (OKLA-) OKLAHOMA MEDICAL RES FOUND.
 PA
 XX Harley JB, James JA, Kaufman KM;
 PI
 XX WPI; 2001-522437/57.
 DR
 XX
 PT Novel vaccine for alleviating or preventing autoimmune disorders induced
 PT Epstein-Barr virus (EBV) infection e.g. systemic lupus erythematosus,
 PT juvenile onset diabetes mellitus, comprises EBV virus or its component.
 PT
 XX Example 1; Fig 3; 11app; English.
 PS

XX The present invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus (EBV),
 CC comprising EBV or its component in a carrier. The vaccine is useful for
 CC preventing or alleviating autoimmune disorders induced by EBV, e.g.
 CC systemic lupus erythematosus (SLE), Sjogren's syndrome, juvenile onset
 CC diabetes mellitus, rheumatoid arthritis, Wegener's granulomatosis,
 CC inflammatory bowel disease, polymyositis, dermatomyositis, multiple
 CC endocrine failure, Schmidt's syndrome, autoimmune uveitis, Addison's
 CC disease, adrenailitis, primary biliary cirrhosis, Graves' disease,
 CC thyroiditis, Hashimoto's thyroiditis, autoimmune thyroid disease,
 CC pernicious and haemolytic anaemia, lupoid hepatitis, demyelinating
 CC disease, multiple sclerosis, subacute cutaneous lupus erythematosus,
 CC hypoparathyroidism, Dressler's syndrome, myasthenia gravis, autoimmune
 CC idiopathic thrombocytopenic purpura, autoimmune pemphigus vulgaris,
 CC pemphigus, bullous pemphigoid, dermatitis herpetiformis, alopecia areata,
 CC autoimmune cystitis, pemphigoid, scleroderma, progressive systemic
 CC sclerosis, CREST syndrome (calcinosis, Raynaud's oesophageal dysmotility,
 CC sclerodactyly and telangiectasia), adult onset diabetes mellitus (type II
 CC diabetes), male or female autoimmune infertility, ankylosing spondylitis,
 CC ulcerative colitis, Crohn's disease, mixed connective tissue disease,
 CC polyarteritis nodosa, systemic necrotising vasculitis,
 CC glomerulonephritis, atopic dermatitis, atopic rhinitis, Goodpasture's
 CC syndrome, Chagas' disease, sarcoidosis, rheumatic fever, asthma,
 CC recurrent abortion, anti-phospholipid syndrome, Farmer's lung, erythema
 CC multiforme, postcardotomy syndrome, Cushing's syndrome, autoimmune
 CC chronic active hepatitis, bird-fancier's lung, allergic
 CC encephalomyelitis, toxic nodular lymphoma, alopecia, Alport's syndrome,
 CC allergic alveolitis, fibrosing alveolitis, interstitial lung disease,
 CC erythema nodosum, pyoderma gangrenosum, transfusion reaction, chronic
 CC fatigue syndrome, fibromyalgia, Takayasu's arteritis, Kawasaki's disease,
 CC polymyalgia rheumatica, temporal arteritis, giant cell arteritis, dengue,
 CC Sampter's syndrome (citraclitis, nasal polyps, eosinophilia) and Behcet's
 CC disease, Sjögren's syndrome, encephalomyelitis, erythema elevatum et
 CC diuturnum, psoriasis, erythroblastosis foetalis, Shulman's syndrome, IGA
 CC nephropathy, Felty's syndrome, fasciitis with eosinophilia, filariasis,
 CC chronic cystitis, heterochromic cystitis, Fuchs' cystitis, Hodgkins and
 CC non-Hodgkin's lymphoma, cardiomyopathy, Henoch-Schönlein purpura, post
 CC vaccination syndromes, renal cell carcinoma, Eaton-Lambert syndrome or

CC relapsing polychondritis. The present sequence is human autoantigen Sm
 CC B/B' octapeptide used in the invention
 XX
 SQ Sequence 8 AA;
 Query Match 32.4%; Score 34; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 9
 DB 1 PAKGMRPP 8
 RSTUT 11
 AAB97330
 ID AAB97330 standard; peptide; 8 AA.
 XX
 AC AAB97330;
 XX
 DT 13-AUG-2001 (first entry)
 XX
 DE UI RNP with A and C proteins epitope peptide.
 XX
 KM B cell; toxin; antigen specific; antibody mediated disease; virucide;
 KM immunosuppressive; antiinflammatory; antiallergic; antidiabetic;
 KM thymometric; antithyroid; vasotropic; cardiac; antitumor;
 KM neuroprotective; antirheumatic; antiarthritic; dermatological;
 KM ophthalmological; nephrotoxic; allergy; autoimmune disorder;
 KM skin diseases; autoimmune endocrinopathy; vasculitic syndrome;
 KM cardiovascular disease; immunohaematologic disorder; neurologic disease;
 KM gastrointestinal disease; collagen vascular disease; renal diseases;
 KM pulmonary disease; infertility disorder; U1-U6 RNP;
 KM systemic lupus erythematosus.
 XX
 XX Unidentified.
 OS
 XX
 XX WO200132853-A1.
 PN
 XX 10-MAY-2001.
 PD
 XX 12-OCT-2000; 2000WO-US028157.
 PF
 XX 29-OCT-1999; 99US-0162464P.
 PR
 XX (BIOM-) INST APPLIED BIOMEDICINE.
 PA
 XX Chaplin JW;
 PI
 XX WPI; 2001-316435/33.
 DR
 XX
 PT B cell clonal toxin useful for treating autoimmune disorders such as
 PT Grave's disease, myocardial infarction, Crohn's disease, multiple
 PT sclerosis, comprises a group that causes toxin to be internalized by B
 PT cell.
 PT
 XX
 PS Disclosure; Page 33; 46pp; English.
 XX
 XX This invention relates to a B cell clonal toxin. The toxin is made from
 CC two moieties, the first causes the toxin to be internalised by a B cell,
 CC and the second is a biologically acceptable toxin. The invention includes
 CC a method for inactivating/filling an antigen specific B cell. A target B
 CC cell is contacted with an effective amount of a B cell clonal toxin. The
 CC method is useful for selective immunosuppression in conditions
 CC characterised by the presence of an unwanted or deleterious immune
 CC response, e.g. in the treatment of antigen specific antibody mediated
 CC disease conditions. Use of the B cell clonal toxin can result in
 CC immunosuppressive; antiinflammatory; antiallergic; virucide; antidiabetic
 CC ; thymometric; antithyroid; vasotropic; cardiac; antitumor;
 CC neuroprotective; antirheumatic; antiarthritic; dermatological;
 CC ophthalmological; and nephrotoxic activity. The toxin is particularly
 CC useful for treating a host suffering from an antigen specific antibody
 CC mediated disease condition, where the antigen specific antibody is

CC produced by an antigen-reactive B cell population present in a host. The
 CC toxin is useful for treating allergies, viral disease conditions, and
 CC autoimmune disorders. Also treated are skin diseases; autoimmune
 CC endocrinopathies; vasculitic syndromes; cardiovascular disease;
 CC immunohematologic disorders; gastrointestinal diseases; neurologic
 CC diseases; collagen vascular diseases; renal diseases; pulmonary diseases;
 CC and infertility disorders. The present sequence represents a UI RNP with
 CC A and C proteins epitope. An antibody response to this antigen is
 CC implicated in systemic lupus erythematosus, a disorder which may be
 CC treated using the toxin of the invention

CC Sequence 8 AA;

Query Match 32.4%; Score 34; DB 4; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMGSP 9
 DB 1 PAKMGSP 8

RESULT 12
 ID ABU07632 standard; peptide; 8 AA.
 XX ABU07632;

DT 23-OCT-2003 (revised)
 DT 10-MAY-2003 (first entry)

DE Epstein-Barr virus nuclear antigen peptide #6.

KM EBV, viral; Epstein-Barr virus nuclear antigen; vaccine;
 KM autoimmune disorder; Epstein-Barr virus infection; diabetes mellitus;
 KM arthritis; multiple sclerosis; dermatitis; psoriasis; asthma; anaemia;
 KM allergy.

OS Human herpesvirus 4.

PN US2002164355-A1.

PD 07-NOV-2002.

PF 24-OCT-2001; 2001US-00012756.

PR 30-NOV-1993; 93US-00160604.

PR 16-MAY-1996; 96US-0019053P.

PR 13-JAN-1997; 97US-00781296.

PA (HARL/) HARLEY J B.

PA (JAME/) JAMES J A.

PI Harley JB, James JA;

PI MPI; 2003-298686/29.

PT New vaccine preventing or alleviating autoimmune disorders induced by the
 PT Epstein-Barr virus, such as diabetes mellitus, rheumatoid arthritis,
 PT multiple sclerosis, systemic lupus erythematosus, atopic dermatitis and
 PT psoriasis.

XX Example 1, Fig 3, 41pp; English.

CC The invention relates to a vaccine for alleviating or preventing
 CC autoimmune disorders induced by infection with Epstein-Barr virus,
 CC comprising an Epstein-Barr virus or a component in a carrier for
 CC administration to alleviate or prevent the autoimmune disorders. The
 CC methods and compositions of the present invention are useful for
 CC diagnosing, preventing, treating and/or alleviating autoimmune disorders,
 CC such as diabetes mellitus, rheumatoid arthritis, juvenile rheumatoid
 CC arthritis, osteoarthritis, psoriatic arthritis, multiple sclerosis,
 CC encephalomyelitis, myasthenia gravis, systemic lupus erythematosus,

CC autoimmune thyroiditis, atopic dermatitis, eczematous dermatitis,
 CC psoriasis, Sjogren's Syndrome, Crohn's disease, aphthous ulcer, lilytis,
 CC conjunctivitis, keratoconjunctivitis, ulcerative colitis, asthma,
 CC allergic asthma, cutaneous lupus erythematosus, scleroderma, vaginitis,
 CC proctitis, drug eruptions, leprosy reversal reactions, erythema
 CC nodosum, leprosy, autoimmune uveitis, allergic encephalomyelitis, acute
 CC necrotizing haemorrhagic encephalopathy, idiopathic bilateral progressive
 CC sensorineural hearing loss, aplastic anaemia, pure red cell anaemia,
 CC idiopathic thrombocytopenia, polychondritis, Wegener's granulomatosis,
 CC chronic active hepatitis, Stevens-Johnson syndrome, idiopathic sprue,
 CC lichen planus, Graves' disease, sarcoidosis, primary biliary cirrhosis,
 CC uveitis posterior, interstitial lung fibrosis, graft-versus-host disease,
 CC and allergy. The present sequence represents an Epstein-Barr virus
 CC nuclear antigen peptide used in the method of the invention. (Updated on
 CC 23-Oct-2003 to standardise OS field)

CC Sequence 8 AA;

Query Match 32.4%; Score 34; DB 6; Length 8;
 Best Local Similarity 75.0%; Pred. No. 2e+06;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMGSP 9
 DB 1 PAKMGSP 8

RESULT 13
 ID ADR43749 standard; peptide; 11 AA.
 XX ADR43749;

AC ADR43749;

DT 04-NOV-2004 (first entry)

DE Maximakinin 8-18 as a bradykinin agonist.

KM bradykinin; Cardiovascular; Vasoactive; Hypotensive; Cytostatic;
 KM vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

PN MO2004069857-A2.

PD 19-AUG-2004.

PF 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UTTE-) UTTECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

PI MPI; 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for
 PT selectively stimulating arterial smooth muscle bradykinin receptors and
 PT for treating cardiovascular disease e.g. ischemic heart disease.

XX Claim 7; SEQ ID NO 3; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the
 CC selective stimulation of arterial smooth muscle bradykinin receptors or
 CC treatment of cardiovascular disease comprises maximakinin, its analogue
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
 CC used in the preparation of a medicament for selectively stimulating
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
 CC organs or organ systems, vascular stenosis, occlusion to peripheral
 CC vessels (such as limb), hypertension; and on the treatment of a condition
 CC or disorder that can be ameliorated with the selective bradykinin

CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor,
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence
CC represents a maximakinin derivative as a bradykinin agonist
XX

SO Sequence 11 AA;

Query Match 32.4%; Score 34; DB 8; Length 11;
Best Local Similarity 75.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
DB 1 KGPRPPGF 8

RESULT 14

ID ADR43750 standard; peptide; 12 AA.

XX ADR43750;

DT 04-NOV-2004 (first entry)

DE Maximakinin 8-19 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

XX Unidentified.

PN WO2004069857-A2.

PD 19-AUG-2004.

PP 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UTRE-) UTRECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

DR WPI; 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.

PS Claim 7; SEQ ID NO 4; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or
CC treatment of cardiovascular disease comprises maximakinin, its analogue
CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
CC used in the preparation of a medicament for selectively stimulating
CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
CC organs or organ systems, vascular stenosis, occlusion to peripheral
CC vessels (such as limb), hypertension; and on the treatment of a condition
CC or disorder that can be ameliorated with the selective bradykinin
CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence

CC represents a maximakinin derivative as a bradykinin agonist
XX
SO Sequence 12 AA;

Query Match 32.4%; Score 34; DB 8; Length 12;
Best Local Similarity 75.0%; Pred. No. 2.8e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
DB 1 KGPRPPGF 8

RESULT 15

ID ADR43752 standard; peptide; 13 AA.

XX ADR43752;

DT 04-NOV-2004 (first entry)

DE Maximakinin 7-19 as a bradykinin agonist.

XX bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.

XX Unidentified.

PN WO2004069857-A2.

PD 19-AUG-2004.

PP 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UTRE-) UTRECH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

DR WPI; 2004-604409/58.

PT Bradykinin agonists comprising maximakinin and its fragments, useful for
PT selectively stimulating arterial smooth muscle bradykinin receptors and
PT for treating cardiovascular disease e.g. ischemic heart disease.

PS Claim 7; SEQ ID NO 6; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the
CC selective stimulation of arterial smooth muscle bradykinin receptors or
CC treatment of cardiovascular disease comprises maximakinin, its analogue
CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
CC used in the preparation of a medicament for selectively stimulating
CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
CC organs or organ systems, vascular stenosis, occlusion to peripheral
CC vessels (such as limb), hypertension; and on the treatment of a condition
CC or disorder that can be ameliorated with the selective bradykinin
CC receptor agonist. Also useful for treatment of a condition for which
CC dilation of vessels is required e.g. treatment of tumours and cancers,
CC and for gene therapy. Maximakinin is a selective bradykinin receptor
CC agonist and exhibits both tissue and receptor specific targeting. This
CC tissue selectivity enables the use of the peptides in the treatment of
CC diseases of the cardiovascular system while minimizing the side effects
CC associated with the use of less selective agents. The present sequence
CC represents a maximakinin derivative as a bradykinin agonist
XX

SO Sequence 13 AA;

Query Match 32.4%; Score 34; DB 8; Length 13;
Best Local Similarity 75.0%; Pred. No. 3.1e+02;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
 |||||
 DB 2 KGRRPPGF 9

RESULT 16

ABP48137
 ID ABP48137 standard; peptide; 18 AA.

AC ABP48137;

DT 23-AUG-2002 (first entry)

DE GHR binding H5 peptide secondary library sequence #13.

KW Growth hormone; receptor; osteopathic; endocrine; hormonal; dwarfism;
 acromegaly; animal husbandry; milk production; GHR.

OS Synthetic.

PN US6387879-B1.

PD 14-MAY-2002.

PF 15-DEC-1997; 97US-00990888.

PR 15-DEC-1997; 97US-00990888.

PA (DGIB-) DGI BIOTECHNOLOGIES INC.

PI Blume AJ, Bissette R, Carcamo J, Mandeckl WS, Tang PM;

DR WPI, 2002-478462/51.

PT New amino acid sequences fully defined in the specification mimic growth
 hormones and are useful to treat conditions such as dwarfism and
 acromegaly, and to promote growth and milk production in cows.

PS Claim 1; Fig 15A; 46pp; English.

CC The invention relates to novel amino acid sequences which bind
 specifically to growth hormone receptor (GHR). The peptides of the
 CC invention have osteopathic, endocrine, and hormonal activity. The amino
 CC acid sequences are useful to treat dwarfism and acromegaly, and in animal
 CC husbandry to promote growth and milk production in cows. The sequence
 CC represents a growth hormone receptor binding peptide of the invention
 SQ Sequence 18 AA;

Query Match 32.4%; Score 34; DB 5; Length 18;
 Best Local Similarity 60.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGFVIG 14
 |||||
 DB 6 GVSYPGMVIG 15

RESULT 17

ADR43748
 ID ADR43748 standard; peptide; 18 AA.

AC ADR43748;

DT 04-NOV-2004 (first entry)

DE Maximakinin 1-18 as a bradykinin agonist.

KW bradykinin; Cardiovascular; Vasotropic; Hypotensive; Cytostatic;
 vascular stenosis; hypertension; tumour; cancer; Maximakinin.

OS Unidentified.

XX NO2004069857-A2.
 PN
 XX
 PD 19-AUG-2004.

XX 06-FEB-2004; 2004WO-GB000470.

PR 06-FEB-2003; 2003GB-00002623.

PR 06-JUN-2003; 2003GB-00012992.

PA (UUTR-) UUTRCH LTD.

PI Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;

DR WPI, 2004-604409/58.

XX

PS Claim 7; SEQ ID NO 2; 67pp; English.

CC The present invention relates to a bradykinin agonist, useful in the
 CC selective stimulation of arterial smooth muscle bradykinin receptors or
 CC treatment of cardiovascular disease comprises maximakinin, its analogue
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
 CC used in the preparation of a medicament for selectively stimulating
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
 CC organs or organ systems, vascular stenosis, occlusion to peripheral
 CC vessels (such as limb), hypertension; and on the treatment of a condition
 CC or disorder that can be ameliorated with the selective bradykinin
 CC receptor agonist. Also useful for treatment of a condition for which
 CC dilation of vessels is required e.g. treatment of tumours and cancers,
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor
 CC agonist and exhibits both tissue and receptor specific targeting. This
 CC tissue selectivity enables the use of the peptides in the treatment of
 CC diseases of the cardiovascular system while minimizing the side effects
 CC associated with the use of less selective agents. The present sequence
 CC represents a maximakinin derivative as a bradykinin agonist
 SQ Sequence 18 AA;

Query Match 32.4%; Score 34; DB 8; Length 18;
 Best Local Similarity 75.0%; Pred. No. 4.4e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
 |||||
 DB 8 KGRRPPGF 15

RESULT 18
 ADN17072
 ID ADN17072 standard; peptide; 19 AA.

AC ADN17072;

DT 15-JUL-2004 (first entry)

DE Second generation G protein library g-alpha peptide, SEQ ID No 81.

KW G alpha subunit; G protein; G protein coupled receptor; GPCR;
 allosteric modulator; g-alpha.

OS Unidentified.

PN WO2004035614-A1.

PD 29-APR-2004.

PF 15-JAN-2003; 2003WO-EP000352.

PR 18-OCT-2002; 2002US-0419143P.
 XX (KARO-) KARO BIO AB.
 XX
 XX Fowlkes DM, Christensen DJ, Hamilton PT, Blasius R, Ramer JK;
 PI Hyde-Deryusche R, Duffin D, Fredericks Z;
 XX WPI; 2004-365151/34.
 DR
 XX New synthetic or partially purified peptides that can bind to specific
 PT subunits of G proteins, useful for detecting the activation or
 PT deactivation of a G protein-coupled receptor (GPCR) or for identifying
 PT allosteric modulators of GPCR.
 XX
 XX Example 300d; SEQ ID NO 81; 242bp; English.
 PS
 XX The invention relates to a novel non-naturally occurring and/or at least
 CC partially purified peptide, which does not comprise a V-H or V-L homology
 CC unit of an antibody and specifically binds to an activated G alpha
 CC subunit of a G protein. The invention further comprises: an assay kit for
 CC the identification of the activation state of a G protein coupled
 CC receptor (GPCR), the kit comprising a first peptide cited above labeled
 CC with a first label; methods of identifying the activation state of a GPCR
 CC; a method of identifying a modulator of a GPCR; a method of determining
 CC the presence or amount of a modulator of a GPCR in a sample; methods of
 CC identifying a substance as an agonist or antagonist of GPCR; and a method
 CC of identifying a G-alpha subunit which interacts with a GPCR. The
 CC composition and methods are useful in detecting the activation or
 CC deactivation of a G protein-coupled receptor or in monitoring the
 CC activation state of a GPCR within a cell. These may also be used for
 CC identifying allosteric modulators of GPCRs. This sequence represents a G
 CC protein library 9-alpha peptide oligo of the invention.
 XX
 SQ Sequence 19 AA;

Query Match 32.4%; Score 34; DB 8; Length 19;
 Best Local Similarity 72.7%; Pred. No. 4.6e+02;
 Matches 8; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 10 GIVGEGVLS 20
 Db 8 GIWVGBEGRLS 18

RESULT 19
 ADR43747
 ID ADR43747 standard; peptide; 19 AA.
 XX
 XX ADR43747;
 AC
 XX
 XX 04-NOV-2004 (first entry)
 DT
 XX
 XX Maximakinin 1-19 as a bradykinin agonist.
 DE
 XX
 XX bradykinin; Cardiovascular; Vasotrophic; Hypotensive; Cytostatic;
 KW vascular stenosis; hypertension; tumour; cancer; Maximakinin.
 XX
 XX Unidentified.
 OS
 XX
 XX WO2004069857-A2.
 PN
 XX
 XX 19-AUG-2004.
 PD
 XX
 XX 06-FEB-2004; 2004WO-GB000470.
 PR
 XX
 XX 06-FEB-2003; 2003GB-00002623.
 PR
 XX
 XX 06-JUN-2003; 2003GB-00012992.
 XX
 XX (UNTE-) UNTECH LTD.
 PA
 XX
 XX Shaw C, Hirst D, Chen T, O'Rourke M, Rao P;
 PI
 XX
 DR WPI; 2004-604409/58.

XX
 XX Bradykinin agonists comprising maximakinin and its fragments, useful for
 PT selectively stimulating arterial smooth muscle bradykinin receptors and
 PT for treating cardiovascular disease e.g. ischemic heart disease.
 XX
 PS Disclosure; SEQ ID NO 1; 67bp; English.
 XX

CC The present invention relates to a bradykinin agonist, useful in the
 CC selective stimulation of arterial smooth muscle bradykinin receptors or
 CC treatment of cardiovascular disease comprises maximakinin, its analogue
 CC or fragment or their encoding nucleic acids. Maximakinin derivatives are
 CC used in the preparation of a medicament for selectively stimulating
 CC arterial smooth muscle bradykinin receptors; for treating cardiovascular
 CC disease (claimed) e.g. ischemic heart disease, ischemic disease of other
 CC organs or organ systems, vascular stenosis, occlusion to peripheral
 CC vessels (such as limb), hypertension; and on the treatment of a condition
 CC or disorder that can be ameliorated with the selective bradykinin
 CC receptor agonist. Also useful for treatment of a condition for which
 CC dilation of vessels is required e.g. treatment of tumours and cancers,
 CC and for gene therapy. Maximakinin is a selective bradykinin receptor
 CC agonist and exhibits both tissue and receptor specific targeting. This
 CC tissue selectivity enables the use of the peptides in the treatment of
 CC diseases of the cardiovascular system while minimizing the side effects
 CC associated with the use of less selective agents. The present sequence
 XX represents maximakinin 1-19 as a bradykinin agonist

SQ Sequence 19 AA;

Query Match 32.4%; Score 34; DB 8; Length 19;
 Best Local Similarity 75.0%; Pred. No. 4.6e+02;
 Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPGF 11
 Db 8 KQPRPPGF 15

RESULT 20
 AAM18175
 ID AAM18175 standard; peptide; 15 AA.
 XX
 XX AAM18175;
 AC
 XX
 XX 13-AUG-1997 (first entry)
 DT
 XX
 XX Immunodominant epitope from Mycobacterium tuberculosis 30KD protein.
 DE
 XX
 XX Vaccine; vaccinating agent; M. tuberculosis; pathogen; bacteria; virus;
 KW fungus; protozoan; HIV.
 KW
 XX
 XX Mycobacterium tuberculosis.
 OS
 XX
 XX WO9637219-A1.
 PN
 XX
 XX 28-NOV-1996.
 PD
 XX
 XX 23-MAY-1996; 96WO-US007781.
 PR
 XX
 XX 23-MAY-1995; 95US-00447398.
 PR
 XX
 XX 20-OCT-1995; 95US-00545926.
 PR
 XX
 XX 31-OCT-1995; 95US-00551149.
 PR
 XX
 XX 06-DEC-1995; 95US-00568357.
 XX
 XX (REGC) UNIV CALIFORNIA.
 PA
 XX
 XX Horwitz MA, Harth G;
 PI
 XX
 DR WPI; 1997-020936/02.
 XX
 XX Vaccines derived from M. tuberculosis major abundant extracellular
 PT proteins - are easy to prepare and less toxic than conventional killed or
 PT attenuated vaccines, useful for protecting against or treating
 PT Mycobacterial infections.

XX Claim 49; Page 162; 193pp; English.
 PS
 XX
 CC A vaccinating agent for promoting an immune response in a mammal against
 CC Mycobacterium pathogens comprises at least one immunodominant epitope of
 CC at least one majorly abundant extracellular protein, i.e. the
 CC M.tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or
 CC 12 kD proteins, or their analogues, homologues and subunits. The present
 CC sequence represents an immunodominant epitope from the major abundant
 CC extracellular product 30 kD protein. The vaccinating agents are used to
 CC protect against (or to treat existing) infections by Mycobacterium
 CC (especially M. tuberculosis) while the epitopes can also be used to
 CC detect presence of an immune response to a Mycobacterium pathogen. The
 CC vectors, containing the DNA for the extracellular proteins, are used to
 CC transform cells for production of recombinant DNA molecules. More
 CC generally the DNA from other pathogens can be used in vaccines, e.g.
 CC against other bacteria, viruses, fungi and protozoa. Since different
 CC combinations of DNA can be used, a wide range of effective compositions
 CC can be produced. They generate a response against the antigens most often
 CC found on infected cells during the infection, regardless of the strength
 CC or specificity of the immune response. The vaccines are easy to produce
 CC and less toxic than known killed or attenuated vaccines, so can be given
 CC to immunocompromised subjects, e.g. those with HIV infection
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 31.4%; Score 33; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DPAKMSP 8
 ||:|||||
 Db 4 DPGQMGMP 11
 RESULT 21
 AAW75617
 ID AAW75617 standard; peptide; 15 AA.
 AC AAW75617;
 XX
 DT 23-OCT-1998 (first entry)
 XX
 DE M. tuberculosis 30 kD protein derived peptide 31 (residues 151-165).
 XX
 KW Mycobacterium tuberculosis; vaccination; extracellular product;
 KM immunodominant epitope; interleukin-12; Mf59; immune response;
 XX opsonising humoral response; intracellular pathogen.
 OS Synthetic.
 OS Mycobacterium tuberculosis.
 XX
 PN WO9831388-A1.
 XX
 PD 23-JUL-1998.
 XX
 PF 15-JAN-1998; 98WO-US000942.
 XX
 PR 21-JAN-1997; 97US-00786533.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Horwitz MA, Harth G, Lee B;
 XX
 DR WPI; 1998-413815/35.
 XX
 PT Vaccines against Mycobacterium containing major extracellular proteins -
 PT used to, e.g. induce protective and therapeutic immune responses, and for
 PT detecting an immune response.
 XX
 PS Example 28; Page 96; 236pp; English.
 XX
 CC Sequences shown in AAW75587 to AAW75641 represent synthetic peptides

CC derived from the native 30kD major secretory protein of M. tuberculosis.
 CC These peptides are used for splenic lymphocyte proliferation assays to
 CC identify the immunodominant T-cell epitope of the 30kD protein. The
 CC invention provides an agent for vaccinating mammals against
 CC Mycobacterium. The agent comprises at least one of the major abundant
 CC extracellular 110, 80, 71, 58, 45, 32A, 32B, 30, 24, 23.5, 23, 16, 14 or
 CC 12 kD proteins of M. tuberculosis, or at least 1 of their immunodominant
 CC epitopes and interleukin-12 (IL-12) or Mf59 as adjuvants. The agent
 CC containing the nucleic acid encoding the extracellular products are used
 CC to raise a protective or therapeutic immune response against
 CC Mycobacterium, specifically M. tuberculosis. The immunodominant epitopes
 CC can also be used (typically in a cutaneous hypersensitivity test) to
 CC detect an immune response to vaccination. Preparation of the agent does
 CC not require selection of the most immunogenic products, so large scale
 CC production and purification are easy, resulting in a consistent,
 CC standardised formulation, having lower toxicity than killed or attenuated
 CC vaccines. The agents provide a rapid and effective response (including a
 CC strong cell-mediated component) and are safe even in immunocompromised
 CC subjects. They prevent development of an opsonising humoral response that
 CC might spread intracellular pathogens
 CC
 XX Sequence 15 AA;
 SQ
 Query Match 31.4%; Score 33; DB 2; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DPAKMSP 8
 ||:|||||
 Db 4 DPGQMGMP 11
 RESULT 22
 ABUS6381
 ID ABUS6381 standard; peptide; 15 AA.
 XX
 AC ABUS6381;
 XX
 DT 31-MAR-2003 (first entry)
 XX
 DE Mycobacterium tuberculosis 30kDa protein fragment #31.
 XX
 KW Antibacterial; tuberculosis; vaccine; gene therapy; 30kDa protein.
 XX
 OS Synthetic.
 OS
 PN US2002131975-A1.
 XX
 PD 19-SEP-2002.
 XX
 PF 14-SEP-2001; 2001US-00953510.
 XX
 PR 23-NOV-1993; 93US-00156358.
 PR 12-AUG-1994; 94US-00288667.
 PR 23-MAY-1995; 95US-00447398.
 PR 31-OCT-1995; 95US-00551149.
 PR 06-DEC-1995; 95US-00568357.
 PR 23-MAY-1996; 96US-00652842.
 PR 21-SEP-1998; 98US-00157689.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Horwitz MA, Harth G;
 XX
 DR WPI; 2003-174073/17.
 XX
 PT New vaccine, useful for promoting an immune response against infectious
 PT pathogens of the genus Mycobacterium in a mammalian host.
 XX
 PS Claim 3; Page 66; 82pp; English.
 XX
 CC The invention describes a vaccine for promoting an immune response, in a
 CC mammalian host, against infectious pathogens of the genus Mycobacterium,

CC comprising at least 1 immunodominant epitope of at least one majority
 CC abundant extracellular product comprising Mycobacterium tuberculosis 110,
 CC 80, 71, 58, 45, 32A, 32B, 30, 24, 32.5, 23, 16, 14, 12 KD protein or
 CC their analogues, homologues or subunits. The proteins and polypeptides of
 CC the invention are useful in gene therapy and treatment of diseases caused
 CC by Mycobacterium such as tuberculosis. This sequence represents a
 CC fragment of the Mycobacterium tuberculosis 30kDa protein

XX
 CC
 SQ Sequence 15 AA;

Query Match 31.4%; Score 33; DB 6; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
 ||:||||
 DB 4 DPGQGMGP 11

RESULT 23

AAE39326
 ID AAE39326 standard; peptide; 15 AA.

XX
 AC AAE39326;

XX
 DT 18-DEC-2003 (first entry)

XX
 DE M. tuberculosis 30 KD protein immunodominant T-cell epitope peptide #31.

XX
 KM Vaccine; antibacterial; fungicide; protozoacide; immunostimulant;
 XX virucide; therapy.

XX
 OS Mycobacterium tuberculosis.

XX
 PN USG59510-BI.

XX
 PD 29-JUL-2003.

XX
 PF 21-SEP-1998; 98US-00157689.

XX
 PR 23-NOV-1993; 93US-00156358.

XX
 PR 12-AUG-1994; 94US-00289667.

XX
 PR 23-MAY-1995; 95US-00447398.

XX
 PR 31-OCT-1995; 95US-00551149.

XX
 PR 06-DEC-1995; 95US-00568357.

XX
 PR 23-MAY-1996; 96US-00652842.

XX
 PA (REBC) UNITV CALIFORNIA.

XX
 PI Horwitz MA, Harth G;

XX
 DR WPI, 2003-669607/63.

XX
 PT A nucleic acid encoding an abundant extracellular protein of
 PT Mycobacterium tuberculosis useful as vaccines for generating protective
 PT or therapeutic immune response against viral, bacterial, fungal or
 PT protozoal infections.

XX
 PS Example 25; Col 64; 82pp; English.

XX
 CC The invention relates to a novel nucleic acid encoding an abundant
 CC extracellular protein of Mycobacterium tuberculosis useful as vaccines
 CC for generating protective or therapeutic immune response against viral,
 CC bacterial, fungal and protozoal infections. They are also used as
 CC immunotherapeutic agents. The present sequence is M. tuberculosis strain
 CC Erdman 30 KD major secretory protein immunodominant T-cell epitope
 CC peptide

XX
 CC
 SQ Sequence 15 AA;

QY 31.4%; Score 33; DB 7; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Query Match 31.4%; Score 33; DB 7; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
 ||:||||
 DB 4 DPGQGMGP 11

RESULT 24

ADP45168
 ID ADP45168 standard; peptide; 15 AA.

XX
 AC ADP45168;

XX
 DT 12-FEB-2004 (first entry)

XX
 DE M. tuberculosis 30kDa extracellular protein fragment seq id 67.

XX
 KM antibacterial; vaccine; immune response; extracellular product;

XX
 KM Mycobacterium; 30KD; extracellular protein.

XX
 OS Mycobacterium tuberculosis.

XX
 PN US2003152584-A1.

XX
 PD 14-AUG-2003.

XX
 PF 15-MAY-2002; 2002US-00147255.

XX
 PR 23-NOV-1993; 93US-00156358.

XX
 PR 12-AUG-1994; 94US-00289667.

XX
 PR 23-MAY-1995; 95US-00447398.

XX
 PR 31-OCT-1995; 95US-00551149.

XX
 PR 23-MAY-1996; 96US-00652842.

XX
 PR 06-DEC-1995; 96US-00568357.

XX
 PR 21-SEP-1998; 98US-00157689.

XX
 PR 06-JAN-1999; 99US-00226539.

XX
 PA (HORW/) HORWITZ M A.

XX
 PI Horwitz MA;

XX
 DR WPI, 2003-897688/82.

XX
 PT Vaccinating agent useful for promoting an immune response in a mammalian
 PT host against Mycobacterium, comprises an immunodominant epitope of a
 PT majorly abundant extracellular product comprising an M. tuberculosis 30
 PT KD protein.

XX
 PS Claim 3; SEQ ID NO 67; 83pp; English.

XX
 CC The invention describes a new vaccinating agent for promoting an immune
 CC response in a mammalian host against Mycobacterium comprising at least
 CC one immunodominant epitope of at least one majority abundant extracellular
 CC product comprising M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30, 24,
 CC 23.5, 23, 16, 14 or 12 KD protein, or its analogue, homologue or subunit.

XX
 CC The bacterium is M. tuberculosis. The vaccinating agent is useful for
 CC promoting an immune response in a mammalian host against Mycobacterium.

XX
 CC This is the amino acid sequence of a Mycobacterium tuberculosis 30KD
 CC extracellular protein fragment that can be used to illicit and immune
 CC response.

XX
 SQ Sequence 15 AA;

QY 31.4%; Score 33; DB 7; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5.1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKGMSP 8
 ||:||||
 DB 4 DPGQGMGP 11

RESULT 25
 ADO36853

ID ADO36853 standard; peptide; 15 AA.
 XX ADO36853;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Majorly abundant extracellular 30kd protein fragment #31.
 XX
 KM antibacterial; virucide; fungicide; protozoacide; vaccine;
 KM vaccinating agent; immune response; infectious pathogen; Mycobacterium;
 KM 110 kDa protein; 80 kDa protein; 71 kDa protein; 58 kDa protein;
 KM 45 kDa protein; 32A kDa protein; 32B kDa protein; 30 kDa protein;
 KM 24 kDa protein; 23.5 kDa protein; 23 kDa protein; 16 kDa protein;
 KM 14 kDa protein; 12 kDa protein; vaccine; immunotherapeutic agent;
 KM 30kd protein.
 XX
 OS Synthetic.
 XX
 PN US2004018209-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 14-SEP-2001; 2001US-00953413.
 XX
 XX 23-NOV-1993; 93US-00156358.
 PR 12-AUG-1994; 94US-00289667.
 PR 23-MAY-1995; 95US-00447398.
 PR 31-OCT-1995; 95US-00551149.
 PR 23-MAY-1996; 96US-00652842.
 PR 06-DEC-1996; 96US-00568357.
 PR 21-SEP-1998; 98US-00157689.
 XX
 PA (REGC) UNIV CALIFORNIA.
 XX
 PI Horwitz MA, Harth G;
 DR WPI; 2004-121994/12.
 XX
 PT New vaccinating agent comprising at least a portion of at least one
 PT majorly abundant extracellular product, useful for promoting an immune
 PT response in a mammalian host against an infectious pathogen from the
 PT genus Mycobacterium.
 PS
 PS Example 25; SEQ ID NO 67; 83pp; English.
 XX
 CC The invention describes a vaccinating agent useful in promoting an immune
 CC response in a mammalian host against an infectious pathogen from the
 CC genus Mycobacterium. The vaccinating agent comprising at least a portion
 CC of at least one majorly abundant extracellular product or a DNA construct
 CC encoding at least a portion of at least one majorly abundant
 CC extracellular product selected from M. tuberculosis 110 kDa protein, 80
 CC kDa protein, 71 kDa protein, 58 kDa protein, 45 kDa protein, 32A kDa
 CC protein, 32B kDa protein, 30 kDa protein, 24 kDa protein, 23.5 kDa
 CC protein, 23 kDa protein, 16 kDa protein, 14 kDa protein or 12 kDa protein
 CC and its analogs, homologs or subunits, and capable of inducing the
 CC expression of the extracellular product upon in vivo introduction into
 CC and resultant uptake by cells of the mammalian host. Also described are:
 CC a DNA molecule containing a coding sequence for at least a portion of the
 CC amino acid sequence of M. tuberculosis 16 kDa protein and fragments and
 CC derivatives; an amino acid sequence encoded by the DNA molecule of (1);
 CC and immunizing a mammalian host against an infectious pathogen of the
 CC genus Mycobacterium. The agent is useful as a vaccine for promoting an
 CC immune response in a mammalian host, against pathogen from genus
 CC Mycobacterium and for producing compounds for use as vaccines and/or
 CC immunotherapeutic agents. It can also be used to protect a mammalian host
 CC against infection by viral, bacterial, fungal or protozoan pathogens.
 CC This is the amino acid sequence of a synthetic Mycobacterium tuberculosis
 CC majorly abundant extracellular 30kd protein fragment used to identify
 CC immunodominant-cell epitopes of the 30kd protein.
 CC
 CC Sequence 15 AA;
 SO

Best Local Similarity 62.5%; Pred. No. 5, 1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DPAKGWSP 8
 DB 4 DPGQWGWSP 11
 RESULT 26
 ID ADU64228 standard; peptide; 15 AA.
 XX
 AC ADU64228;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE 30 KD protein peptide fragment residues 151-165, SEQ ID 67.
 XX
 KM Antibacterial; Tuberculostatic; Protozoacide; Fungicide; Virucide;
 KM Anti-HIV, Vaccine.
 XX
 OS Mycobacterium tuberculosis.
 XX
 PN US2004228873-A1.
 XX
 PD 18-NOV-2004.
 XX
 PF 27-OCT-2003; 2003US-00695155.
 XX
 XX 23-NOV-1993; 93US-00156358.
 PR 12-AUG-1994; 94US-00289667.
 PR 23-MAY-1995; 95US-00447398.
 PR 20-OCT-1995; 95US-00545926.
 PR 31-OCT-1995; 95US-00551149.
 PR 23-MAY-1996; 96US-00652842.
 PR 06-DEC-1996; 96US-00568357.
 PR 21-JAN-1997; 97US-00786533.
 XX
 PA (HORN/) HORWITZ M A.
 PA (HART/) HARTH G.
 PA (LEEB/) LEE B.
 XX
 PI Horwitz MA, Harth G, Lee B;
 DR WPI; 2004-813210/80.
 XX
 PT New vaccinating agent for promoting an immune response against infectious
 PT Mycobacterium pathogen and HIV infection using majorly abundant
 PT extracellular products from Mycobacterium tuberculosis.
 XX
 XX Example 28; SEQ ID NO 67; 109pp; English.
 XX
 CC The present invention relates to a vaccinating agent for promoting an
 CC immune response in a mammalian host against an infectious Mycobacterium
 CC pathogen. The vaccinating agent comprises at least a portion or at least
 CC one immunodominant epitope of at least one majorly abundant extracellular
 CC product selected from M. tuberculosis 110, 80, 71, 58, 45, 32A, 32B, 30,
 CC 24, 23.5, 23, 16, 14 or 12 KD protein and their analogs, homologs, and
 CC subunits, and an IL-12 or IL-59 adjuvant. The compositions of the present
 CC invention are useful for stimulating a protective immune response in
 CC mammalian hosts against intracellular pathogens, such as bacteria,
 CC protozoa, viruses and fungus, particularly Mycobacterium tuberculosis and
 CC the HIV virus. The present sequence is a peptide fragment of M.
 CC tuberculosis 30 KD protein which was used for immunodominant epitope
 CC mapping of the 30 KD protein.
 CC
 CC Sequence 15 AA;
 SO
 Query Match 31.4%; Score 33; DB 8; Length 15;
 Best Local Similarity 62.5%; Pred. No. 5, 1e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DPAKGWSP 8

Db 4 DPGGWGP 11

```

RESULT 27
AAU07809
ID AAU07809 standard; peptide; 16 AA.
XX
AC AAU07809;
XX
DT 07-NOV-2001 (first entry)
XX
DE Peptide encoded by oligonucleotide ONV510.
XX
XX Vascular endothelial growth factor receptor-1; VEGF; psoriasis;
KM angiogenesis mediated disease; birth control; neovascularisation;
KM inflammatory disorder; neoplastic disorder; anti tumour; anti rheumatic;
KM anti arthritic; anti psoriatic; anti diabetic; anti atherosclerotic;
KM anti ulcer; osteopathic; cycostatic; anti inflammatory; ophthalmological;
KM dermatological.
XX
OS Synthetic.
XX
PN WO200157067-A1.
XX
PD 09-AUG-2001.
XX
PP 02-FEB-2001; 2001WO-IB000135.
XX
PR 04-FEB-2000; 2000US-0180568P.
XX
PA (SUPR-) SUPRATEK PHARMA INC.
XX
PI Tcheletikova L, Li S, Pietrzynski G, Alakhov V;
XX
DR WPI; 2001-529780/58.
XX
DR N-PSDB; AAS09208.
XX
PT Composition for treating angiogenesis mediated diseases such as tumor and
PT psoriasis, comprises a peptide or its derivative capable of specific
PT binding with high affinity vascular endothelial growth factor receptor-1.
XX
XX Example 16; Page 70; 86pp; English.
XX
XX The present invention relates to a pharmaceutical composition comprising
CC of a peptide ligand, or its derivative, which is capable of specific
CC binding with high affinity to vascular endothelial growth factor (VEGF)
CC receptor-1 or its derivative and structurally similar receptors. The
CC invention also provides peptide ligands that are capable of inhibiting
CC angiogenesis induced by VEGF. The peptide ligands of the invention are
CC useful for treating a disease associated with angiogenesis in a patient.
CC They are also useful for treating angiogenesis mediated diseases e.g.
CC solid tumours, rheumatoid arthritis and psoriasis, for treating diseases
CC of excessive or abnormal stimulation of endothelial cells e.g. Crohn's
CC disease, atherosclerosis and scleroderma, for treating diseases that have
CC angiogenesis as a pathological consequence e.g. cat scratch disease and
CC ulcers, as a birth control agent, and for treating diseases associated
CC with neovascularisation of the eye e.g. atopic keratitis and Pagen's
CC disease, inflammatory disorders e.g. ulcerative colitis and inflammatory
CC bowel disease, and neoplastic and non-neoplastic diseases and disorders.
CC The peptide ligands are also useful as a targeting group to improve the
CC delivery of a biological agent used for therapeutic or diagnostic
CC purpose. The present sequence represents peptide encoded by
CC oligonucleotide ONV5.10
XX
SQ Sequence 16 AA;

```

Query Match 31.4%; Score 33; DB 4; Length 16;
 Best Local Similarity 50.0%; Pred. No. 5.5e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFI 12
 :|:|:|:|

Db 2 EPEVRLSPGH1 13

```

RESULT 28
ABP30905
ID ABP30905 standard; protein; 20 AA.
XX
AC ABP30905;
XX
DT 02-JUL-2002 (first entry)
XX
DE OE8 antibody epitope peptide #4.
XX
XX Human; immunostimulant; cycostatic; cancer; ovarian carcinoma.
XX
OS Homo sapiens.
XX
PN WO200206317-A2.
XX
PD 24-JAN-2002.
XX
PP 17-JUL-2001; 2001WO-US022635.
XX
PR 17-JUL-2000; 2000US-00617747.
XX
PR 10-AUG-2000; 2000US-00636801.
XX
PR 20-SEP-2000; 2000US-00667857.
XX
PR 04-APR-2001; 2001US-00827271.
XX
PR 18-JUN-2001; 2001US-00884441.
XX
PA (CORI-) CORIXA CORP.
XX
PI Mitcham JL, King GE, Algate PA, Fling SP, Retter MW, Fanger GR,
PI Reed SG, Vedrick TS, Carter D, Hill P, Albone B;
XX
DR WPI; 2002-164781/21.
XX
XX Polypeptides comprising an immunogenic portion of an ovarian carcinoma
PT protein or its variants, useful for stimulating an immune response in a
PT patient and treating ovarian cancer.
XX
PS Claim 34; Page 323; 408pp; English.
XX
XX This invention relates to polypeptides comprising an immunogenic portion
CC of an ovarian carcinoma protein which acts as an immunostimulant and is
CC cytostatic. The polypeptides, polynucleotides, antibodies, fusion
CC proteins, T cell populations and antigen presenting cells that express
CC the polypeptides are useful for eliciting an immune response in a
CC patient and treating ovarian cancer. This sequence represents protein
CC related to the invention
XX
SQ Sequence 20 AA;

```

Query Match 31.4%; Score 33; DB 5; Length 20;
 Best Local Similarity 62.5%; Pred. No. 7e+02;
 Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGEBSVLS 20
 :|:|:|:|

Db 3 IGEDSILS 10

```

RESULT 29
ADA08550
ID ADA08550 standard; peptide; 20 AA.
XX
AC ADA08550;
XX
DT 06-NOV-2003 (first entry)
XX
DE Human OE8 antibody epitope #4.
XX
KW epitope; human; gene therapy; ovarian cancer; cancer.
XX

```

OS Homo sapiens.
 XX
 PN US2003091580-A1.
 XX
 PD 15-MAY-2003.
 XX
 PF 17-JUL-2001; 2001US-00907969.
 XX
 PR 18-JUN-2001; 2001US-00884441.
 XX
 PA (MITC/) MITCHAM J L.
 PA (KING/) KING G B.
 PA (ALGA/) ALGATE P A.
 PA (PLIN/) FLING S P.
 PA (RETT/) RETTER M W.
 PA (FANG/) FANGER G R.
 PA (VEDV/) VEDVICK T S.
 PA (CART/) CARTER D.
 PA (HILL/) HILL P.
 PA (ALBO/) ALBONE E.
 XX
 PI Mitcham JL, King GB, Algate PA, Fling SP, Retter MW, Fanger GR;
 PI Reed SG, Vedvick TS, Carter D, Hill P, Albone E;
 XX
 DR WPI, 2003-532352/50.
 XX
 PT New isolated 0772P polypeptides and polynucleotides, useful in gene
 PT therapy, particularly for treating or diagnosing cancer, e.g. ovarian
 PT cancer.
 XX
 PS Claim 34; SEQ ID NO 397; 371pp; English.
 XX
 CC The invention relates to an isolated 0772P polypeptide, which has the
 CC structure fully defined in the specification. The composition containing
 CC the polypeptides, polynucleotides, fusion proteins, antibodies, T-cells
 CC or antigen presenting cells are useful for stimulating an immune response
 CC and treating ovarian cancer. Detecting the presence of the
 CC polynucleotides and polypeptides is useful for diagnosing cancer. Ovarian
 CC carcinoma CNAs and protein CDNs were identified using microarray
 CC technology. The present sequence represents a human OES antibody epitope.
 CC
 SQ Sequence 20 AA;
 XX
 QY Query Match 31.4%; Score 33; DB 7; Length 20;
 QY Best Local Similarity 62.5%; Pred. No. 7e+02;
 QY Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 DB 13 VGBEGVLS 20
 DB :||:|:
 DB 3 IGEDGILS 10
 XX
 RESULT 30
 ADF09099
 ID ADF09099 standard; peptide; 20 AA.
 XX
 AC ADF09099;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Secreted ovarian carcinoma antigen seqid 603.
 XX
 KW gene therapy; protein therapy; vaccine; antibody inhibition;
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KW secreted ovarian carcinoma antigen.
 XX
 OS Homo sapiens.
 XX
 PN US2003124140-A1.
 XX
 PD 03-JUL-2003.
 XX

PF 17-JUL-2002; 2002US-00198053.
 XX
 PR 17-DEC-1998; 98US-00215681.
 PR 17-DEC-1998; 98US-00216003.
 PR 23-JUN-1999; 99US-00338933.
 PR 24-SEP-1999; 99US-00404879.
 PR 17-JUL-2000; 2000US-00617747.
 PR 10-AUG-2000; 2000US-00635801.
 PR 20-SEP-2000; 2000US-00667857.
 PR 04-APR-2001; 2001US-00827271.
 PR 18-JUN-2001; 2001US-00884441.
 PR 17-JUL-2001; 2001US-00907969.
 XX
 PA (CORI-) CORIXA CORP.
 XX
 PI Bangur CS, Retter MW, Fanger GR, Hill P;
 PI WPI; 2003-697152/82.
 XX
 DR Oncogenic nucleic acids useful for the prevention, diagnosis and
 DR treatment of breast cancer.
 XX
 PT Claim 2; SEQ ID NO 603; 399pp; English.
 XX
 PS The invention describes nucleic acids (I) and the polypeptides (II) they
 PS encode. The nucleic acids (I) may be used for preventing, diagnosing and
 PS treating diseases related to their aberrant expression i.e. breast
 PS cancers. For example, (I) and (II) may be used to treat disorders
 PS associated with decreased expression by rectifying mutations or deletions
 PS in a patient's genome that affect the activity of (II) by expressing
 PS inactive proteins or to supplement the patient's own production of (II).
 PS Additionally, (I) may be used to produce (II), by inserting (I) into a
 PS host cell and culturing the cell to express the protein (II). (I) And its
 PS complementary sequences may also be used as DNA probes in diagnostic
 PS assays to detect and quantitate the presence of similar nucleic acids in
 PS samples, and therefore which patients may be in need of restorative
 PS therapy. The host cell may also be used as antigens in the production of
 PS antibodies against (II) and in assays to identify modulators of (II)'s
 PS expression and activity. The anti-(II) antibodies, agonists and
 PS antagonists may be used to regulate expression and activity and as
 PS diagnostic agents for detecting the presence of (II) in samples (e.g. by
 PS immunoassay). This sequence represents a secreted ovarian carcinoma
 PS antigen.
 XX
 SQ Sequence 20 AA;
 XX
 QY Query Match 31.4%; Score 33; DB 7; Length 20;
 QY Best Local Similarity 62.5%; Pred. No. 7e+02;
 QY Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 DB 13 VGBEGVLS 20
 DB :||:|:
 DB 3 IGEDGILS 10
 XX
 RESULT 31
 ADF08893
 ID ADF08893 standard; peptide; 20 AA.
 XX
 AC ADF08893;
 XX
 DT 12-FEB-2004 (first entry)
 XX
 DE Secreted ovarian carcinoma antigen seqid 397.
 XX
 KW gene therapy; protein therapy; vaccine; antibody inhibition;
 KW breast cancer; restorative therapy; diagnostic agent; immunoassay;
 KW secreted ovarian carcinoma antigen.
 XX
 OS Homo sapiens.
 XX
 PN US2003124140-A1.
 XX

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PD 03-JUL-2003.
XX
XX 17-JUL-2002; 2002US-00198053.
XX
XX 17-DEC-1998; 98US-00215681.
XX 17-DEC-1998; 98US-00216003.
XX 23-JUN-1999; 99US-00338933.
XX 24-SEP-1999; 99US-00404879.
XX 17-JUL-2000; 2000US-00617747.
XX 10-AUG-2000; 2000US-00636801.
XX 20-SEP-2000; 2000US-00667857.
XX 04-APR-2001; 2001US-00827271.
XX 18-JUN-2001; 2001US-00884441.
XX 17-JUL-2001; 2001US-00907969.
XX
XX (COR-) CORIXA CORP.
XX
XX Bangur CS, Reltter MW, Fanger GR, Hall P;
XX WPI; 2003-897152/82.
XX
XX Oncogenic nucleic acids useful for the prevention, diagnosis and
XX treatment of breast cancer.
XX
XX Example 3; SEQ ID NO 397; 399pp; English.
XX
XX The invention describes nucleic acids (I) and the polypeptides (II) they
XX encode. The nucleic acids (I) may be used for preventing, diagnosing and
XX treating diseases related to their aberrant expression i.e. breast
XX cancers. For example, (I) and (II) may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of (II) by expressing
XX inactive proteins or to supplement the patient's own production of (II).
XX Additionally, (I) may be used to produce (II), by inserting (I) into a
XX host cell and culturing the cell to express the protein (II). (I) And its
XX complementary sequences may also be used as DNA probes in diagnostic
XX assays to detect and quantitate the presence of similar nucleic acids in
XX samples, and therefore which patients may be in need of restorative
XX therapy. The host cell may also be used as antigens in the production of
XX antibodies against (II) and in assays to identify modulators of (II)'s
XX expression and activity. The anti-(II) antibodies, agonists and as
XX antagonists may be used to regulate expression and activity and as
XX diagnostic agents for detecting the presence of (II) in samples (e.g. by
XX immunoassay). This sequence represents a secreted ovarian carcinoma
XX antigen.
XX
XX SQ Sequence 20 AA;
XX
XX Query Match 31.4%; Score 33; DB 7; Length 20;
XX Best Local Similarity 62.5%; Pred. No. 7e+02;
XX Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 VGESEGVLS 20
XX :||:|:|
XX DB 3 IGSDGILS 10
XX
XX RESULT 32
XX ADG46180
XX ID ADG46180 standard; peptide; 20 AA.
XX
XX AC ADG46180;
XX
XX DT 26-FEB-2004 (first entry)
XX
XX DE O8E antibody epitope #4.
XX
XX O8E antibody epitope #4.
XX
XX Human; ovarian carcinoma; O8E; ovarian cancer; secreted tumour antigen;
XX cytostatic; O772P; epitope.
XX
XX OS Homo sapiens.
XX
XX PN US2003165504-A1.
XX

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XX
XX PD 04-SEP-2003.
XX
XX PF 04-APR-2001; 2001US-00827271.
XX
XX 17-DEC-1998; 98US-00215681.
XX 17-DEC-1998; 98US-00216003.
XX 23-JUN-1999; 99US-00338933.
XX 24-SEP-1999; 99US-00404879.
XX 17-JUL-2000; 2000US-00617747.
XX 10-AUG-2000; 2000US-00636801.
XX 20-SEP-2000; 2000US-00667857.
XX
XX (RETT/) RETTER M W.
XX (FANG/) FANGER G R.
XX
XX Reltter MW, Fanger GR;
XX WPI; 2003-898035/82.
XX
XX New isolated O8E or O772P polypeptides, useful for diagnosing,
XX preventing, treating and monitoring cancer, e.g. ovarian cancer,
XX stimulating the immune response in patient.
XX
XX Example 3; SEQ ID NO 397; 290pp; English.
XX
XX The invention relates to human ovarian carcinoma polypeptides, designated
XX O8E or O772P, and the polynucleotides encoding them. The invention also
XX relates to methods for inhibiting the development of cancer, e.g. ovarian
XX cancer in a patient, methods for stimulating and/or expanding T cells and
XX methods for identifying secreted tumour antigens. The polypeptides,
XX compositions, antibodies to the polypeptides and methods are useful for
XX diagnosing, preventing, treating and monitoring cancer, e.g. ovarian
XX cancer. The composition is particularly useful for stimulating an immune
XX response in patient. This sequence represents an O8E antibody epitope of
XX the invention.
XX
XX SQ Sequence 20 AA;
XX
XX Query Match 31.4%; Score 33; DB 7; Length 20;
XX Best Local Similarity 62.5%; Pred. No. 7e+02;
XX Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
XX
XX QY 13 VGESEGVLS 20
XX :||:|:|
XX DB 3 IGSDGILS 10
XX
XX RESULT 33
XX ADK40495
XX ID ADK40495 standard; peptide; 20 AA.
XX
XX AC ADK40495;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE KDR & VEGF/KDR complex binding peptide of a Lin20 peptide library ID146.
XX
XX endotheelial cell; vacular endotheelial growth factor; VEGF;
XX receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;
XX foetal liver kinase-1; Flk-1; VEGF/KDR complex; angiogenesis;
XX neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;
XX simian haemorrhagic fever virus;
XX enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;
XX virucidal; antibacterial; cytostatic.
XX
XX Synthetic.
XX
XX OS
XX PN WO2003074005-A2.
XX
XX PD 12-SEP-2003.
XX
XX PF 03-MAR-2003; 2003WO-US006731.
XX

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PF 02-JUN-2004; 2004US-00860790.
XX
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.
PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
PR 17-JUL-2002; 2002US-00198053.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Retter MW, Fanger GR, Hill P;
XX
DR WPI; 2005-151645/16.
XX
PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT for eliciting humoral and/or cellular immune response.
XX
XX
PS Disclosure; SEQ ID NO 397; 398bp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC of, a sequence hybridizing under highly stringent conditions to, or
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen peptide of the invention.
XX
SQ Sequence 20 AA;
XX
Query Match 31.4%; Score 33; DB 9; Length 20;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 13 VSEEGVLS 20
DB 3 IGEDGILS 10
XX
RESULT 36
ADXL17982
ID ADXL17982 standard; peptide; 20 AA.
XX
AC ADXL17982;
XX
DT 21-APR-2005 (first entry)
XX
DE Human ovarian carcinoma antigen O8B peptide #4.
XX
KW diagnosis; cytostatic; immunostimulant; gene therapy; tumor;
KW ovarian tumor; cancer; carcinoma; antigen.
XX
OS Homo sapiens.
XX
PN US2005031634-A1.
XX
PD 10-FEB-2005.
XX
PF 02-JUN-2004; 2004US-00860790.
XX
PR 17-DEC-1998; 98US-00216003.
PR 23-JUN-1999; 99US-00338933.
PR 24-SEP-1999; 99US-00404879.
PR 17-JUL-2000; 2000US-00617747.
PR 10-AUG-2000; 2000US-00636801.
PR 20-SEP-2000; 2000US-00667857.

PR 04-APR-2001; 2001US-00827271.
PR 18-JUN-2001; 2001US-00884441.
PR 17-JUL-2001; 2001US-00907969.
PR 17-JUL-2002; 2002US-00198053.
XX
PA (CORI-) CORIXA CORP.
XX
PI Bangur CS, Retter MW, Fanger GR, Hill P;
XX
DR WPI; 2005-151645/16.
XX
PT New ovarian carcinoma polynucleotides, preferably cDNAs, useful for
PT diagnosing, preventing and treating diseases, such as ovarian cancer, and
PT for eliciting humoral and/or cellular immune response.
XX
XX
PS Claim 2; SEQ ID NO 603; 398bp; English.
XX
CC The invention relates to an isolated polynucleotide comprising a sequence
CC of, a sequence hybridizing under highly stringent conditions to, or
CC having at least 75, or 90% identity to a 849 or 1399 bp, fully defined in
CC the specification, its complement or degenerate variants, or a sequence
CC of at least 20 contiguous residues of the 849 or 1399 bp sequence. The
CC polynucleotides and polypeptides are useful for diagnosing, preventing
CC and treating diseases, such as ovarian cancer, and for eliciting humoral
CC and/or cellular immune response. This sequence corresponds to an ovarian
CC carcinoma antigen peptide of the invention.
XX
SQ Sequence 20 AA;
XX
Query Match 31.4%; Score 33; DB 9; Length 20;
Best Local Similarity 62.5%; Pred. No. 7e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 13 VSEEGVLS 20
DB 3 IGEDGILS 10
XX
RESULT 37
AAO14949
ID AAO14949 standard; peptide; 10 AA.
XX
AC AAO14949;
XX
DT 06-AUG-2002 (first entry)
XX
DE Survivin-like protein-related peptide.
XX
KW Survivin-like protein; diagnosis; screening; cancer;
KW apoptosis abnormality; gene therapy.
XX
OS Unidentified.
XX
PN WO200233071-A1.
XX
PD 25-APR-2002.
XX
PF 16-OCT-2001; 2001WO-0P009071.
XX
PR 17-OCT-2000; 2000JP-00316721.
PR 20-DEC-2000; 2000JP-00386809.
XX
PA (TAKE) TAKEDA CHEM IND LTD.
XX
PI Tanaka H, Kaleda I;
XX
DR WPI; 2002-435536/46.
XX
PT Baculovirus TAP repeat domain or RING-finger domain-containing survivin-
PT like polypeptides and encoded DNAs, applicable in diagnosis and screening
PT compounds for treating various cancers and apoptosis abnormality.
XX
PS Example 4; Page 91; 136pp; Japanese.

XX The invention comprises the amino acid and coding sequences of survivin-
CC like proteins. The survivin-like DNA and protein sequences are useful in
CC diagnostics and screening compounds for treating various cancers and
CC apoptosis abnormally, including gene therapy. The present amino acid
CC sequence was used in an example of the invention
XX

XX Sequence 10 AA;
SQ

Query Match 30.5%; Score 32; DB 5; Length 10;
Best Local Similarity 50.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
DB 1 DPAKMSPPG 10
1 EFGAGPGPPG 10

RESULT 38
ADS92606
ID ADS92606 standard; peptide; 10 AA.
AC ADS92606;
XX
DT 02-DEC-2004 (first entry)
XX
DE Platelet aggregation inhibition method-related mutated gp38p peptide #3.
XX
XX platelet aggregation inhibition; gp44-expressing; screening;
XX colon cancer; rectal cancer; testicular cancer; seminoma;
XX flat-epithelial carcinoma; cancer metastasis; pulmonary thrombosis;
XX cerebral infarction; myocardial infarction; arteriosclerosis;
XX bleeding tendency; blood clotting disorder; haemophilia; uremia;
XX chronic myeloproliferative disorder; gp38p; mutant; mutein.
XX
OS Synthetic.
OS Unidentified.
XX
XX WO2004036681-A1.
XX
XX 22-APR-2004.
XX
XX 09-OCT-2003; 2003WO-JP012996.
XX
XX 11-OCT-2002; 2002JP-00298400.
XX
XX 08-MAY-2003; 2003JP-00129954.
XX
XX (SANY) SANKYO CO LTD.
XX
XX Teuruo T, Fujita N, Osawa M, Kato Y,
XX
XX WPI; 2004-330453/30.
XX
XX Substances with activity of promoting or inhibiting platelet aggregation
XX screened by using factor gp4, applicable in treatment of its
XX accompanying diseases like colon cancer, myocardial infarction and
XX arteriosclerosis.
XX
XX Example 12; SEQ ID NO 46; 219pp; Japanese.
XX
XX The invention comprises a method for screening substances for promoting
XX or inhibiting platelet aggregation. The method involves: culturing gp44-
XX expressing cells in the presence/absence of a test substance, detecting
XX expression of mRNAs, and measuring the expression doses of the detected
XX mRNAs for comparison and selection. The method of the invention is useful
XX in the development of drugs for the treatment of: colon cancer, rectal
XX cancer, testicular cancer, seminoma, flat-epithelial carcinoma, cancer
XX metastasis, pulmonary thrombosis, cerebral infarction, myocardial
XX infarction, arteriosclerosis, bleeding tendency, blood clotting disorder,
XX haemophilia, uremia and chronic myeloproliferative disorder. The present
XX amino acid sequence represents a mutated gp38p peptide that was used in
XX an example of the invention.

SQ Sequence 10 AA;
XX

Query Match 30.5%; Score 32; DB 8; Length 10;
Best Local Similarity 83.3%; Pred. No. 4.7e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
DB 2 GMSPPG 10
2 GMAAPG 7

RESULT 39
ADB49200
ID ADB49200 standard; peptide; 15 AA.
AC ADB49200;
XX
DT 04-DEC-2003 (first entry)
XX
DE Biotinylated peptide recognition unit #1.
XX
XX WW domain; drug candidate screening; drug discovery; drug modification;
XX drug refinement; immunogen; WW binding protein; WW domain;
XX peptide recognition unit.
XX
OS Synthetic.
XX
XX US2003077577-A1.
XX
XX 24-APR-2003.
XX
XX 28-JUN-2002; 2002US-00185050.
XX
XX 03-APR-1996; 96US-00630916.
XX
XX 03-APR-1997; 97US-00826516.
XX
XX (PIROZ) PIROZZI G.
XX (KAYB/) KAY B K.
XX (FOWL/) FOWLKES D M.
XX
XX Pirozzi G, Kay BK, Fowlkes DW,
XX
XX WPI; 2003-635075/60.
XX
XX Novel purified polypeptide comprising WW domain, useful for drug
XX discovery, modification and refinement, for discovering polypeptides
XX involved in pharmacological activities, or as an immunogen to generate
XX antibodies.
XX
XX Example; Page 22; 133pp; English.
XX
XX The invention describes a purified polypeptide (I) comprising a WW domain
XX which has a sequence (S1) selected from 11 sequences fully defined in the
XX specification, a sequence (S2) selected from 48 sequences fully defined
XX in the specification or a sequence (S3) comprising 683, 906, 224 or 725
XX amino acids fully defined in the specification. (I) is useful for
XX screening a potential drug candidate, by allowing (I) to come into
XX contact with at least one recognition unit having a selective affinity
XX for the WW domain in (I), in the presence of an amount of a potential
XX drug candidate, such that (I) and the recognition unit are capable of
XX interacting when brought into contact with one another in the absence of
XX the drug candidate, and determining the effect, if any, of the presence
XX of the amount of the drug candidate on the interaction of (I) with the
XX recognition unit. (I) is useful for drug discovery, modification and
XX refinement, for discovering polypeptides involved in pharmacological
XX activities, or as an immunogen to generate antibodies. This is the amino
XX acid sequence of a peptide recognition unit used to screen cDNA
XX expression libraries for WW domain binding proteins.
XX

Sequence 15 AA;
SQ

Query Match 30.5%; Score 32; DB 7; Length 15;
Best Local Similarity 46.2%; Pred. No. 7.3e+02;

Matches 6; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFIYG 14
| | | | |
Db 2 PHEGTPPPPIYVG 14

RESULT 40
AAU10333
ID AAU10333 standard; peptide; 16 AA.
XX
AC AAU10333;
XX
DT 14-FEB-2002 (first entry)
XX
DE Human PROST 03 immunogenic fragment, Pep8.
XX
KW Human; PROST 03; metastasis; prostate cancer; tumour; immune response;
KW cytostatic; vaccine; immunogenic.
XX
OS Homo sapiens.
XX
PN WO200181577-A2.
XX
PD 01-NOV-2001.
XX
PF 26-APR-2001; 2001WO-US013323.
XX
PR 27-APR-2000; 2000US-0200065P.
PR 20-APR-2001; 2001US-00838785.
XX
PA (SCHD) SCHERING AG.
XX
PI Lau T, Lin RJ, Parkes D, Parry G, Schneider DW, Streibbrecher R;
PI Van Heut PT, Wu J;
XX
DR WPI; 2002-041404/05.
XX
PT Novel PROST 03 polypeptides and polynucleotides useful in research,
PT diagnosis and therapeutic applications, particularly for use in cancer
PT therapeutics.
XX
PS Claim 18; Page 50; 77pp; English.
XX
CC The invention relates to an isolated PROST 03 polypeptide (I) and to the
CC polynucleotide (II) encoding PROST 03. Fragments of (I) were used to
CC generate antibodies (III) to PROST 03. (III) is useful for selectively
CC destroying a cell expressing (I), and for treating a disease-state
CC associated with expression of PROST 03 in a human patient. (III) is
CC useful for diagnosing metastasis associated with (I), in a subject. (I)
CC is also useful for diagnosing and treating diseases of cell proliferation
CC such as prostate cancer. (I) is also useful for generating antibodies to
CC PROST 03. (III) is useful in detecting the levels of PROST 03
CC polypeptides in cells and tissues, and in targeting drugs to primary and
CC metastatic tumours. (I) is also useful for stimulating immune response to
CC PROST 03 containing cells. (II) is useful in diagnostic assays for
CC detecting the levels of polynucleotides encoding PROST 03 in cells and
CC tissues. (II) is useful as DNA probes, as targets for antisense and
CC ribozyme therapy, and as templates for the production of antisense
CC polynucleotides. (I) and (II) are useful in research, biological,
CC clinical and therapeutic purposes. The present sequence represents the
CC amino acid sequence of human PROST 03 immunogenic fragment Pep8, used to
CC generate anti-PROST 03 antibodies
XX
SQ Sequence 16 AA;

Query Match 30.5%; Score 32; DB 5; Length 16;
Best Local Similarity 55.6%; Pred. No. 7.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMSPP 9
:|:|:|:
DB 3 EPAEGISAP 11

RESULT 41
AEC13757
ID AEC13757 standard; peptide; 16 AA.
XX
AC AEC13757;
XX
DT 20-OCT-2005 (first entry)
XX
DE Staphylococcus aureus lysyl-tRNA synthetase peptide.
XX
KW protein purification; antibacterial; antimicrobial; infection;
KW drug screening; lysyl-tRNA synthetase.
XX
OS Staphylococcus aureus.
XX
PN US2005181464-A1.
XX
PD 18-AUG-2005.
XX
PF 29-SEP-2004; 2004US-00953901.
XX
PR 04-APR-2002; 2002US-0369819P.
PR 04-APR-2002; 2002US-0369826P.
PR 04-APR-2002; 2002US-0369831P.
PR 04-APR-2002; 2002US-0370060P.
PR 08-APR-2002; 2002US-0370681P.
PR 08-APR-2002; 2002US-0370805P.
PR 08-APR-2002; 2002US-0370852P.
PR 08-APR-2002; 2002US-0370868P.
PR 09-APR-2002; 2002US-0370959P.
PR 09-APR-2002; 2002US-0370979P.
PR 09-APR-2002; 2002US-0371008P.
PR 09-APR-2002; 2002US-0371009P.
PR 09-APR-2002; 2002US-0371014P.
PR 09-APR-2002; 2002US-0371025P.
PR 09-APR-2002; 2002US-0371064P.
PR 09-APR-2002; 2002US-0371065P.
PR 09-APR-2002; 2002US-0371094P.
PR 09-APR-2002; 2002US-0371114P.
PR 09-APR-2002; 2002US-0371180P.
PR 09-APR-2002; 2002US-0371189P.
PR 31-MAY-2002; 2002US-0384634P.
PR 31-MAY-2002; 2002US-0385157P.
PR 04-JUN-2002; 2002US-0385542P.
PR 04-JUN-2002; 2002US-0385611P.
PR 04-JUN-2002; 2002US-0385747P.
PR 04-JUN-2002; 2002US-0385750P.
PR 04-JUN-2002; 2002US-0385752P.
PR 04-JUN-2002; 2002US-0385773P.
PR 04-JUN-2002; 2002US-0385780P.
PR 04-JUN-2002; 2002US-0385785P.
PR 04-JUN-2002; 2002US-0385797P.
PR 05-JUN-2002; 2002US-0385962P.
PR 05-JUN-2002; 2002US-0386022P.
PR 05-JUN-2002; 2002US-0386024P.
PR 05-JUN-2002; 2002US-0386087P.
PR 05-JUN-2002; 2002US-0386141P.
PR 05-JUN-2002; 2002US-0386350P.
PR 05-JUN-2002; 2002US-0386586P.
PR 06-JUN-2002; 2002US-0386368P.
PR 06-JUN-2002; 2002US-0386369P.
PR 06-JUN-2002; 2002US-0386436P.
PR 06-JUN-2002; 2002US-0386441P.
PR 06-JUN-2002; 2002US-0386528P.
PR 06-JUN-2002; 2002US-0386573P.
PR 06-JUN-2002; 2002US-0386834P.
PR 31-JUL-2002; 2002US-0399839P.
PR 31-JUL-2002; 2002US-0399861P.
PR 31-JUL-2002; 2002US-0399869P.
PR 31-JUL-2002; 2002US-0399970P.
PR 31-JUL-2002; 2002US-0399983P.

PR	31-JUL-2002;	2002US-039984P.
PR	31-JUL-2002;	2002US-039985P.
PR	01-AUG-2002;	2002US-0400154P.
PR	01-AUG-2002;	2002US-0400230P.
PR	01-AUG-2002;	2002US-0400268P.
PR	01-AUG-2002;	2002US-0400363P.
PR	01-AUG-2002;	2002US-0400374P.
PR	01-AUG-2002;	2002US-0400380P.
PR	01-AUG-2002;	2002US-0400433P.
PR	01-AUG-2002;	2002US-0400434P.
PR	01-AUG-2002;	2002US-0400436P.
PR	01-AUG-2002;	2002US-0400442P.
PR	01-AUG-2002;	2002US-0400463P.
PR	04-APR-2003;	2003WO-CA000465.
PR	08-APR-2003;	2003WO-CA000482.
PR	08-APR-2003;	2003WO-CA000483.
PR	02-JUN-2003;	2003WO-CA000786.
XX		
PA	(AFPI-) AFFINITY PHARM INC.	
XX		
P1	Edwards A, Dharamel A, Vedadi M, Alam MZ, Arrowsmith C, Awrey DE;	
P1	Beattie B, Buzzadlaja K, Clarke T, Domagala M, Houston S;	
P1	Kangasrajan D, Li Q, Mansoury K, McDonnald M, Nethery-Brooks K, Ng I;	
P1	Ouyang H, Richards D, Vallee F, Virag C;	
XX		
DR	WPI; 2005-628190/64.	
XX		
PT	Novel crystallized, recombinant bacterial polypeptide, useful as targets	
PT	for pathogenic bacteria such as Helicobacter pylori, Staphylococcus	
PT	aureus, for detecting pathogenic species in biological sample, and in	
PT	drug designing.	
XX		
PS	Example 1, Fig 8; 637pp; English.	
XX		
CC	The invention relates to a composition (1) comprising purified	
CC	polypeptides from bacteria. Also described: (1) a crystallized,	
CC	recombinant polypeptide comprising an amino acid sequence of (1), where	
CC	the crystallized, recombinant polypeptide and a co-factor or a small	
CC	organic molecule, where the complex is in crystal form; and (3) a host	
CC	cell comprising a nucleic acid encoding a polypeptide of (1), where a	
CC	culture of the host cell produces at least about 1 mg of the polypeptide	
CC	per liter of culture and the polypeptide is at least about one-third	
CC	soluble as measured by gel electrophoresis. (1) can be used as a target	
CC	for pathogenic bacteria, useful for detecting the presence of a	
CC	pathogenic species in a biological sample. (1) is useful for monitoring	
CC	the effectiveness of anti-pathogenic treatments in an individual	
CC	suffering from a disease or disorder caused by a pathogenic bacteria,	
CC	such as infections. (1) is also useful in drug design and screening, for	
CC	identifying inhibitors of (1), for designing a potential compound that is	
CC	useful for treating or preventing pathogenic diseases or disorders, for	
CC	assessing the activity of small molecules and other modulators in in	
CC	vitro assay, and for developing antimicrobial agents. The present	
CC	sequence represents a Staphylococcus aureus lyeal tRNA synthetase	
CC	peptide, which is used in an example from the present invention.	
XX		
SQ	Sequence 16 AA;	
	Query Match	30.5%
	Best Local Similarity	70.0%; Pred. No. 7.9e+02;
	Matches	7, Conservative 1, Mismatches 2, Indels 0, Gaps 0,
QY	10 GFIVGESEVVL 19	
DB	5 GDIVGVEGVWL 14	
RESULT 42		
ABP57840		
ID	ABP57840 standard; protein; 18 AA.	
XX		
NC	ABP57840;	

XX 19-APR-2000; 2000DK-00000666.
PR 21-FEB-2001; 2001DK-00000283.

XX (STAT-) STATENS SERUM INST.

XX Agger EM, Andersen P, Okkels LMW, Wellingh K;

XX WPI; 2002-061970/08.

PT New Mycobacterium tuberculosis antigens, useful for diagnosing
PT tuberculosis, and as a vaccine for treating or preventing infections
PT caused by species of tuberculosis complex.

PS Example 3; Page 96; 11pp; English.

XX The invention relates to a substantially pure polypeptide comprising an
CC amino acid sequence selected from RV0284, RV0285, RV0455C, RV0569,
CC RV1195, RV1386, RV3477, RV3878, RV3879C or W3106.1 (also disclosed are
CC ORF13A and RV0284Ct), or their immunogenic portion, nucleic acids
CC encoding them and an amino acid sequence analogue having at least 70%
CC sequence identity to the polypeptide and is immunogenic. The protein is
CC useful in preparing a pharmaceutical composition for diagnosing
CC tuberculosis and in preparing a vaccine against tuberculosis caused by
CC virulent mycobacteria. The vaccine or immunogenic/ pharmaceutical
CC composition can be used prophylactically in a subject not infected with a
CC virulent mycobacterium, or therapeutically in a subject already infected
CC with a virulent mycobacterium. The protein is useful for preventing,
CC treating and detecting infections caused by species of tuberculosis
CC complex (M. tuberculosis, M. bovis, M. africanum). The nucleic acids may
CC be used for effecting in vivo expression of the antigen, and in
CC diagnostic assays for detecting the presence of pathogenic organisms in a
CC sample. The vaccine is an improvement of the living BCG vaccine presently
CC available, where one or more copies of the DNA sequence encoding one or
CC more polypeptide has been incorporated into the genome of the
CC microorganism to allow the microorganism to express and secrete the
CC polypeptide. Incorporation of more than one copy of a nucleotide sequence
CC enhances the immune response. The present sequence represents an
CC immunogenic peptide derived from an M. tuberculosis protein of the
CC invention

XX SQ Sequence 20 AA;

Query Match 30.5%; Score 32; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14
DB 9 GMSPPGPIVG 18

RESULT 44

ADK40519
ID ADK40519 standard; peptide; 20 AA.

AC ADK40519;

DT 06-MAY-2004 (first entry)

DE KDR & VEGF/KDR complex binding peptide of a Lin20 peptide library ID170.

XX endothelial cell; vascular endothelial growth factor; VEGF;
KM receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;
KM foetal liver kinase-1; Flk-1; VEGF/KDR complex; angiogenesis;
KM neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;
KM simian haemorrhagic fever virus;
KM enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;
KM vincidol; antibacterial; cytostatic.

OS Synthetic.

XX WO2003074005-A2.

XX 12-SEP-2003.
PD
XX 03-MAR-2003; 2003WO-US006731.
PP

XX 01-MAR-2002; 2002US-0360851P.
PR
XX 15-JAN-2003; 2003US-0440411P.

XX (DYAX-) DYAX CORP.
PA (BRAC) BRACCO INT BV.

PI Sato AK, Sexton DJ, Ladner RC, Dransfield DT, Swenson RE;
PI Marinelli ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;
PI Pochon S, Buesat P, Arbogast C, Pillat R, Fan H, Linder KE, Song B;
PI Nanjappa P;

XX WPI; 2003-779009/73.

PT New polypeptide that binds to vascular endothelial growth factor receptor
PT -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates
PT with therapeutic or imaging agents.

PS Claim 80; SEQ ID NO 170; 350pp; English.

XX This invention relates to novel peptides useful for detecting and
CC targeting primary receptors on endothelial cells that bind vascular
CC endothelial growth factor (VEGF). Specifically, it refers to detecting
CC the receptor tyrosine kinase identified as VEGF-2, which is also known as
CC kinase domain region (KDR) and foetal liver kinase-1 (Flk-1). The present
CC invention describes the involvement of the VEGF/KDR complex as important
CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding
CC polypeptides can be used for imaging neoplastic tumours. Furthermore,
CC these compositions are useful for targeting radiotherapeutics to specific
CC sites for treating diseases associated with KDR activation, which include
CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and
CC enterohaemorrhagic Escherichia coli infection. Accordingly, these
CC compositions exhibit various activities including protozoacidal, anti-
CC HIV, vincidol, antibacterial and cytostatic. This peptide sequence is a
CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of
CC the Lin20 peptide library of the invention.

XX SQ Sequence 20 AA;

Query Match 30.5%; Score 32; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 8 PPGFVSGEVL 19
DB 2 PPGFVSGEVL 13

RESULT 45

ADR40737
ID ADR40737 standard; peptide; 20 AA.

AC ADR40737;

DT 21-OCT-2004 (first entry)

DE KDR/ VEGF binding peptide of the secondary linear Lin20 library Seq 170.

XX kinase domain region; KDR; vascular endothelial growth factor; VEGF;
KM VEGF receptor 2; VEGFR2; foetal liver kinase 1; Flk-1; angiogenesis;
KM neoplastic tumour; malaria; HIV infection; SIV infection;
KM simian haemorrhagic fever virus infection;
KM enterohaemorrhagic Escherichia coli infection; cytostatic;
KM antidiabetic; antimalarial; anti-HIV; vincidol; antibacterial;
KM Lin20 library.

OS Synthetic.

XX WO2004065621-A1.

XX 05-AUG-2004.
 PD
 XX
 XX 11-SEP-2003; 2003MO-US028787.
 PF
 XX 15-JAN-2003; 2003US-0440411P.
 PR 03-MAR-2003; 2003US-00382082.
 PR 03-MAR-2003; 2003MO-US006731.
 XX
 XX (DYAX-) DYAX CORP.
 PA (BRAC) BRACCO INT BV.
 XX
 XX Sato AK, Sexton DJ, Dransfield DT, Ladner RC, Arboresc C;
 PI Buesse P, Fan H, Khurana S, Linder KE, Martinelli ER, Nanjappa P;
 PI Nunn A, Pillai R, Pochon S, Ramalingam K, Shrivastava A, Song B;
 PI Swenson RE, Von Wronski M;
 XX
 DR WPI, 2004-580734/56.
 XX
 PT Novel isolated polypeptide having ability to bind to kinase domain region
 PT or vascular endothelial growth factor/kinase domain region complex,
 PT useful in inhibiting vascular endothelial growth factor activation of
 PT kinase domain region.
 XX
 PS Claim 12; SEQ ID NO 170; 470pp; English.
 XX
 CC This invention relates to novel isolated peptides that can bind to a
 CC kinase domain region (KDR) or vascular endothelial growth factor
 CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide
 CC dimers and multimeric complexes that bind with high affinity to KDR (also
 CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (Flk-1))
 CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and
 CC KDR in angiogenesis these binding peptides can be used for imaging
 CC important sites of angiogenesis, as well as in targeting therapeutics to
 CC such sites. The present invention describes these peptides as useful for
 CC promoting or inhibiting angiogenesis and pathogenic conditions associated
 CC thereof such as neoplastic tumours. Furthermore, these binding peptides
 CC are useful for treating malaria, HIV infection, SIV infection, simian
 CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia
 CC coli infection. Accordingly, they exhibit cytostatic, antiangiogenic,
 CC antimalarial, anti-HIV, virucidal and antibacterial activities. In
 CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and
 CC enable efficient detection, imaging and localisation of activated
 CC endothelial cells exhibiting upregulated KDR expression. This peptide
 CC sequence is a high affinity KDR and VEGF/KDR binding peptide belonging to
 CC the secondary linear linc20 library of the invention.
 XX
 SQ Sequence 20 AA;
 XX
 Query Match 30.5%; Score 32; DB 8; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
 QY 8 PPGFIVGEGVL 19
 Db 2 PPGFSYMEQAL 13
 XX
 RESULT 46
 ID AAM49486
 AA AAM49486 standard; peptide; 9 AA.
 AC AAM49486;
 XX
 DT 05-JUN-1998 (first entry)
 XX
 DE Human leucocyte antigen DQ4 binding peptide #377.
 XX
 KM Human leucocyte antigen; HLA-DQ4; combinatorial library;
 KW autoimmune disease; chronic articular rheumatism.
 XX
 OS Synthetic.
 XX

PN JP08151396-A.
 XX
 XX 11-JUN-1996.
 PD
 XX 28-NOV-1994; 94JP-00292657.
 PP
 XX 28-NOV-1994; 94JP-00292657.
 PR 28-NOV-1994; 94JP-00292657.
 XX
 XX (TEIJ) TEIJIN LTD.
 PA
 XX WPI; 1996-329479/33.
 DR
 XX
 PT HLA-binding oligopeptide and an immunoregulator contg it - used in the
 PT treatment of auto-immune disease.
 XX
 PS Claim 4; Page 43; 61pp; Japanese.
 XX
 CC This peptide is an example of a peptide which binds to a human leucocyte
 CC antigen HLA-DQ4 molecule. The peptide was isolated from a phagemid
 CC combinatorial library comprising the sequence AAV05953, by screening with
 CC an HLA-DQ4 molecule. The peptide is used for the treatment of autoimmune
 CC disease, or especially for treatment of viral diseases
 CC
 SQ Sequence 9 AA;
 XX
 Query Match 29.5%; Score 31; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2e+06;
 Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
 QY 7 SPFGIV 13
 Db 1 APFGIV 7
 XX

RESULT 47
 ID ADO68173
 AA ADO68173 standard; peptide; 9 AA.
 AC ADO68173;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213P1F11 HLA motif bearing epitope #4263.
 XX
 KM cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leucocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KM HLA vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 PR 01-APR-2002; 2002US-00114432.
 XX
 PA (CHAL/) CHALLITA-ETD P M.
 PA (RAT/) RAITANO A B.
 PA (FAR/) FARIS M.
 PA (HUB/) HUBERT R S.
 PA (MOR/) MORRISON R K.
 PA (GEW/) GR W.
 PA (JAKO/) JAKOBYITS A.
 XX
 PI Challita-ETD PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 XX
 DR WPI, 2004-132240/13.
 XX

PT New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.

XX Example 13; Page 130; 334pp; English.

PS The invention describes a composition comprising a substance that
XX modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.

CC Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRTVGESE 17
||: ||:|

Db 1 GFLKGESE 8

RESULT 48

ADO69472

ID ADO69472 standard; peptide; 9 AA.

XX ADO69472;

DT 15-JUL-2004 (first entry)

DE Human 213P1F11 HLA motif bearing epitope #5562.

XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.

XX Homo sapiens.

XX US2004019915-A1.

PD 29-JAN-2004.

PF 01-APR-2002; 2002US-00114432.

PR 01-APR-2002; 2002US-00114432.

PA (CHAL/) CHALLITA-EID P M.

PA (RAIT/) RAITANO A B.

PA (HUBB/) HUBERT R S.

PA (MORR/) MORRISON R K.

PA (GEWW/) GE W.

PA (JAKO/) JAKOBOVITS A.

PI Chailita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX WPI; 2004-132240/13.

XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.

XX Example 13; Page 151; 334pp; English.

PS The invention describes a composition comprising a substance that
XX modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.

CC Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRTVGESE 17
||: ||:|

Db 2 GFLKGESE 9

RESULT 49

ADO69312

ID ADO69312 standard; peptide; 9 AA.

XX ADO69312;

DT 15-JUL-2004 (first entry)

DE Human 213P1F11 HLA motif bearing epitope #5402.

XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.

XX Homo sapiens.

XX US2004019915-A1.

PD 29-JAN-2004.

PF 01-APR-2002; 2002US-00114432.

PR 01-APR-2002; 2002US-00114432.

PA (CHAL/) CHALLITA-EID P M.

PA (RAIT/) RAITANO A B.

PA (HUBB/) HUBERT R S.

PA (MORR/) MORRISON R K.

PA (GEWW/) GE W.

PA (JAKO/) JAKOBOVITS A.

PI Chailita-Eid PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX

DR WPI, 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13, Page 149, 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 9 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFLVGEEDG 17
DB 2 GFLVGEEDG 9
RESULT 50
AD069700
ID ADO69700 standard; peptide; 9 AA.
XX
XX ADO69700;
AC
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F11 HLA motif bearing epitope #5790.
XX
XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
PD 01-APR-2002; 2002US-00114432.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-BID P M.
XX (RAIT/) RAITANO A B.
XX (PARI/) PARIS M.
XX (HUBER/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GERW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;

XX
XX WPI, 2004-132240/13.
DR
XX
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13, Page 155, 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 9 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFLVGEEDG 17
DB 2 GFLVGEEDG 9
RESULT 51
AD071975
ID ADO71975 standard; peptide; 9 AA.
XX
XX ADO71975;
AC
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F11 HLA motif bearing epitope #6074.
XX
XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
PD 01-APR-2002; 2002US-00114432.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-BID P M.
XX (RAIT/) RAITANO A B.
XX (PARI/) PARIS M.
XX (HUBER/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GERW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI

PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
XX 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 160; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form, an antibody or its fragment, a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
SQ Sequence 9 AA;
XX
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GETVGEEG 17
||: ||: |
Db 1 GFLKGEDG 8
XX
RESULT 52
AD068215
ID AD068215 standard; peptide; 9 AA.
XX
AC AD068215;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213p1f1 HLA motif bearing epitope #4305.
XX
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX

PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
XX 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 131; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form, an antibody or its fragment, a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
SQ Sequence 9 AA;
XX
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GETVGEEG 17
||: ||: |
Db 2 GFLKGEDG 9
XX
RESULT 53
AD068624
ID AD068624 standard; peptide; 9 AA.
XX
AC AD068624;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213p1f1 HLA motif bearing epitope #4714.
XX
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX

XX Cha11ita-B1d PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 XX WPI, 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13, Page 137, 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213P1F1, or a molecule that is modulated by
 CC 213P1F1, where the status of the cell that expresses 213P1F1 is
 CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213P1F1; generating a
 CC mammalian immune response; detecting the presence of 213P1F1-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213P1F1 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213P1F1.
 XX
 SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2e+06;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GFIYGEBSG 17
 ||: ||: ||:
 Db 2 GFLKGEBSG 9

RESULT 54
 ADO72059
 ID ADO72059 standard; peptide; 9 AA.
 XX
 AC ADO72059;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213P1F1 HLA motif bearing epitope #6158.
 XX
 KW cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 XX HLA vaccine.
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 PA (CHAL/) CHALLITA-BID P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) PARIS M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEW/) GE W.

PA (JAKO/) JAKOBOVITS A.
 XX
 PI Cha11ita-B1d PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 XX WPI, 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213P1F1, or a molecule that is modulated by 213P1F1, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13, Page 161, 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213P1F1, or a molecule that is modulated by
 CC 213P1F1, where the status of the cell that expresses 213P1F1 is
 CC modulated and 213P1F1 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213P1F1; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213P1F1; generating a
 CC mammalian immune response; detecting the presence of 213P1F1-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213P1F1 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213P1F1.
 XX
 SQ Sequence 9 AA;

Query Match 29.5%; Score 31; DB 8; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2e+06;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GFIYGEBSG 17
 ||: ||: ||:
 Db 2 GFLKGEBSG 9

RESULT 55
 ADO68890
 ID ADO68890 standard; peptide; 9 AA.
 XX
 AC ADO68890;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213P1F1 HLA motif bearing epitope #4980.
 XX
 KW cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 XX HLA vaccine.
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 PA (CHAL/) CHALLITA-BID P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) PARIS M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.

PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 142; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
SQ Sequence 9 AA;
QY 10 GFLVGEDEG 17
DB 1 GFLVGEDEG 8
QY 10 GFLVGEDEG 17
DB 1 GFLVGEDEG 8
RESULT 56
AD068347
ID AD068347 standard; peptide; 9 AA.
XX
AC AD068347;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213p1f1 HLA motif bearing epitope #4437.
XX
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBR/) HUBERT R S.

PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 133; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
SQ Sequence 9 AA;
QY 10 GFLVGEDEG 17
DB 2 GFLVGEDEG 9
QY 10 GFLVGEDEG 17
DB 2 GFLVGEDEG 9
RESULT 57
AD068354
ID AD068354 standard; peptide; 9 AA.
XX
AC AD068354;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213p1f1 HLA motif bearing epitope #4444.
XX
KW cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.

PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 XX
 DR WPI, 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13, Page 133, 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213p1f1, or a molecule that is modulated by
 CC 213p1f1, where the status of the cell that expresses 213p1f1 is
 CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produces the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
 CC mammalian immune response; detecting the presence of 213p1f1-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213p1f1.
 CC
 SQ Sequence 9 AA;
 XX
 Query Match 29.5%; Score 31; DB 8; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2e+06;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GFLVGEKG 17
 Db 1 GFLVGEKG 8
 XX
 RESULT 58
 ADO68030
 ID ADO68030 standard; peptide, 9 AA.
 XX
 AC ADO68030;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213p1f1 HLA motif bearing epitope #4120.
 XX
 KW cytotoxic; gene therapy; 213p1f1, 213p1f1 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KW HLA vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 PA (CHAL/) CHALLITA-EID P M.
 PA (RAIT/) RAITANO A B.

PA (FARI/) FARIS M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 XX
 DR WPI, 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13, Page 128, 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213p1f1, or a molecule that is modulated by
 CC 213p1f1, where the status of the cell that expresses 213p1f1 is
 CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produces the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
 CC mammalian immune response; detecting the presence of 213p1f1-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213p1f1.
 CC
 SQ Sequence 9 AA;
 XX
 Query Match 29.5%; Score 31; DB 8; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2e+06;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GFLVGEKG 17
 Db 2 GFLVGEKG 9
 XX
 RESULT 59
 ADO68858
 ID ADO68858 standard; peptide, 9 AA.
 XX
 AC ADO68858;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213p1f1 HLA motif bearing epitope #4948.
 XX
 KW cytotoxic; gene therapy; 213p1f1, 213p1f1 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KW HLA vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 PA (CHAL/) CHALLITA-EID P M.

PA	(PAIT//)	PAITANO A B.
PA	(PARI//)	PARIS M.
PA	(HUBE//)	HUBERT R S.
PA	(MORR//)	MORRISON R K.
PA	(GEWM//)	GE W.
PA	(JAKO//)	JAKOBOVITS A.
PI	Challita-Eld PM,	Raitano AB, Paris M, Hubert RS, Morrison RK,
PI	Ge W, Jakobovits A,	
DR	WPI, 2004-132240/13.	
XX		
PT	New composition comprising a substance that modulates the status of	
PT	213p1F11, or a molecule that is modulated by 213p1F11, useful for	
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.	
XX		
PS	Example 13; Page 141, 334pp; English.	
XX		
CC	The invention describes a composition comprising a substance that	
CC	modulates the status of 213p1F11, or a molecule that is modulated by	
CC	213p1F11, where the status of the cell that expresses 213p1F11 is	
CC	modulated and 213p1F11 is a gene overexpressed in many cancers. Also	
CC	described are: a pharmaceutical composition comprising the composition	
CC	cited above in a unit dose form; an antibody or its fragment; a non-human	
CC	transgenic animal that produced the antibody; a hybridoma that produces	
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the	
CC	cell that expresses 213p1F11; a polynucleotide that encodes the protein;	
CC	inhibiting growth of cancer cells that express 213p1F11, generating a	
CC	mammalian immune response; detecting the presence of 213p1F11-related	
CC	protein or polynucleotide in a sample; and detecting the presence of	
CC	cancer in an individual. The compositions, molecules and methods are	
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal	
CC	cancer. This is the amino acid sequence of a human 213p1F11 peptide	
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif	
CC	useful in the creation of an HLA vaccine to modulate 213p1F11.	
XX		
SO	Sequence 9 AA;	
XX		
Query Match	29.5%;	Score 31; DB 8; Length 9;
Best Local Similarity	62.5%;	Pred. No. 28+06;
Matches 5; Conservative	2;	Mismatches 1; Indels 0; Gaps 0
OY	10 GPTVGEBG 17	
	: :	
DB	2 GFLKGEDG 9	
RESULT 60		
AD069100		
ID	AD069100 standard; peptide; 9 AA.	
XX		
AC	AD069100;	
XX		
DT	15-JUL-2004 (first entry)	
DE	Human 213p1F11 HLA motif bearing epitope #5190.	
XX		
KW	cytostatic; gene therapy; 213p1F11; 213p1F11 modulation; cancer;	
KW	transgenic; cytotoxic agent delivery; diagnostic agent delivery;	
KW	immune response; pancreatic cancer; rectal cancer; bladder cancer; human;	
KW	human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;	
XX	HLA vaccine.	
XX		
OS	Homo sapiens.	
XX		
PN	US2004019915-A1.	
XX		
PD	29-JAN-2004.	
XX		
PF	01-APR-2002; 2002US-00114432.	
XX		
PR	01-APR-2002; 2002US-00114432.	
XX		

PA	(CHAL//)	CHALLITA-EID P. M.
PA	(RAIT//)	RAITANO A. B.
PA	(FARI//)	FARIS M.
PA	(HUBE//)	HUBERT R. S.
PA	(MORR//)	MORRISON R. K.
PA	(GERW//)	GE W.
PA	(JAKO//)	JAKOBOWITS A.
PA		
PI	Challita-Bid PM,	Raitano AB, Faris M, Hubert RS, Morrison RK,
PI	Ge W, Jakobovits A,	
DR	WPI, 2004-1332240/13.	
XX		
XX		
PT	New composition comprising a substance that modulates the status of	
PT	213P1F11, or a molecule that is modulated by 213P1F11, useful for	
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.	
XX		
PS	Example 13, Page 145, 334pp; English.	
XX		
CC	The invention describes a composition comprising a substance that	
CC	modulates the status of 213P1F11, or a molecule that is modulated by	
CC	213P1F11, where the status of the cell that expresses 213P1F11 is	
CC	modulated and 213P1F11 is a gene overexpressed in many cancers. Also	
CC	described are: a pharmaceutical composition comprising the composition	
CC	cited above in a unit dose form; an antibody or its fragment; a non-human	
CC	transgenic animal that produced the antibody; a hybridoma that produces	
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the	
CC	cell that expresses 213P1F11; a polynucleotide that encodes the protein;	
CC	inhibiting growth of cancer cells that expresses 213P1F11; generating a	
CC	mammalian immune response; detecting the presence of 213P1F11-related	
CC	protein or polynucleotide in a sample; and detecting the presence of	
CC	cancer in an individual. The compositions, molecules and methods are	
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal	
CC	cancer. This is the amino acid sequence of a human 213P1F11 peptide	
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif	
CC	useful in the creation of an HLA vaccine to modulate 213P1F11.	
XX		
SQ	Sequence 9 AA:	
Query Match	29.5%;	Score 31; DB 8; Length 9;
Best Local Similarity	62.5%;	Pred. No. 2e+06;
Matches	5; Conservative	2; Mismatches 1; Indels 0; Gaps 0
Qy	10	GFIVGEEG 17
	: :	
	: :	
Db	1	GLKGGEDG 8
RESULT 61		
ADO67954		
ID	ADO67954	standard; peptide; 9 AA.
XX		
AC	ADO67954;	
XX		
DT	15-JUN-2004	(first entry)
XX		
DE	Human 213P1F11	HLA motif bearing epitope #4044.
XX		
KW	cytostatic; gene therapy; 213P1F11, 213P1F11 modulation; cancer;	
KW	transgenic; cytotoxic agent delivery; diagnostic agent delivery;	
KW	immune response; pancreatic cancer; rectal cancer; bladder cancer; human;	
KW	human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;	
KW	HLA vaccine.	
XX		
OS	Homo sapiens.	
XX		
PN	US2004019915-A1.	
XX		
PD	29-JAN-2004.	
XX		
PF	01-APR-2002; 2002US-00114432.	
XX		
PR	01-APR-2002; 2002US-00114432.	

XX (CHAL/) CHALLITA-BID P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARI M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-Bid PM, Raitano AB, Fari M, Hubert RS, Morrison RK,
 PI Ge W, Jakobovits A,
 DR WPI; 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13; Page 127; 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213p1f1, or a molecule that is modulated by
 CC 213p1f1, where the status of the cell that expresses 213p1f1 is
 CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
 CC mammalian immune response; detecting the presence of 213p1f1-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213p1f1.
 CC
 XX
 SO Sequence 9 AA;
 Query Match 29.5%; Score 31; DB 8; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2e+06;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GPRVGEQ 17
 ||: ||: ||:
 DB 1 GFLKGEQD 8
 RESULT 62
 ADO66277
 ID ADO66277 standard; peptide; 9 AA.
 AC ADO66277;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213p1f1 HLA motif bearing epitope #2367.
 XX
 KW cytotoxic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KW HLA vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX

PR 01-APR-2002; 2002US-00114432.
 XX
 XX (CHAL/) CHALLITA-BID P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARI M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-Bid PM, Raitano AB, Fari M, Hubert RS, Morrison RK,
 PI Ge W, Jakobovits A,
 DR WPI; 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13; Page 103; 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213p1f1, or a molecule that is modulated by
 CC 213p1f1, where the status of the cell that expresses 213p1f1 is
 CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
 CC mammalian immune response; detecting the presence of 213p1f1-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213p1f1.
 CC
 XX
 SO Sequence 9 AA;
 Query Match 29.5%; Score 31; DB 8; Length 9;
 Best Local Similarity 62.5%; Pred. No. 2e+06;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 10 GPRVGEQ 17
 ||: ||: ||:
 DB 1 GFLKGEQD 8
 RESULT 63
 ADO68944
 ID ADO68944 standard; peptide; 9 AA.
 AC ADO68944;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213p1f1 HLA motif bearing epitope #5034.
 XX
 KW cytotoxic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KW HLA vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 PF

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XX 01-APR-2002; 2002US-00114432.
PR
XX
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
XX MPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 143; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
XX Sequence 9 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFTVGEEG 17
DB 2 GFLKGEDG 9
RESULT 64
ADO69211
ID ADO69211 standard; peptide; 9 AA.
XX
XX ADO69211;
AC
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213p1f1 HLA motif bearing epitope #5301.
XX
XX cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX

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PF 01-APR-2002; 2002US-00114432.
XX
XX
XX 01-APR-2002; 2002US-00114432.
PR
XX
PA (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWM/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
XX MPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 147; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
XX Sequence 9 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 9;
Best Local Similarity 62.5%; Pred. No. 2e+06;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFTVGEEG 17
DB 1 GFLKGEDG 8
RESULT 65
ADO68650
ID ADO68650 standard; peptide; 9 AA.
XX
XX ADO68650;
AC
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213p1f1 HLA motif bearing epitope #4740.
XX
XX cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX

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XX	01-APR-2002; 2002US-00114432.	XX
PE		XX
XX	01-APR-2002; 2002US-00114432.	XX
XX		XX
FR	01-APR-2002; 2002US-00114432.	XX
XX		XX
PA	(CHAL/) CHALLITA-BID P M.	XX
PA	(RAIT/) RAITANO A B.	XX
PA	(PARI/) PARIS M.	XX
PA	(HUBE/) HUBERT R S.	XX
PA	(MORR/) MORRISON R K.	XX
PA	(GEWM/) GE W.	XX
PA	(JAKO/) JAKOBOVITS A.	XX
PI		XX
PI	Challita-Bid PM, Raitano AB, Paris M, Hubert RS, Morrison RK,	XX
PI	Ge W, Jakobovits A;	XX
DR	WPI, 2004-132240/13.	XX
XX		XX
PT	New composition comprising a substance that modulates the status of	XX
PT	213p11, or a molecule that is modulated by 213p11, useful for	XX
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.	XX
XX		XX
PS	Example 13; Page 138; 334pp; English.	XX
XX		XX
CC	The invention describes a composition comprising a substance that	XX
CC	modulates the status of 213p11, or a molecule that is modulated by	XX
CC	213p11, where the status of the cell that expresses 213p11 is	XX
CC	modulated and 213p11 is a gene overexpressed in many cancers. Also	XX
CC	described are: a pharmaceutical composition comprising the composition	XX
CC	cted above in a unit dose form, an antibody or its fragment, a non-human	XX
CC	transgenic animal that produced the antibody; a hybridoma that produces	XX
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the	XX
CC	cell that expresses 213p11; a polynucleotide that encodes the protein;	XX
CC	inhibiting growth of cancer cells that expresses 213p11; generating a	XX
CC	mammalian immune response; detecting the presence of 213p11-related	XX
CC	protein or polynucleotide in a sample; and detecting the presence of	XX
CC	cancer in an individual. The compositions, molecules and methods are	XX
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal	XX
CC	cancer. This is the amino acid sequence of a human 213p11 peptide	XX
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif	XX
CC	useful in the creation of an HLA vaccine to modulate 213p11.	XX
XX		XX
SO	Sequence 9 AA;	XX
		XX
Query Match	29.5%; Score 31; DB 8; Length 9;	
Best Local Similarity	62.5%; Pred. No. 26+06;	
Matches	5; Conservative 2; Mismatches 1; Indels 0; Gaps 0	
QY	10 GPTVGEEG 17	
	: :	
	1 GFLKGEDG 8	
DB		
RESULT 66		
ID	ADO69433	
ID	ADO69433 standard; peptide; 9 AA.	
AC	ADO69433;	
XX		
XX	15-JUL-2004 (first entry)	
XX		
DE	Human 213p11 HLA motif bearing epitope #5523.	
XX		
KW	Cytostatic; gene therapy; 213p11, 213p11 modulation; cancer;	
KW	transgenic; cytotoxic agent delivery; diagnostic agent delivery;	
KW	immune response; pancreatic cancer; rectal cancer; bladder cancer; human;	
KW	human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;	
XX	HLA vaccine.	
XX		
OS	Homo sapiens.	
XX		
XX	US2004019915-A1.	
XX		

PD	29-JAN-2004.
XX	
PF	01-APR-2002; 2002US-00114432.
XX	
PR	01-APR-2002; 2002US-00114432.
XX	
PA	(CHAL/) CHALLITA-BID P M.
PA	(RAIT/) RAITANO A B.
PA	(FARI/) PARIS M.
PA	(HUBB/) HUBERT R S.
PA	(MORR/) MORRISON R K.
PA	(GEWM/) GE W.
PA	(JAKO/) JAKOBOVITS A.
XX	
PI	Challita-Bid PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
PI	Ge W, Jakobovits A;
XX	
DR	WPI; 2004-132240/13.
XX	
PT	New composition comprising a substance that modulates the status of
PT	213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX	
PS	Example 13; Page 151; 334pp; English.
XX	
CC	The invention describes a composition comprising a substance that
CC	modulates the status of 213P1F11, or a molecule that is modulated by
CC	213P1F11, where the status of the cell that expresses 213P1F11 is
CC	modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC	described are: a pharmaceutical composition comprising the composition
CC	cited above in a unit dose form; an antibody or its fragment; a non-human
CC	transgenic animal that produced the antibody; a hybridoma that produces
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC	cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC	inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC	mammalian immune response; detecting the presence of 213P1F11-related
CC	cancer in an individual. The compositions, molecules and methods are
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal
CC	cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC	useful in the creation of an HLA vaccine to modulate 213P1F11.
XX	
SO	Sequence 9 AA;
XX	
Query Match	29.5%; Score 31; DB 8; Length 9;
Best Local Similarity	62.5%; Pred. No. 2e+06;
Matches	5; Conservative 2; Mismatches 1; Indels 0; Gaps 0
QY	10 GFIVGESEG 17
	: :
Db	1 GFLKGEDEG 8
XX	
RESULT 67	
ID	ADO69643
AC	ADO69643 standard; peptide; 9 AA.
XX	
XX	ADO69643;
DT	15-JUL-2004 (first entry)
XX	
DE	Human 213P1F11 HLA motif bearing epitope #5733.
XX	
KW	cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KW	transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW	immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW	human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW	HLA vaccine.
XX	
OS	Homo sapiens.
XX	
PN	US2004019915-A1.

```
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EID P M.
XX
XX (RAIT/) RAITANO A B.
XX
XX (FARI/) FARIS M.
XX
XX (HUBE/) HUBERT R S.
XX
XX (MORR/) MORRISON R K.
XX
XX (GEWM/) GE W.
XX
XX (JAKO/) JAKOBOVITS A.
XX
XX
XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
XX
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F1, or a molecule that is modulated by 213P1F1, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 154; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F1, or a molecule that is modulated by
XX 213P1F1, where the status of the cell that expresses 213P1F1 is
XX modulated, and 213P1F1 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F1; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F1; generating a
XX mammalian immune response; detecting the presence of 213P1F1-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F1 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F1.
XX
XX Sequence 9 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 2e+06;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GFLVGEHG 17
XX ||: ||:|
XX 1 GFLKGEHG 8
XX
XX Db
XX
XX RESULT 68
XX ADO71860
XX ID ADO71860 standard; peptide; 9 AA.
XX
XX ADO71860;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213P1F1 HLA motif bearing epitope #5959.
XX
XX cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX
```

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PN US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EID P M.
XX
XX (RAIT/) RAITANO A B.
XX
XX (FARI/) FARIS M.
XX
XX (HUBE/) HUBERT R S.
XX
XX (MORR/) MORRISON R K.
XX
XX (GEWM/) GE W.
XX
XX (JAKO/) JAKOBOVITS A.
XX
XX
XX Chailita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
XX
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F1, or a molecule that is modulated by 213P1F1, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 158; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F1, or a molecule that is modulated by
XX 213P1F1, where the status of the cell that expresses 213P1F1 is
XX modulated, and 213P1F1 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F1; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F1; generating a
XX mammalian immune response; detecting the presence of 213P1F1-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F1 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F1.
XX
XX Sequence 9 AA;
XX
XX Query Match 29.5%; Score 31; DB 8; Length 9;
XX Best Local Similarity 62.5%; Pred. No. 2e+06;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 10 GFLVGEHG 17
XX ||: ||:|
XX 2 GFLKGEHG 9
XX
XX Db
XX
XX RESULT 69
XX ADO72141
XX ID ADO72141 standard; peptide; 9 AA.
XX
XX ADO72141;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213P1F1 HLA motif bearing epitope #6240.
XX
XX cytostatic; gene therapy; 213P1F1; 213P1F1 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX
```


OS Homo sapiens.
XX
XX US2004019915-A1.
XX
PD 29-JAN-2004.
XX
XX
PF 01-APR-2002; 2002US--00114432.
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL// CHALLITA-BID P M.
PA (RAIT// RAITANO A B.
PA (FARI// FARIS M.
PA (HUBE// HUBERT R S.
PA (MORR// MORRISON R K.
PA (GEWM// GE W.
PA (JAKO// JAKOBOVITS A.
PI Challita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX
DR WPI, 2004-132240/13.

PS Example 13; Page 207; 334pp; English.

CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.

XX
SQ Sequence 10 AA;

Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0

DY 10 GFIVGEG 17
||: ||:
| |:
Db 1 GFLKGDD 8

RESULT 71
ADO67058
ID ADO67058 standard; peptide; 10 AA.
XX
XX ADO67058;
DT 15-JUL-2004 (first entry)
XX
XX Human 213P1F11 HLA motif bearing epitope #3148.
DB
XX cyrostatic; gene therapy; 213P1F11, 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KM HLA vaccine.

```
XX Homo sapiens.
OS
XX US2004019915-A1.
PN
XX
XX 29-JAN-2004.
PD
XX
XX 01-APR-2002; 2002US-00114432.
PF
XX
XX 01-APR-2002; 2002US-00114432.
PR
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX
XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
DR
XX
XX New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 114; 334pp; English.
PS
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
XX
XX Sequence 10 AA;
SQ
XX
XX
XX Query Match 29.5%; Score 31; DB 8; Length 10;
XX Best Local Similarity 62.5%; Pred. No. 6.8e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 10 GIVGREG 17
XX ||: ||:|
XX 1 GFLKGBDG 8
XX
XX
XX
XX RESULT 72
XX ADO74471
XX ID ADO74471 standard; peptide; 10 AA.
XX
XX
XX ADO74471;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213p1f1 HLA motif bearing epitope #8570.
XX
XX cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
```

```
KW HLA vaccine.
XX
XX Homo sapiens.
OS
XX US2004019915-A1.
PN
XX
XX 29-JAN-2004.
PD
XX
XX 01-APR-2002; 2002US-00114432.
PF
XX
XX 01-APR-2002; 2002US-00114432.
PR
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX
XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
DR
XX
XX New composition comprising a substance that modulates the status of
PT 213p1f1, or a molecule that is modulated by 213p1f1, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX
XX Example 13; Page 200; 334pp; English.
PS
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213p1f1, or a molecule that is modulated by
CC 213p1f1, where the status of the cell that expresses 213p1f1 is
CC modulated and 213p1f1 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213p1f1; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213p1f1; generating a
CC mammalian immune response; detecting the presence of 213p1f1-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213p1f1 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213p1f1.
XX
XX
XX Sequence 10 AA;
SQ
XX
XX
XX Query Match 29.5%; Score 31; DB 8; Length 10;
XX Best Local Similarity 62.5%; Pred. No. 6.8e+02;
XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
XX
XX 10 GIVGREG 17
XX ||: ||:|
XX 3 GFLKGBDG 10
XX
XX
XX
XX RESULT 73
XX ADO74828
XX ID ADO74828 standard; peptide; 10 AA.
XX
XX
XX ADO74828;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213p1f1 HLA motif bearing epitope #8927.
XX
XX cytostatic; gene therapy; 213p1f1; 213p1f1 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
```

KM	human leukocyte antigen; HLA, class I, class II; epitope, HLA motif;
KM	HLA vaccine.
XX	
OS	Homo sapiens.
XX	
PN	US2004019915-A1.
XX	
PD	29-JAN-2004.
XX	
PF	01-APR-2002; 2002US-00114432.
XX	
PR	01-APR-2002; 2002US-00114432.
XX	
PA	(CHAL/) CHALLITA-BID P M.
PA	(RAIT/) RAITANO A B.
PA	(FARI/) FARI S M.
PA	(HUBE/) HUBERT R S.
PA	(MORR/) MORRISON R K.
PA	(GEW/) GE W.
PA	(JAKO/) JAKOBOVITS A.
XX	
PI	Challita-Bid PM, Raitano AB, Farris M, Hubert RS, Morrison RK,
PI	Ge W, Jakobovits A;
XX	
DR	WPI; 2004-132240/13.
XX	
PT	New composition comprising a substance that modulates the status of
PT	213P1P1, or a molecule that is modulated by 213P1P1, useful for
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX	
PS	Example 13; Page 205; 334pp; English.
XX	
CC	The invention describes a composition comprising a substance that
CC	modulates the status of 213P1P1, or a molecule that is modulated by
CC	213P1P1, where the status of the cell that expresses 213P1P1 is
CC	modulated and 213P1P1 is a gene overexpressed in many cancers. Also
CC	described are: a pharmaceutical composition comprising the composition
CC	cited above in a unit dose form; an antibody or its fragment; a non-human
CC	transgenic animal that produced the antibody; a hybridoma that produces
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC	cell that expresses 213P1P1; a polynucleotide that encodes the protein;
CC	inhibiting growth of cancer cells that expresses 213P1P1; generating a
CC	mammalian immune response; detecting the presence of 213P1P1-related
CC	antigen or polynucleotide in a sample; and detecting the presence of
CC	cancer in an individual. The compositions, molecules and methods are
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal
CC	cancer. This is the amino acid sequence of a human 213P1P1 peptide
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC	useful in the creation of an HLA vaccine to modulate 213P1P1.
XX	
SQ	Sequence 10 AA;
XX	
QY	Query Match 29.5%; Score 31; DB 8; Length 10;
Db	Best local similarity 62.5%; Pred. No. 6; 8e+02;
XX	Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX	
QY	10 GFIIVGEIG 17
XX	: :
Db	3 GFLKGEDG 10
XX	
RESULT 74	
ID	ADO66467
XX	ADO66467 standard; peptide; 10 AA.
AC	ADO66467;
XX	
DT	15-JUN-2004 (first entry)
XX	
DE	Human 213P1P1 HLA motif bearing epitope #2557.
XX	
KM	cytotoxic; gene therapy; 213P1P1; 213P1P1 modulation; cancer;
KM	transgenic; cytotoxic agent delivery; diagnostic agent delivery;

KW		immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KV		human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX		HLA vaccine.
OS	Homo sapiens.	
XX	US2004019915-A1.	
FN		
PD	29-JAN-2004.	
XX		
PF	01-APR-2002; 2002US-00114432.	
XX		
PR	01-APR-2002; 2002US-00114432.	
XX		
PA	(CHAL/) CHALLITA-BID P M.	
PA	(RAIT/) RAITANO A B.	
PA	(FARI/) FARIIS M.	
PA	(HUBB/) HUBERT R S.	
PA	(MORR/) MORRISON R K.	
PA	(GEWW/) GE W.	
PA	(JAKO/) JAKOBOVITS A.	
PI	Challita-Bid PM, Raitano AB, Fariis M, Hubert RS, Morrison RK,	
PI	Ge W, Jakobovits A;	
XX		
DR	WPI; 2004-132240/13.	
XX		
PT	New composition comprising a substance that modulates the status of	
PT	213PFI1, or a molecule that is modulated by 213PFI1, useful for	
PT	detecting or treating cancer, e.g. pancreatic or rectal cancer.	
PS	Example 13; Page 105; 334pp; English.	
XX		
CC	The invention describes a composition comprising a substance that	
CC	modulates the status of 213PFI1, or a molecule that is modulated by	
CC	213PFI1, where the status of the cell that expresses 213PFI1 is	
CC	modulated and 213PFI1 is a gene overexpressed in many cancers. Also	
CC	described are: a pharmaceutical composition comprising the composition	
CC	cited above in a unit dose form; an antibody or its fragment; a non-human	
CC	transgenic animal that produced the antibody; a hybridoma that produces	
CC	the antibody; delivering a cytotoxic agent or a diagnostic agent to the	
CC	cell that expresses 213PFI1; a polynucleotide that encodes the protein;	
CC	inhibiting growth of cancer cells that expresses 213PFI1; generating a	
CC	mammalian immune response; detecting the presence of 213PFI1-related	
CC	protein or polynucleotide in a sample; and detecting the presence of	
CC	cancer in an individual. The compositions, molecules and methods are	
CC	useful for detecting and treating cancer, e.g. pancreatic or rectal	
CC	cancer. This is the amino acid sequence of a human 213PFI1 peptide	
CC	epitope bearing a human leukocyte antigen (HLA) class I or class II motif	
CC	useful in the creation of an HLA vaccine to modulate 213PFI1.	
XX		
SQ	Sequence 10 AA;	
OY	Query Match 29.5%; Score 31; DB 8; Length 10;	
	Best Local Similarity 62.5%; Pred. No. 6.8e+02;	
	Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;	
	10 GFIVGEGS 17	
	: :	
DB	1 GFLKGEDG 8	
RESULT 75		
ADOT5227		
ID	ADOT5227 standard; peptide; 10 AA.	
XX		
AC	ADO75227;	
XX		
DT	15-JUN-2004 (first entry)	
XX		
XX	Human 213PFI1 HLA motif bearing epitope #9326.	
KV	cytostatic; gene therapy; 213PFI1; 213PFI1 modulation; cancer;	

XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KM HLA vaccine.
XX
OS Homo sapiens.
PN US2004019915-A1.
PD 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-ElD P M.
PA (RAIT/) RAITANO A B.
PA (PARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Challita-ElD PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 208; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated, and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 10 AA;
SQ

Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEEG 17
||:|:|:
Db 1 GFLKGEDEG 8

RESULT 78
ADO65940
ID ADO65940 standard; peptide; 10 AA.
XX
AC ADO65940;
XX
XX 15-JUL-2004 (first entry)
XX

DE Human 213P1F11 HLA motif bearing epitope #2030.
XX
XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KM HLA vaccine.
XX
OS Homo sapiens.
PN US2004019915-A1.
PD 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-ElD P M.
PA (RAIT/) RAITANO A B.
PA (PARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
XX Challita-ElD PM, Raitano AB, Paris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
XX WPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 98; 334pp; English.
XX
XX The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated, and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 10 AA;
SQ

Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEEG 17
||:|:|:
Db 1 GFLKGEDEG 8

RESULT 79
AD074212
ID AD074212 standard; peptide; 10 AA.
XX
AC AD074212;
XX
XX 15-JUL-2004 (first entry)
XX

```
XX Human 213P1F11 HLA motif bearing epitope #8311.
DE cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
OS Homo sapiens.
XX US2004019915-A1.
XX 29-JAN-2004.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-ElD P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIIS M.
XX (HUBE/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX Chailita-ElD PM, Raitano AB, Fariis M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX WPI; 2004-132240/13.
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX Example 13; Page 197; 334pp; English.
XX The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX Sequence 10 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFLVGEKG 17
DB 3 GFLVGEKG 10
RESULT 80
AD075255
ID AD075255 standard; peptide; 10 AA.
XX AC AD075255;
XX
```

```
DT 15-JUL-2004 (first entry)
XX Human 213P1F11 HLA motif bearing epitope #9354.
XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
OS Homo sapiens.
XX US2004019915-A1.
XX 29-JAN-2004.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-ElD P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIIS M.
XX (HUBE/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX Chailita-ElD PM, Raitano AB, Fariis M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX WPI; 2004-132240/13.
XX New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX Example 13; Page 212; 334pp; English.
XX The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX Sequence 10 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFLVGEKG 17
DB 2 GFLVGEKG 9
RESULT 81
AD067592
ID AD067592 standard; peptide; 10 AA.
XX AC AD067592;
XX
```

XX 15-JUL-2004 (first entry)
DT Human 213P1P11 HLA motif bearing epitope #3682.
DE
XX cytotoxic; gene therapy; 213P1P11; 213P1P11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX Homo sapiens.
OS
XX US2004019915-A1.
PN
XX 29-JAN-2004.
PD
XX 01-APR-2002; 2002US-00114432.
PF
XX 01-APR-2002; 2002US-00114432.
PR
XX 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GERW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
PI WPI; 2004-132240/13.
DR
XX New composition comprising a substance that modulates the status of
PT 213P1P11, or a molecule that is modulated by 213P1P11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 121; 334pp; English.
PS
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1P11, or a molecule that is modulated by
CC 213P1P11, where the status of the cell that expresses 213P1P11 is
CC modulated and 213P1P11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1P11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1P11; generating a
CC mammalian immune response; detecting the presence of 213P1P11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1P11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1P11.
CC
CC Sequence 10 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFIGVEEG 17
||:|:|:|
Db 1 GFLKGBDG 8

RESULT 82
ADO74085
ID ADO74085 standard; peptide; 10 AA.
XX

AC ADO74085;
XX 15-JUL-2004 (first entry)
DT Human 213P1P11 HLA motif bearing epitope #8184.
DE
XX cytotoxic; gene therapy; 213P1P11; 213P1P11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX Homo sapiens.
OS
XX US2004019915-A1.
PN
XX 29-JAN-2004.
PD
XX 01-APR-2002; 2002US-00114432.
PF
XX 01-APR-2002; 2002US-00114432.
PR
XX 01-APR-2002; 2002US-00114432.
XX (CHAL/) CHALLITA-EID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GERW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
PI WPI; 2004-132240/13.
DR
XX New composition comprising a substance that modulates the status of
PT 213P1P11, or a molecule that is modulated by 213P1P11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 195; 334pp; English.
PS
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1P11, or a molecule that is modulated by
CC 213P1P11, where the status of the cell that expresses 213P1P11 is
CC modulated and 213P1P11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1P11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1P11; generating a
CC mammalian immune response; detecting the presence of 213P1P11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1P11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1P11.
CC
CC Sequence 10 AA;
SQ
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFIGVEEG 17
||:|:|:|
Db 1 GFLKGBDG 8

RESULT 83
ADO74939
ID ADO74939 standard; peptide; 10 AA.
XX

```
XX AD074939;
AC
XX 15-JUL-2004 (first entry)
XX
XX Human 213P1F11 HLA motif bearing epitope #9038.
XX
XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EBD P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIS M.
XX (HUBB/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Challita-EBD PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A,
XX
XX WPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 207, 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F11, or a molecule that is modulated by
XX 213P1F11, where the status of the cell that expresses 213P1F11 is
XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F11; generating a
XX mammalian immune response; detecting the presence of 213P1F11-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F11 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 10 AA;
XX
XX
```

```
Query Match          29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GIVGEG 17
   ||: ||:|
DB 2 GFLKGEDG 9

RESULT 84
AD075094
```

```
ID AD075094 standard; peptide; 10 AA.
XX
XX AD075094;
XX
XX 15-JUL-2004 (first entry)
XX
XX Human 213P1F11 HLA motif bearing epitope #9193.
XX
XX cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
XX HLA vaccine.
XX
XX Homo sapiens.
XX
XX US2004019915-A1.
XX
XX 29-JAN-2004.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX 01-APR-2002; 2002US-00114432.
XX
XX (CHAL/) CHALLITA-EBD P M.
XX (RAIT/) RAITANO A B.
XX (FARI/) FARIS M.
XX (HUBB/) HUBERT R S.
XX (MORR/) MORRISON R K.
XX (GEWW/) GE W.
XX (JAKO/) JAKOBOVITS A.
XX
XX Challita-EBD PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
XX Ge W, Jakobovits A,
XX
XX WPI; 2004-132240/13.
XX
XX New composition comprising a substance that modulates the status of
XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for
XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
XX Example 13; Page 209, 334pp; English.
XX
XX The invention describes a composition comprising a substance that
XX modulates the status of 213P1F11, or a molecule that is modulated by
XX 213P1F11, where the status of the cell that expresses 213P1F11 is
XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also
XX described are: a pharmaceutical composition comprising the composition
XX cited above in a unit dose form; an antibody or its fragment; a non-human
XX transgenic animal that produced the antibody; a hybridoma that produces
XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;
XX inhibiting growth of cancer cells that expresses 213P1F11; generating a
XX mammalian immune response; detecting the presence of 213P1F11-related
XX protein or polynucleotide in a sample; and detecting the presence of
XX cancer in an individual. The compositions, molecules and methods are
XX useful for detecting and treating cancer, e.g. pancreatic or rectal
XX cancer. This is the amino acid sequence of a human 213P1F11 peptide
XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
XX useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
XX Sequence 10 AA;
XX
XX
```

```
Query Match          29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GIVGEG 17
   ||: ||:|
DB 3 GFLKGEDG 10

RESULT 85
AD075094
```


AD075374
 ID AD075374 standard; peptide; 10 AA.
 AC AD075374,
 XX
 XX 15-JUL-2004 (first entry)
 XX
 DE Human 213P1F11 HLA motif bearing epitope #9473.
 XX
 XX cytotoxic; gene therapy; 213P1F11, 213P1F11 modulation; cancer;
 KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KM HLA vaccine.
 KM
 OS Homo sapiens.
 XX
 XX US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 XX (CHAL/) CHALLITA-RID P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chalita-Rid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 PI WPI; 2004-132240/13.
 DR
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 PT
 XX
 PS Example 13; Page 213; 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213P1F11, or a molecule that is modulated by
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
 CC mammalian immune response; detecting the presence of 213P1F11-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.
 CC
 XX
 XX Sequence 10 AA;
 SQ

Query Match 29.5%; Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GPTVGEEG 17
 ||: ||: |
 DB 1 GFLKGEDG 8

RESULT 86
 ID AD074213
 AC AD074213 standard; peptide; 10 AA.
 XX
 XX AD074213,
 XX
 XX 15-JUL-2004 (first entry)
 XX
 DE Human 213P1F11 HLA motif bearing epitope #8312.
 XX
 XX cytotoxic; gene therapy; 213P1F11, 213P1F11 modulation; cancer;
 KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KM HLA vaccine.
 KM
 OS Homo sapiens.
 XX
 XX US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 XX (CHAL/) CHALLITA-RID P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARIS M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Chalita-Rid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 PI WPI; 2004-132240/13.
 DR
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 PT
 XX
 PS Example 13; Page 197; 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213P1F11, or a molecule that is modulated by
 CC 213P1F11, where the status of the cell that expresses 213P1F11 is
 CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
 CC mammalian immune response; detecting the presence of 213P1F11-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213P1F11.
 CC
 XX
 XX Sequence 10 AA;
 SQ

Query Match 29.5%; Score 31; DB 8; Length 10;
 Best Local Similarity 62.5%; Pred. No. 6.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GPTVGEEG 17
 ||: ||: |
 DB 2 GFLKGEDG 9

RESULT 87
ADO75134
ID ADO75134 standard; peptide; 10 AA.
XX
AC ADO75134;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F11 HLA motif bearing epitope #9233.
XX
KW cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Chalita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 210; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
SQ Sequence 10 AA;
XX
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFIGVEEG 17
DB 2 GFLKSGDG 9

RESULT 88
ADO74599
ID ADO74599 standard; peptide; 10 AA.
XX
AC ADO74599;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F11 HLA motif bearing epitope #8698.
XX
KW cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KW HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (FARI/) FARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEWW/) GE W.
PA (JAKO/) JAKOBOVITS A.
XX
PI Chalita-Bid PM, Raitano AB, Faris M, Hubert RS, Morrison RK;
PI Ge W, Jakobovits A;
XX
DR WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 202; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
SQ Sequence 10 AA;
XX
Query Match 29.5%; Score 31; DB 8; Length 10;
Best Local Similarity 62.5%; Pred. No. 6.8e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 10 GFIGVEEG 17
DB 2 GFLKSGDG 9

Db 2 GFLKGEDG 9

RESULT 89
ID ABP62415 standard; peptide; 11 AA.
XX
XX ABP62415;
AC
XX
DT 10-OCT-2002 (first entry)
XX
XX Human immunopeptide to HCV E2 glycoprotein light chain CDR #92.
DE
XX
XX Viruslike; human; immunopolypeptide; immunopeptide; envelope glycoprotein;
KM nonstructural protein; hepatitis C virus; HCV; E2 glycoprotein;
KM NS3 protein; viral infection.
XX
XX Homo sapiens.
OS
PN MO200259340-A1.
XX
XX 01-AUG-2002.
PD
XX 25-JAN-2002; 2002WO-US002303.
PF
XX 26-JAN-2001; 2001US-0264451P.
PR
XX (SCRI) SCRIIPS RES INST.
PA
XX Maruyama T, Jones IM, Burton DR, Fox RI,
PI WPI; 2002-599801/64.
XX
XX New human immunopolypeptide with binding specificity for certain envelope
PT glycoproteins and nonstructural proteins of hepatitis C virus (HCV), for
PT diagnosing or treating patients having or suspected of having HCV
PT infection.
XX
XX Claim 1; Fig 17; 308bp; English.
PS
XX
XX The present invention relates to human immunopolypeptides, produced by a
CC phage transected cell library. The present sequence is one such
CC immunopolypeptide. The immunopolypeptides have binding specificity for
CC envelope glycoprotein E2 and nonstructural protein NS3 of hepatitis C
CC virus (HCV). E2 glycoprotein is believed to be responsible for target
CC cell binding and contains neutralizing epitopes, while NS3 is thought to
CC be involved in the replication of HCV. The immunopolypeptides are useful
CC for diagnosing and treating a patient having or suspected to be having
CC HCV infection.
CC
XX
SQ Sequence 11 AA;

Query Match 29.5%; Score 31; DB 5; Length 11;
Best Local Similarity 71.4%; Pred. No. 7.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 11
| | | | |
DB 4 GSPSPGY 10

RESULT 90
ID AAR13452
XX AAR13452 standard; peptide; 13 AA.
XX
XX AAR13452;
AC
XX
XX 25-MAR-2003 (revised)
DT 28-OCT-1991 (first entry)
XX
XX Residues 145-157 of 152(I) bovine factor VII.
DE
XX
XX Thrombosis; tissue factor; heparin.
KM

XX OS Bos taurus.
XX
XX Key Location/Qualifiers
XX Cleavage-site 8..9
FT Region
FT /label= mutation
FT /note= "Arg -> Leu"
XX
XX WO9111514-A.
PN
XX
XX 08-AUG-1991.
PD
XX
XX 29-JAN-1990; 90US-00471313.
PF
XX 29-JAN-1990; 90US-00471313.
PR
XX (ZYMO) ZYMOGENETICS INC.
PA
XX
XX Berkner KL;
PI
XX
XX WPI; 1991-252647/34.
DR
XX
XX New modified factor VII to treat and prevent coagulation disorders - has
PT a reduced susceptibility to activation by plasma factor Xa and inhibits
PT clotting activity of wild type factor VIIa.
PT
XX
XX Claim 1; Fig 1; 40bp; English.
PS
XX
XX The Arg-11e cleavage site is modified to reduce susceptibility to
CC activation by plasma factor Xa. It therefore has a longer plasma half-
CC life and a correspondingly longer period of anticoagulative activity. The
CC modified factor VII binds tissue factor, and competes with wild type
CC factor VIIa. It is more selective than heparin, being active only in the
CC presence of tissue factor, and because it does not destroy other
CC coagulation proteins it is likely to be more effective and cause less
CC bleeding complications. See also AAR13446-R13455. (Updated on 25-MAR-2003
CC to correct PA field.)
CC
XX
XX Sequence 13 AA;

Query Match 29.5%; Score 31; DB 2; Length 13;
Best Local Similarity 60.0%; Pred. No. 9e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14
| | | | |
DB 2 GSKPGSLVIG 11

RESULT 91
ID AAR13455
XX AAR13455 standard; peptide; 13 AA.
XX
XX AAR13455;
AC
XX
XX 25-MAR-2003 (revised)
DT 28-OCT-1991 (first entry)
XX
XX Residues 145-157 of 152(I) bovine factor VII.
DE
XX
XX Thrombosis; tissue factor; heparin.
KM
XX
XX Bos taurus.
OS
XX
XX Key Location/Qualifiers
XX Cleavage-site 8..9
FT Region
FT /label= mutation
FT /note= "Arg -> Ile"
XX
XX WO9111514-A.
PN
XX

PD 08-AUG-1991.
 XX
 PF 29-JAN-1990; 90US-00471313.
 XX
 PR 29-JAN-1990; 90US-00471313.
 XX
 PA (ZYMO) ZYMOGENETICS INC.,
 XX
 PI Berkner KI;
 XX
 DR WPI; 1991-252647/34.
 XX
 PT New modified factor VII to treat and prevent coagulation disorders - has
 PT a reduced susceptibility to activation by plasma factor Xa and inhibits
 PT clotting activity of wild type factor VIIA.
 XX
 PS Claim 1; Fig 1; 40pp; English.
 XX
 CC The Arg-116 cleavage site is modified to reduce susceptibility to
 CC activation by plasma factor Xa. It therefore has a longer plasma half-
 CC life and a correspondingly longer period of anticoagulative activity. The
 CC modified factor VII binds tissue factor, and competes with wild type
 CC factor VIIa. It is more selective than heparin, being active only in the
 CC presence of tissue factor, and because it does not destroy other
 CC coagulation proteins it is likely to be more effective and cause less
 CC bleeding complications. See also AAR13446-R13454. (Updated on 25-MAR-2003
 CC to correct PA field.)
 XX
 S0 Sequence 13 AA;

Query Match	29.5%	Score 31;	DB 2;	Length 13;
Best Local Similarity	60.0%	Pred. No. 9e+02;		
Matches	6;	Conservative	0;	Mismatches 4;
			Indels	0;
			Gaps	0

QY	5	GMSPGRIVG	14
Db	2	GSKPGIIVG	11

RESULT 92
AAB83040
ID AAB83040 standard; peptide; 14 AA.

DT	25-JUN-2001	(first entry)
XX		
DE	Human Smad PY motif #6.	

KM Human; HCT; homologous to E6 carboxyl terminus; ubiquitination;
KM HECT E3 ubiquitin ligase; antiinflammatory; cytostatic; osteopontic;
KM antimicrobial; neuroprotective; transforming growth factor beta;
KM TGF-beta; bone morphogenic protein; BMP; Smad; cell signaling;
KM inflammation; ageing; cancer infection; bone anabolism; osteoporosis
KM renal failure; neurodegeneration; fibrosis; py motif.

Homo sapiens.

PN WO200116604-A1.

PD 08-MAR-2001.

PF 29-AUG-2000; 2000WO-US023729.

PR 30-AUG-1999; 99US-00385918.

PA (SIGN-) SIGNAL PHARM INC.

PI Hoekstra MF, Xie W, Murray BW, Mercurio FM;

DR WPI; 2001-327913/34.

PT Screening for modulators of TGF-beta and/or bone morphogenic protein

PT (BMP) mediated signaling useful for treating cancer and osteoporosis by
 PT evaluating the ability of agents to modulate Smad protein degradation.
 XX
 PS Example 2; Page 31; 75pp; English.

CC The present sequence is a Smad pY motif. The pY motif binds to the WW
CC domain of HECT (homologous to E6 carboxyl terminus) E3 ubiquitin ligase.
CC resulting in ubiquitination of Smad by the E3 ubiquitin ligase. The
CC sequence is provided in a specification relating to a method for
CC screening for agents that modulate transforming growth factor (TGF)-beta
CC and/or bone morphogenic protein (BMP)-mediated signaling. The method
CC involves evaluating the effect of an agent on binding of HECT E3
CC ubiquitin ligase WW domain to Smad pY motif, on ubiquitination of Smad
CC protein by E3 ubiquitin ligase, or on the cellular levels of Smad protein
CC HECT E3 ubiquitin ligase activity. The method is useful for stimulating
CC bone formation in a patient or treating a condition associated with
CC insufficient TGF-beta and/or BMP-mediated cell signaling. Agents that
CC inhibit BMP-mediated signaling are useful for treating inflammation,
CC ageing, cancer and infectious diseases. Agents that augment BMP-mediated
CC signaling are useful for stimulating bone anabolism as well as treating
CC broken bones, osteoporosis, and acute or chronic renal failure. Agents
CC that inhibit TGF-mediated signaling are useful for treating cancer,
CC inflammation, neurodegeneration and fibrosis

SQ Sequence 14 AA;

Query Match	29.5%	Score 31;	DB 4;	Length 14;
Best Local Similarity	38.5%	Pred. No. 9.7e+02;		
Matches	5;	Conservative	4;	Mismatches 4;
				Indels 0;
				Gaps 0

QY	5	GMSPPGFIVGEEG	17
		:: : :	
Db	2	GLTPPPGYLSEDG	14

RESULT	93
ADC22507	
ID	ADC22507 standard; peptide; 15 AA

AC ADC22507;

DT 18-DEC-2003 (first entry)

DE Protein binding domain amino acid sequence SEQ ID NO:356.

KW recombinant fusion protein; fusion protein; binding; detection;

KW subcellular compartment localisation.

OS Homo sapiens.

PN WO2003012068-A2.

PD 13-FEB-2003

PF 01-AUG-2002; 2002WO-US024572.

PR 01-AUG-2001; 2001US-0309395P.

XX

XX

XX

DR N-PSDB; ADC22506.

PT New recombinant fusion protein comprising detection and first

PT useful for detecting binding of a molecule of interest.

PS Claim 8; SEQ ID NO 356; 101pp; English.

CC The present invention describes a recombinant fusion protein (1) for
CC detecting binding of a molecule of interest. (1) comprises: (a) a
CC detection domain; (b) a first localisation domain; and (c) a binding
CC domain for the molecule of interest. The detection domain, the first
CC localisation domain and the binding domain for the molecule of interest
CC constituting the recombinant fusion protein for detecting binding of a
CC molecule of interest are operably linked. The binding domain for the
CC -20 amino acid residues. The first localisation domain and the binding
CC domain for the molecule of interest both do not occur in a single non-
CC recombinant protein with the same spacing as in the recombinant fusion
CC protein for detecting binding of a molecule of interest. Also described:
CC (1) a recombinant nucleic acid encoding the recombinant fusion protein;
CC (2) a recombinant expression vector comprising the nucleic acid control
CC sequences operably linked to the recombinant nucleic acid molecule; (3) a
CC genetically engineered host cell transfected with the recombinant
CC expression vector; (4) a kit for detecting binding of the molecule of
CC interest; and (5) a method for identifying compounds that alter the
CC binding of the molecule of interest. The recombinant fusion protein is
CC useful for detecting binding of a molecule of interest. The recombinant
CC fusion protein eliminates the need to construct two or more chimeric
CC proteins and enables the monitoring of biochemical events in live, intact
CC or fixed cells. The present sequence is used in the exemplification of
CC the present invention.

SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. NO. 1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPPG 10
| | | | |
DB 2 PGKGVKSPG 10

RESULT 94

ADP89482
ID ADF89482 standard; peptide; 15 AA.

AC ADF89482;

DT 26-FEB-2004 (first entry)

DE Human E2F1-derived P49 peptide.

KM histone-deacetylase; inhibitor; subtype; human; E2F1.

OS Homo sapiens.

PN JP2003221399-A.

PD 05-AUG-2003.

PF 19-NOV-2002; 2002JP-00335851.

PR 22-NOV-2001; 2001JP-00358583.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA WPI; 2003-883175/82.

PT Novel peptide substrate or its salt, useful for measuring histone-
deacetylase activity and screening of histone-deacetylase inhibitors.

PS Disclosure; SEQ ID NO 57; 40pp; Japanese.

CC The invention relates to a novel compound or its salt. The compound of
CC the invention may be useful for measuring the activity of histone-
CC deacetylase, screening for a histone-deacetylase inhibitor and
CC identifying the subtypes of histone-deacetylase. The current sequence is
CC that of the human E2F1-derived peptide of the invention.

SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 7; Length 15;
Best Local Similarity 55.6%; Pred. NO. 1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPPG 10
| | | | |
DB 5 PGKGVKSPG 13

RESULT 95

ADK48864
ID ADK48864 standard; peptide; 15 AA.

AC ADK48864;

DT 06-MAY-2004 (first entry)

DE C-terminal acetylated human EFLF derived peptide SegID 57.

KM human; EFLF; erythroid Kruppel like factor; histone-deacetylase; HDAC;
fluorescence; colour developing substrate; histone deacetylase inhibitor;

KM cancer; cytostatic.

OS Homo sapiens.

PN JP2003221398-A.

PD 05-AUG-2003.

PF 19-NOV-2002; 2002JP-00335840.

PR 22-NOV-2001; 2001JP-00358583.

XX (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN.

PA WPI; 2004-102668/11.

PT Novel peptide substrate or its salt, useful for measuring histone
deacetylase activity.

PS Disclosure; SEQ ID NO 57; 39pp; Japanese.

CC This invention relates to a novel method for measuring the histone-
CC deacetylase (HDAC) activity of a substrate using specific radioactivity,
CC fluorescence or a colour developing substrate. Specifically, it refers to
CC compound such as peptidyl-Lys(NAC)-WCA, which comprises a protecting group
CC of a hydrogen atom or an amino terminus, a group in which deacetylation
CC is carried out by the histone deacetylase linked to an acetylated lysine
CC residue that in turn is linked to the fluorescent group MCA (7-amino 4-
CC methylcoumarin). The present invention describes a method for measuring
CC HDAC activity, as well as identifying the subtype of histone deacetylase.
CC Furthermore, it can be used to screen for histone deacetylase inhibitors,
CC such that they can be used to regulate gene expression. Accordingly,
CC these compositions can be used to treat cancer and exhibit cytostatic
CC activities. This peptide sequence is a C-terminal acetylated human
CC peptide used to determine HDAC activity of the invention.

SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 8; Length 15;
Best Local Similarity 55.6%; Pred. NO. 1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

OY 2 PAKGMSPPG 10
| | | | |
DB 5 PGKGVKSPG 13

RESULT 96

ADO76533
ID ADO76533 standard; peptide; 15 AA.

XX AD076533;
 XX 15-JUL-2004 (first entry)
 XX Human 213P1F11 HLA motif bearing epitope #10632.
 XX
 XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
 XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 XX HLA vaccine.
 XX
 XX Homo sapiens.
 XX US2004019915-A1.
 XX 29-JAN-2004.
 XX 01-APR-2002; 2002US-00114432.
 XX 01-APR-2002; 2002US-00114432.
 XX 01-APR-2002; 2002US-00114432.
 XX
 XX (CHAL/) CHALLITA-EID P M.
 XX (RAIT/) RAITANO A B.
 XX (FARI/) FARIS M.
 XX (HUB/) HUBERT R S.
 XX (MORR/) MORRISON R K.
 XX (GEW/) GE W.
 XX (JAKO/) JAKOBOVITS A.
 XX
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
 XX Ge W, Jakobovits A;
 XX WPI; 2004-132240/13.
 XX
 XX New composition comprising a substance that modulates the status of
 XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for
 XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 XX Example 13; Page 231; 334pp; English.
 XX
 XX The invention describes a composition comprising a substance that
 XX modulates the status of 213P1F11, or a molecule that is modulated by
 XX 213P1F11, where the status of the cell that expresses 213P1F11 is
 XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also
 XX described are: a pharmaceutical composition comprising the composition
 XX cited above in a unit dose form; an antibody or its fragment; a non-human
 XX transgenic animal that produced the antibody; a hybridoma that produces
 XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;
 XX inhibiting growth of cancer cells that expresses 213P1F11; generating a
 XX mammalian immune response; detecting the presence of 213P1F11-related
 XX protein or polynucleotide in a sample; and detecting the presence of
 XX cancer in an individual. The compositions, molecules and methods are
 XX useful for detecting and treating cancer, e.g. pancreatic or rectal
 XX cancer. This is the amino acid sequence of a human 213P1F11 peptide
 XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 XX useful in the creation of an HLA vaccine to modulate 213P1F11.
 XX
 XX Sequence 15 AA;
 XX
 XX Query Match 29.5%; Score 31; DB 8; Length 15;
 XX Best Local Similarity 62.5%; Pred. No. 1e+03;
 XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEGB 17
 ||: ||: ||:
 DB 4 GFLKGEGB 11

RESULT 97
 AD076718

ID AD076718 standard; peptide; 15 AA.
 XX
 XX AD076718;
 XX 15-JUL-2004 (first entry)
 XX Human 213P1F11 HLA motif bearing epitope #10817.
 XX
 XX cytotoxic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
 XX transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 XX immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 XX human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 XX HLA vaccine.
 XX
 XX Homo sapiens.
 XX US2004019915-A1.
 XX 29-JAN-2004.
 XX 01-APR-2002; 2002US-00114432.
 XX 01-APR-2002; 2002US-00114432.
 XX 01-APR-2002; 2002US-00114432.
 XX
 XX (CHAL/) CHALLITA-EID P M.
 XX (RAIT/) RAITANO A B.
 XX (FARI/) FARIS M.
 XX (HUB/) HUBERT R S.
 XX (MORR/) MORRISON R K.
 XX (GEW/) GE W.
 XX (JAKO/) JAKOBOVITS A.
 XX
 XX Challita-Eid PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
 XX Ge W, Jakobovits A;
 XX WPI; 2004-132240/13.
 XX
 XX New composition comprising a substance that modulates the status of
 XX 213P1F11, or a molecule that is modulated by 213P1F11, useful for
 XX detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 XX Example 13; Page 234; 334pp; English.
 XX
 XX The invention describes a composition comprising a substance that
 XX modulates the status of 213P1F11, or a molecule that is modulated by
 XX 213P1F11, where the status of the cell that expresses 213P1F11 is
 XX modulated and 213P1F11 is a gene overexpressed in many cancers. Also
 XX described are: a pharmaceutical composition comprising the composition
 XX cited above in a unit dose form; an antibody or its fragment; a non-human
 XX transgenic animal that produced the antibody; a hybridoma that produces
 XX the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 XX cell that expresses 213P1F11; a polynucleotide that encodes the protein;
 XX inhibiting growth of cancer cells that expresses 213P1F11; generating a
 XX mammalian immune response; detecting the presence of 213P1F11-related
 XX protein or polynucleotide in a sample; and detecting the presence of
 XX cancer in an individual. The compositions, molecules and methods are
 XX useful for detecting and treating cancer, e.g. pancreatic or rectal
 XX cancer. This is the amino acid sequence of a human 213P1F11 peptide
 XX epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 XX useful in the creation of an HLA vaccine to modulate 213P1F11.
 XX
 XX Sequence 15 AA;
 XX
 XX Query Match 29.5%; Score 31; DB 8; Length 15;
 XX Best Local Similarity 62.5%; Pred. No. 1e+03;
 XX Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEGB 17
 ||: ||: ||:
 DB 8 GFLKGEGB 15

RESULT 98

AD076801
ID ADO76801 standard; peptide; 15 AA.
XX
AC ADO76801;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F11 HLA motif bearing epitope #10900.
XX
KM cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KM HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (PARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
PI Challita-Eld PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 235; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
SQ Sequence 15 AA;
XX

Query Match 29.5%; Score 31; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEKG 17
||:|:|:|
Db 2 GFLKGBDG 9

RESULT 99
ID ADO77052
XX ADO77052 standard; peptide; 15 AA.
XX
AC ADO77052;
XX
DT 15-JUL-2004 (first entry)
XX
DE Human 213P1F11 HLA motif bearing epitope #11151.
XX
KM cytostatic; gene therapy; 213P1F11; 213P1F11 modulation; cancer;
KM transgenic; cytotoxic agent delivery; diagnostic agent delivery;
KM immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
KM human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
KM HLA vaccine.
XX
OS Homo sapiens.
XX
PN US2004019915-A1.
XX
PD 29-JAN-2004.
XX
PF 01-APR-2002; 2002US-00114432.
XX
PR 01-APR-2002; 2002US-00114432.
XX
PA (CHAL/) CHALLITA-BID P M.
PA (RAIT/) RAITANO A B.
PA (PARI/) PARIS M.
PA (HUBE/) HUBERT R S.
PA (MORR/) MORRISON R K.
PA (GEMW/) GE W.
PA (JAKO/) JAKOBOVITS A.
PI Challita-Eld PM, Raitano AB, Faris M, Hubert RS, Morrison RK,
PI Ge W, Jakobovits A;
XX WPI; 2004-132240/13.
XX
PT New composition comprising a substance that modulates the status of
PT 213P1F11, or a molecule that is modulated by 213P1F11, useful for
PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
XX
PS Example 13; Page 239; 334pp; English.
XX
CC The invention describes a composition comprising a substance that
CC modulates the status of 213P1F11, or a molecule that is modulated by
CC 213P1F11, where the status of the cell that expresses 213P1F11 is
CC modulated and 213P1F11 is a gene overexpressed in many cancers. Also
CC described are: a pharmaceutical composition comprising the composition
CC cited above in a unit dose form; an antibody or its fragment; a non-human
CC transgenic animal that produced the antibody; a hybridoma that produces
CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
CC cell that expresses 213P1F11; a polynucleotide that encodes the protein;
CC inhibiting growth of cancer cells that expresses 213P1F11; generating a
CC mammalian immune response; detecting the presence of 213P1F11-related
CC protein or polynucleotide in a sample; and detecting the presence of
CC cancer in an individual. The compositions, molecules and methods are
CC useful for detecting and treating cancer, e.g. pancreatic or rectal
CC cancer. This is the amino acid sequence of a human 213P1F11 peptide
CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
CC useful in the creation of an HLA vaccine to modulate 213P1F11.
XX
SQ Sequence 15 AA;
XX

Query Match 29.5%; Score 31; DB 8; Length 15;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFLVGEKG 17
||:|:|:|
Db 3 GFLKGBDG 10

Search completed: January 20, 2006, 19:05:17
 Job time : 78.5769 secs

RESULT 100
 ADO76676
 ID ADO76676 standard; peptide; 15 AA.
 XX
 AC ADO76676;
 XX
 DT 15-JUL-2004 (first entry)
 XX
 DE Human 213P1P11 HLA motif bearing epitope #10775.
 XX
 KW cytostatic; gene therapy; 213P1P11; 213P1P11 modulation; cancer;
 KW transgenic; cytotoxic agent delivery; diagnostic agent delivery;
 KW immune response; pancreatic cancer; rectal cancer; bladder cancer; human;
 KW human leukocyte antigen; HLA; class I; class II; epitope; HLA motif;
 KW HLA vaccine.
 XX
 OS Homo sapiens.
 XX
 PN US2004019915-A1.
 XX
 PD 29-JAN-2004.
 XX
 PF 01-APR-2002; 2002US-00114432.
 XX
 PR 01-APR-2002; 2002US-00114432.
 XX
 PA (CHAL/) CHALLITA-ETD P M.
 PA (RAIT/) RAITANO A B.
 PA (FARI/) FARI M.
 PA (HUBE/) HUBERT R S.
 PA (MORR/) MORRISON R K.
 PA (GEMW/) GE W.
 PA (JAKO/) JAKOBOVITS A.
 XX
 PI Challita-ETD PM, Raitano AB, Fari M, Hubert RS, Morrison RK;
 PI Ge W, Jakobovits A;
 XX
 DR WPI; 2004-132240/13.
 XX
 PT New composition comprising a substance that modulates the status of
 PT 213P1P11, or a molecule that is modulated by 213P1P11, useful for
 PT detecting or treating cancer, e.g. pancreatic or rectal cancer.
 XX
 PS Example 13; Page 233; 334pp; English.
 XX
 CC The invention describes a composition comprising a substance that
 CC modulates the status of 213P1P11, or a molecule that is modulated by
 CC 213P1P11, where the status of the cell that expresses 213P1P11 is
 CC modulated and 213P1P11 is a gene overexpressed in many cancers. Also
 CC described are: a pharmaceutical composition comprising the composition
 CC cited above in a unit dose form; an antibody or its fragment; a non-human
 CC transgenic animal that produced the antibody; a hybridoma that produces
 CC the antibody; delivering a cytotoxic agent or a diagnostic agent to the
 CC cell that expresses 213P1P11; a polynucleotide that encodes the protein;
 CC inhibiting growth of cancer cells that expresses 213P1P11; generating a
 CC mammalian immune response; detecting the presence of 213P1P11-related
 CC protein or polynucleotide in a sample; and detecting the presence of
 CC cancer in an individual. The compositions, molecules and methods are
 CC useful for detecting and treating cancer, e.g. pancreatic or rectal
 CC cancer. This is the amino acid sequence of a human 213P1P11 peptide
 CC epitope bearing a human leukocyte antigen (HLA) class I or class II motif
 CC useful in the creation of an HLA vaccine to modulate 213P1P11.
 XX
 SQ Sequence 15 AA;

Query Match 29.5%; Score 31; DB 8; Length 15;
 Best Local Similarity 62.5%; Pred. No. 1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GPTVGEEG 17
 ||: ||:
 DB 4 GPLKGEDG 11

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 / Search time 20.9615 Seconds
(Without alignments)
78.883 Million cell updates/sec

Title: US-09-662-293-4

Sequence: 1 DPAKGMSPRGIVGEGVLIS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: /cgn2_6/ptcodata/1/aa/5.COMB.pep.*
2: /cgn2_6/ptcodata/1/aa/6.COMB.pep.*
3: /cgn2_6/ptcodata/1/aa/H.COMB.pep.*
4: /cgn2_6/ptcodata/1/aa/PCUS.COMB.pep.*
5: /cgn2_6/ptcodata/1/aa/RT.COMB.pep.*
6: /cgn2_6/ptcodata/1/aa/backfile1.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	105	100.0	20	2	US-09-292-225-4
2	105	100.0	20	2	US-09-292-225-13
3	34	32.4	8	2	US-08-475-955-116
4	34	32.4	9	2	US-07-867-819D-116
5	34	32.4	9	2	US-08-475-955-100
6	34	32.4	9	2	US-07-867-819D-100
7	34	32.4	18	2	US-08-990-888-28
8	33	31.4	15	2	US-09-157-689-67
9	33	31.4	15	2	US-09-353-510-67
10	33	31.4	20	2	US-09-667-857-397
11	33	31.4	20	2	US-10-198-053-397
12	33	31.4	20	2	US-10-198-053-603
13	33	31.4	20	2	US-09-827-711-397
14	31	29.5	16	1	US-08-482-142-185
15	31	29.5	16	1	US-08-478-572-185
16	31	29.5	16	1	US-08-484-396-185
17	31	29.5	18	2	US-08-990-888-36
18	31	29.5	18	2	US-09-570-022-13
19	31	29.5	20	2	US-09-635-501-29
20	31	29.5	20	2	US-10-007-700-463
21	30	28.6	8	2	US-08-475-955-12
22	30	28.6	8	2	US-08-475-955-205
23	30	28.6	8	2	US-08-475-955-206
24	30	28.6	8	2	US-07-867-819D-112
25	30	28.6	8	2	US-07-867-819D-112
26	30	28.6	8	2	US-07-867-819D-113
27	30	28.6	10	2	US-08-476-509B-32

28	30	28.6	10	2	US-08-476-509B-35	Sequence 35, App1
29	30	28.6	10	2	US-08-988-242-11	Sequence 11, App1
30	30	28.6	11	1	US-08-526-764-1	Sequence 1, App1
31	30	28.6	12	2	US-08-988-242-10	Sequence 10, App1
32	30	28.6	12	2	US-07-867-819D-14	Sequence 14, App1
33	30	28.6	14	2	US-08-630-916A-53	Sequence 53, App1
34	30	28.6	14	2	US-08-630-916A-54	Sequence 54, App1
35	30	28.6	14	2	US-09-509-595B-20	Sequence 20, App1
36	30	28.6	18	2	US-08-990-888-25	Sequence 25, App1
37	30	28.6	18	2	US-08-990-888-65	Sequence 65, App1
38	30	28.6	19	2	US-09-010-999-9	Sequence 9, App1
39	30	28.6	19	2	US-09-470-830A-27	Sequence 27, App1
40	30	28.6	20	2	US-08-928-213B-128	Sequence 128, App1
41	30	28.6	20	2	US-08-928-213B-129	Sequence 129, App1
42	29.5	28.1	14	1	US-07-721-761A-17	Sequence 17, App1
43	29.5	28.1	14	1	US-07-978-687-17	Sequence 17, App1
44	29.5	28.1	14	1	PCT-US91-05801-17	Sequence 17, App1
45	29.5	28.1	17	1	US-07-721-761A-10	Sequence 10, App1
46	29.5	28.1	17	1	US-07-978-687-10	Sequence 10, App1
47	29.5	28.1	17	4	PCT-US91-05801-10	Sequence 10, App1
48	29	27.6	8	2	US-08-160-604-1	Sequence 1, App1
49	29	27.6	8	2	US-08-475-955-123	Sequence 123, App1
50	29	27.6	8	2	US-09-718-693A-3	Sequence 3, App1
51	29	27.6	8	2	US-07-867-819D-147	Sequence 147, App1
52	29	27.6	8	2	US-07-867-819D-149	Sequence 149, App1
53	29	27.6	8	2	US-07-867-819D-157	Sequence 157, App1
54	29	27.6	11	2	US-08-475-955-10	Sequence 10, App1
55	29	27.6	11	2	US-07-867-819D-10	Sequence 10, App1
56	29	27.6	12	2	US-08-475-955-14	Sequence 14, App1
57	29	27.6	16	1	US-07-994-469A-21	Sequence 21, App1
58	29	27.6	16	1	US-08-478-572-186	Sequence 186, App1
59	29	27.6	16	2	US-08-484-296-186	Sequence 186, App1
60	29	27.6	18	2	US-08-990-888-24	Sequence 24, App1
61	29	27.6	18	2	US-08-990-888-46	Sequence 46, App1
62	29	27.6	19	2	US-08-990-888-62	Sequence 62, App1
63	29	27.6	19	2	US-09-010-999-8	Sequence 8, App1
64	29	27.6	20	2	US-09-980-177A-77	Sequence 77, App1
65	29	27.6	20	2	US-10-007-700-413	Sequence 413, App1
66	29	27.6	18	2	US-10-394-980-140	Sequence 140, App1
67	28.5	27.1	5	1	US-08-488-470A-7	Sequence 7, App1
68	28	26.7	5	1	US-07-946-239-15	Sequence 15, App1
69	28	26.7	5	1	US-08-484-505A-7	Sequence 7, App1
70	28	26.7	5	2	US-08-383-766-3	Sequence 3, App1
71	28	26.7	5	2	US-09-151-467-15	Sequence 15, App1
72	28	26.7	5	2	US-09-078-403A-7	Sequence 7, App1
73	28	26.7	5	2	US-09-256-838-15	Sequence 15, App1
74	28	26.7	5	4	PCT-US92-07815-15	Sequence 15, App1
75	28	26.7	8	2	US-08-475-955-117	Sequence 117, App1
76	28	26.7	8	2	US-07-867-819D-31	Sequence 31, App1
77	28	26.7	9	2	US-09-769-180-31	Sequence 31, App1
78	28	26.7	11	2	US-08-476-509B-30	Sequence 30, App1
79	28	26.7	14	2	US-08-630-916A-85	Sequence 85, App1
80	28	26.7	14	2	US-08-630-916A-85	Sequence 85, App1
81	28	26.7	15	6	5187078-4	Patent No. 5187078
82	28	26.7	18	2	US-08-530-916A-9	Sequence 9, App1
83	28	26.7	18	2	US-08-990-888-30	Sequence 30, App1
84	28	26.7	18	2	US-08-990-888-69	Sequence 69, App1
85	28	26.7	18	2	US-09-292-225-12	Sequence 12, App1
86	28	26.7	19	2	US-09-570-022-12	Sequence 12, App1
87	28	26.7	19	2	US-09-068-624-2	Sequence 2, App1
88	28	26.7	20	1	US-09-068-624-3	Sequence 3, App1
89	28	26.7	20	1	US-07-956-848A-17	Sequence 17, App1
90	28	26.7	20	1	US-08-468-514-7	Sequence 7, App1
91	28	26.7	20	1	US-08-471-956-17	Sequence 17, App1
92	28	26.7	20	2	US-08-786-455B-2	Sequence 2, App1
93	28	26.7	20	2	US-09-715-838A-6	Sequence 6, App1
94	28	26.7	20	2	US-08-475-955-195	Sequence 195, App1
95	27.5	25.7	8	2		
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100	27	25.7	8	2		

ALIGNMENTS

RESULT 1

US-09-292-225-4
; Sequence 4, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-4

Query Match 100.0%; Score 105; DB 2; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFTVGEVGLS 20
Db 1 DPAKMSPPGFTVGEVGLS 20

RESULT 2

US-09-292-225-13
; Sequence 13, Application US/09292225
; Patent No. 6455686
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/09/292,225
; EARLIER FILING DATE: 1999-04-15
; EARLIER APPLICATION NUMBER: 60/098,909
; EARLIER FILING DATE: 1998-09-02
; EARLIER APPLICATION NUMBER: 60/085,295
; EARLIER FILING DATE: 1998-05-13
; EARLIER APPLICATION NUMBER: 60/098,565
; EARLIER FILING DATE: 1998-04-17
; EARLIER APPLICATION NUMBER: 09/062,013
; EARLIER FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-09-292-225-13

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
Db 1 PAKGMSPP 8

RESULT 4
US-07-867-819D-116
; Sequence 116, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:

Best Local Similarity 100.0%; Pred. No. 1.8e-10;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFTVGEVGLS 20
Db 1 DPAKMSPPGFTVGEVGLS 20

RESULT 3

US-08-475-955-116
; Sequence 116, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Patricia L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/475,955
; FILING DATE: June 7, 1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/667,819
; FILING DATE: April 13, 1992
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patricia L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMF114CIP (2) DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404) -873-8794
; TELEFAX: (404) -873-8795
; INFORMATION FOR SEQ ID NO: 116:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 8 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-475-955-116

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
Db 1 PAKGMSPP 8

RESULT 4
US-07-867-819D-116
; Sequence 116, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:

APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRP 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 116
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapien
US-07-867-819D-116

Query Match 32.4%; Score 34; DB 2; Length 8;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSP 9
Db 1 PAKGMRP 8

RESULT 5
US-08-475-955-100
Sequence 100, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
US-08-475-955-100

Query Match 32.4%; Score 34; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSP 9
Db 2 PAKGMRP 9

RESULT 6
US-07-867-819D-100
Sequence 100, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRP 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 100
LENGTH: 9
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (1)..(8)
OTHER INFORMATION: Binding site
US-07-867-819D-100

Query Match 32.4%; Score 34; DB 2; Length 9;
Best Local Similarity 75.0%; Pred. No. 4.6e+05;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSP 9
Db 2 PAKGMRP 9

RESULT 7
US-08-990-888-28
Sequence 28, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandelk, Wlodek S.
TITLE OF INVENTION: Assays for Compounds which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 28
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence

US-08-990-888-28

Query Match 32.4%; Score 34; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 60;
Matches 6; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPGPIVG 14
|:|:|:|
Db 6 GVSYPGWLVG 15

RESULT 8

US-09-157-689-67
; Sequence 67, Application US/09157689
; Patent No. 6599510
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; APPLICANT: Harth, Gunter
; TITLE OF INVENTION: Abundant Extracellular Products and
; TITLE OF INVENTION: Methods for Their Production and Use
; NUMBER OF SEQUENCES: 95
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. Maclean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/157,689
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/568,357
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/551,149
; FILING DATE: 31-OCT-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Maclean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 118-119
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: B7man
; US-09-157-689-67

Query Match 31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKGMSP 8
|:|:|:|
Db 4 DPGQGMGP 11

RESULT 9

US-09-953-510-67
; Sequence 67, Application US/09953510
; Patent No. 6818223
; GENERAL INFORMATION:
; APPLICANT: Horwitz, Marcus A.
; TITLE OF INVENTION: Abundant Extracellular
; Products and Methods for Their Production and Use
; NUMBER OF SEQUENCES: 91
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Kurt A. Maclean
; STREET: 2029 Century Park East, Suite 3800
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90067
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0,
; Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/953,510
; FILING DATE: 14-SEP-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/447,398
; FILING DATE: 23-MAY-1995
; APPLICATION NUMBER: US 08/289,667
; FILING DATE: 12-AUG-1994
; APPLICATION NUMBER: US 08/156,358
; FILING DATE: 23-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Maclean, Kurt A.
; REGISTRATION NUMBER: 31,118
; REFERENCE/DOCKET NUMBER: 112-272
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (310) 788-5000
; TELEFAX: (310) 277-1297
; INFORMATION FOR SEQ ID NO: 67:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 15 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: Internal
; ORIGINAL SOURCE:
; ORGANISM: Mycobacterium tuberculosis
; STRAIN: B7man
; SEQUENCE DESCRIPTION: SEQ ID NO: 67:
; US-09-953-510-67

Query Match 31.4%; Score 33; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 71;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKGMSP 8
|:|:|:|
Db 4 DPGQGMGP 11

```
RESULT 10
US-09-667-857-397
; Sequence 397, Application US/09667857
; Patent No. 6699664
; GENERAL INFORMATION:
; APPLICANT: Mitchem, Jennifer L.
; APPLICANT: King, Gordon E.
; APPLICANT: Algate, Paul A.
; APPLICANT: Fling, Steven P.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary Richard
; APPLICANT: Reed, Steven G.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Derrick
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C5
; CURRENT APPLICATION NUMBER: US/09/667,857
; CURRENT FILING DATE: 2000-09-20
; NUMBER OF SEQ ID NOS: 455
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-667-857-397
```

```
Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      13 VGESEGVLS 20
       :|||:|||
Db      3 IGEDGILS 10
```

```
RESULT 11
US-10-198-053-397
; Sequence 397, Application US/10198053
; Patent No. 6858710
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-397
```

```
Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      13 VGESEGVLS 20
       :|||:|||
Db      3 IGEDGILS 10
```

```
RESULT 12
US-10-198-053-603
; Sequence 603, Application US/10198053
; Patent No. 6858710
```

```
; GENERAL INFORMATION:
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Hill, Paul
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.462C9
; CURRENT APPLICATION NUMBER: US/10/198,053
; CURRENT FILING DATE: 2002-07-17
; NUMBER OF SEQ ID NOS: 624
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 603
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-198-053-603
```

```
Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      13 VGESEGVLS 20
       :|||:|||
Db      3 IGEDGILS 10
```

```
RESULT 13
US-09-827-271-397
; Sequence 397, Application US/09827271
; Patent No. 6962980
; GENERAL INFORMATION:
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; FILE REFERENCE: 210121.462C6
; CURRENT APPLICATION NUMBER: US/09/827,271
; CURRENT FILING DATE: 2001-04-04
; NUMBER OF SEQ ID NOS: 461
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 397
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-271-397
```

```
Query Match      31.4%; Score 33; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 99;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      13 VGESEGVLS 20
       :|||:|||
Db      3 IGEDGILS 10
```

```
RESULT 14
US-08-482-142-185
; Sequence 185, Application US/08482142
; Patent No. 5820862
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mel-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Pranzan, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
```

ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-482-142-185

Query Match 29.5%; Score 31; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 12 IYGEBCVLS 20
:|::|||:
Db 6 LVGDGCVLA 14

RESULT 15
US-08-478-572-185
; Sequence 185, Application US/08478572
; Patent No. 5968526
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/478,572

FILING DATE: 07-June-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 185:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-478-572-185

Query Match 29.5%; Score 31; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

Qy 12 IYGEBCVLS 20
:|::|||:
Db 6 LVGDGCVLA 14

RESULT 16
US-08-484-296-185
; Sequence 185, Application US/08484296
; Patent No. 6268491
; GENERAL INFORMATION:
; APPLICANT: Garman, Richard
; APPLICANT: Greenstein, Julia
; APPLICANT: Kuo, Mei-chang
; APPLICANT: Rogers, Bruce
; APPLICANT: Franzen, Henry
; APPLICANT: Chen, Xian
; APPLICANT: Evans, Sean
; APPLICANT: Shaked, Ze'ev
; TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
; TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
; NUMBER OF SEQUENCES: 207
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
; STREET: 610 LINCOLN STREET
; CITY: WALTHAM
; STATE: MA
; COUNTRY: USA
; ZIP: 02154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII TEXT
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,296
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/445,307
; FILING DATE: 07 June 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: CRAIG, ANNE I.
; REGISTRATION NUMBER: 32,976
; REFERENCE/DOCKET NUMBER: 017.6US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 466-6000
; TELEFAX: (617) 466-6040
; INFORMATION FOR SEQ ID NO: 185:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-484-296-185

Query Match 29.5%; Score 31; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGSEGVLS 20
DB 6 LVGDDGVLA 14

RESULT 17
US-08-990-888-36
Sequence 36, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 36
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-36

Query Match 29.5%; Score 31; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 5; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14
DB 6 GVTYPGMLVG 15

RESULT 18
US-09-570-022-13
Sequence 13, Application US/09570022
Patent No. 6573244
GENERAL INFORMATION:
APPLICANT: GORDON, RICHARD K.
APPLICANT: MOORAD, DEBORAH R.
APPLICANT: DOCTOR, BHUPENDRA P.
APPLICANT: GARCIA, GREGORY B.
TITLE OF INVENTION: PREVING AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
FILE REFERENCE: 38644-170531
CURRENT APPLICATION NUMBER: US/09/570,022
CURRENT FILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: 60/134,446
PRIOR FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide
US-09-570-022-13

Query Match 29.5%; Score 31; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGPIV 13
DB 5 AKGIQPPGLMV 15

RESULT 19
US-09-635-501-29
Sequence 29, Application US/09635501
Patent No. 6884771
GENERAL INFORMATION:
APPLICANT: Actor, Susan L. et al.
TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
FILE REFERENCE: NMT-132CP3
CURRENT APPLICATION NUMBER: US/09/635,501
CURRENT FILING DATE: 2000-08-09
PRIOR APPLICATION NUMBER: 09/407,427
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: 09/163,648
PRIOR FILING DATE: 1998-09-30
PRIOR APPLICATION NUMBER: 08/989,299
PRIOR FILING DATE: 1997-12-11
NUMBER OF SEQ ID NOS: 107
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 29
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: motifs
US-09-635-501-29

Query Match 29.5%; Score 31; DB 2; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKMSPPGPI 11
DB 1 DISKGNPPGF 11

RESULT 20
US-10-007-700-463
Sequence 463, Application US/10007700
Patent No. 6960570
GENERAL INFORMATION:
APPLICANT: Wang, Tongtong
APPLICANT: Wang, Aljun
APPLICANT: Skelky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margareta
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
AND DIAGNOSIS OF LUNG CANCER

FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 463
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-700-463

Query Match 29.5%; Score 31; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPPP 16

RESULT 21

US-08-475-955-12
Sequence 12, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
US-08-475-955-12

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 3 GMPPPG 8

RESULT 22

US-08-475-955-205
Sequence 205, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-205

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 2 GMPPPG 7

RESULT 23
US-08-475-955-206
Sequence 206, Application US/08475955

/ Patent No. 6641813
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ NUMBER OF INVENTION: AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patricia L. Pabst
/ STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3450
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,955
/ FILING DATE: June 7, 1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/867,819
/ FILING DATE: April 13, 1992
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/472,947
/ FILING DATE: January 31, 1990
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Pabst, Patricia L.
/ REGISTRATION NUMBER: 31,284
/ REFERENCE/DOCKET NUMBER: OMRF14CIP(2)DIV
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (404)-873-8794
/ TELEFAX: (404)-873-8795
/ INFORMATION FOR SEQ ID NO: 206:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 8 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-475-955-206

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10
Db 1 GMPPPG 6

RESULT 24
US-07-867-819D-12
/ Sequence 12, Application US/07867819D
/ Patent No. 6897287
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
/ FILE REFERENCE: OMRF 114 CIP (2)
/ CURRENT APPLICATION NUMBER: US/07/867,819D
/ CURRENT FILING DATE: 1992-04-13
/ PRIOR APPLICATION NUMBER: 07/472,947
/ PRIOR FILING DATE: 1990-01-31
/ PRIOR APPLICATION NUMBER: 07/648,205
/ PRIOR FILING DATE: 1991-01-31
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: PatentIn version 3.1

/ SEQ ID NO 12
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: homo sapien
/ FEATURE:
/ NAME/KEY: MISC FEATURE
/ LOCATION: (1)-(8)
/ OTHER INFORMATION: Binding site
/ US-07-867-819D-12

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10
Db 3 GMPPPG 8

RESULT 25
US-07-867-819D-112
/ Sequence 112, Application US/07867819D
/ Patent No. 6897287
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
/ FILE REFERENCE: OMRF 114 CIP (2)
/ CURRENT APPLICATION NUMBER: US/07/867,819D
/ CURRENT FILING DATE: 1992-04-13
/ PRIOR APPLICATION NUMBER: 07/472,947
/ PRIOR FILING DATE: 1990-01-31
/ PRIOR APPLICATION NUMBER: 07/648,205
/ PRIOR FILING DATE: 1991-01-31
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 112
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: homo sapien
/ US-07-867-819D-112

Query Match 28.6%; Score 30; DB 2; Length 8;
Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10
Db 2 GMPPPG 7

RESULT 26
US-07-867-819D-113
/ Sequence 113, Application US/07867819D
/ Patent No. 6897287
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
/ FILE REFERENCE: OMRF 114 CIP (2)
/ CURRENT APPLICATION NUMBER: US/07/867,819D
/ CURRENT FILING DATE: 1992-04-13
/ PRIOR APPLICATION NUMBER: 07/472,947
/ PRIOR FILING DATE: 1990-01-31
/ PRIOR APPLICATION NUMBER: 07/648,205
/ PRIOR FILING DATE: 1991-01-31
/ NUMBER OF SEQ ID NOS: 161
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 113
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: homo sapien
/ US-07-867-819D-113

Query Match 28.6%; Score 30; DB 2; Length 8;

Best Local Similarity 83.3%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 5 GMSPPG 10
Db 1 GMPPG 6

RESULT 27

US-08-476-509B-32
Sequence 32, Application US/08476509B
Patent No. 6034212
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 32:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-08-476-509B-32

Query Match 28.6%; Score 30; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 5 GMSPPG 14
Db 1 GTPPPYTVG 10

RESULT 28
US-08-476-509B-35
Sequence 35, Application US/08476509B
Patent No. 6034212
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A

TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS
TITLE OF INVENTION: THEREOF
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauder & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
US-08-476-509B-35

Query Match 28.6%; Score 30; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPG 14
Db 1 GTPPPYTVG 10

RESULT 29

US-08-988-242-11
Sequence 11, Application US/08988242
Patent No. 6403103
GENERAL INFORMATION:
APPLICANT: PARANHOS-BACCALA, GLAUCIA
APPLICANT: LESENCHAL, MYLENE
APPLICANT: JOLIVET, MICHEL
APPLICANT: MANDRAND, BERNARD
TITLE OF INVENTION: NEW TYROSINOMYOMA CRUIZ ANTIGEN, GENE
TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
TITLE OF INVENTION: CHAGAS DISEASE
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
ADDRESSEE: OLIFF & BERRIDGE, PLC
STREET: P. O. BOX 19928
CITY: Alexandria
STATE: Virginia
COUNTRY: U.S.A.
ZIP: 22320
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

```

/ APPLICATION NUMBER: US/08/988,242
/ FILING DATE: 10-DEC-1997
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/   NAME: Berridge, William P.
/   REGISTRATION NUMBER: 30,024
/   REFERENCE/DOCKET NUMBER: WPB 36400A
/   TELECOMMUNICATION INFORMATION:
/     TELEPHONE: 703-836-6400
/     TELEFAX: 703-836-2787
/   INFORMATION FOR SEQ ID NO: 11:
/     SEQUENCE CHARACTERISTICS:
/       LENGTH: 10 amino acids
/       TYPE: amino acid
/       STRANDEDNESS: single
/       TOPOLOGY: linear
/     MOLECULE TYPE:
/     DESCRIPTION: /desc = "protein"
US-08-988-242-11

Query Match      28.6%; Score 30; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 PAKGMSPP 9
Db      1 PAKGAAP 8

RESULT 30
US-08-526-764-1
/ Sequence 1, Application US/08526764
/ Patent No. 5834431
/ GENERAL INFORMATION:
/   APPLICANT:
/   TITLE OF INVENTION: DES-ARG9-BK ANTAGONISTS
/   NUMBER OF SEQUENCES: 1
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
/   CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/526,764
/     INFORMATION FOR SEQ ID NO: 1:
/       SEQUENCE CHARACTERISTICS:
/         LENGTH: 11 amino acids
/         TYPE: amino acid
/         STRANDEDNESS: single
/         TOPOLOGY: linear
/       MOLECULE TYPE: peptide
US-08-526-764-1

Query Match      28.6%; Score 30; DB 1; Length 11;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy      5 GMSPPGF 11
Db      2 GKRPFGF 8

RESULT 31
US-08-988-242-10
/ Sequence 10, Application US/08988242
/ Patent No. 6403103
/ GENERAL INFORMATION:
/   APPLICANT: PARANHOS-BACCALA, GLAUCIA
/   APPLICANT: LESNECHAL, MYLENE
/   APPLICANT: JOLIVET, MICHEL
/   APPLICANT: MANDRAND, BERNARD
/   TITLE OF INVENTION: NEW TRYPAANOSOMA CRUZI ANTIGEN, GENE
/   TITLE OF INVENTION: ENCODING THEREFOR, AND METHODS OF DETECTING AND TREATING
```

```

/ TITLE OF INVENTION: CHAGAS DISEASE
/ NUMBER OF SEQUENCES: 19
/ CORRESPONDENCE ADDRESS:
/   ADDRESSER: OLIF & BERRIDGE, PLC
/   STREET: P.O. BOX 19928
/   CITY: Alexandria
/   STATE: Virginia
/   COUNTRY: U.S.A.
/   ZIP: 22320
/   COMPUTER READABLE FORM:
/   MEDIUM TYPE: Floppy disk
/   COMPUTER: IBM PC compatible
/   OPERATING SYSTEM: PC-DOS/MS-DOS
/   SOFTWARE: Patentin Release #1.0, Version #1.30
/   CURRENT APPLICATION DATA:
/     APPLICATION NUMBER: US/08/988,242
/     FILING DATE: 10-DEC-1997
/     CLASSIFICATION: 435
/     ATTORNEY/AGENT INFORMATION:
/       NAME: Berridge, William P.
/       REGISTRATION NUMBER: 30,024
/       REFERENCE/DOCKET NUMBER: WPB 36400A
/       TELECOMMUNICATION INFORMATION:
/         TELEPHONE: 703-836-6400
/         TELEFAX: 703-836-2787
/       INFORMATION FOR SEQ ID NO: 10:
/         SEQUENCE CHARACTERISTICS:
/           LENGTH: 12 amino acids
/           TYPE: amino acid
/           STRANDEDNESS: single
/           TOPOLOGY: linear
/         MOLECULE TYPE:
/         DESCRIPTION: /desc = "protein"
US-08-988-242-10

Query Match      28.6%; Score 30; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy      2 PAKGMSPP 9
Db      3 PAKGAAP 10

RESULT 32
US-07-867-819D-14
/ Sequence 14, Application US/07867819D
/ Patent No. 6897287
/ GENERAL INFORMATION:
/   APPLICANT: Harley, John
/   TITLE OF INVENTION: Method and Reagents for Diagnosis of Autoantibodies
/   FILE REFERENCE: OMRP 114 CIP (2)
/   CURRENT APPLICATION NUMBER: US/07/867,819D
/   PRIOR FILING DATE: 1992-04-13
/   PRIOR APPLICATION NUMBER: 07/472,947
/   PRIOR FILING DATE: 1990-01-31
/   PRIOR APPLICATION NUMBER: 07/648,205
/   PRIOR FILING DATE: 1991-01-31
/   NUMBER OF SEQ ID NOS: 161
/   SOFTWARE: Patentin version 3.1
/   SEQ ID NO 14
/   LENGTH: 12
/   TYPE: PRT
/   ORGANISM: homo sapien
/   FEATURE:
/     NAME/KEY: MISC FEATURE
/     LOCATION: (3)_(10)
/   OTHER INFORMATION: Binding site
/   FEATURE:
/     NAME/KEY: VARIANT
/     LOCATION: (9)_(9)
/   OTHER INFORMATION: Can be R, F, G, H, I, K, S, T, V or Y
US-07-867-819D-14
```

Query Match 28.6%; Score 30; DB 2; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
| | | |
| | | |
Db 4 PPGKXPP 11

RESULT 33
US-08-630-916A-53
; Sequence 53, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: United States
; ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-53

Query Match 28.6%; Score 30; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPFTVG 14
| | | |
| | | |
Db 2 GTPPPYTVG 11

RESULT 34
US-08-630-916A-54
; Sequence 54, Application US/08630916A
; Patent No. 601137
; GENERAL INFORMATION:
; APPLICANT: Pirozzi, Gregorio
; APPLICANT: Kay, Brian K.
; APPLICANT: Fowlkes, Dana M.
; TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
; TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
; NUMBER OF SEQUENCES: 124

CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/630,916A
; FILING DATE: 03-APR-1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: MISROCK, S. LESLIE
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 1101-203
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 790-9090
; TELEFAX: (212) 896-8864/9741
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 14 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
US-08-630-916A-54

Query Match 28.6%; Score 30; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPFTVG 14
| | | |
| | | |
Db 2 GTPPPYTVG 11

RESULT 35
US-09-509-595B-20
; Sequence 20, Application US/09509595B
; Patent No. 6951928
; GENERAL INFORMATION:
; APPLICANT: MAX-PLANCK-GESELLSCHAFT ZUR FORDERUNG DER WISSENSCHAFTEN E.V.
; APPLICANT: NATIONAL PUBLIC HEALTH INSTITUTE
; APPLICANT: PELTONEN, Leena
; APPLICANT: ALTONEN, Johanna
; APPLICANT: BJORSES, Petra
; APPLICANT: PERHENTUPA, Jaakko
; APPLICANT: PALOTIE, Aarno
; APPLICANT: HORELI-KUITUNEN, Nina
; APPLICANT: VASPO, Marie-Laure
; APPLICANT: LEHACH, Hans
; TITLE OF INVENTION: NUCLEIC ACID MOLECULE ENCODING A (POLY) PEPTIDE CO-SEGREGATING IN
; TITLE OF INVENTION: FORM WITH AUTOTMONE POLYENDOCRINOPATHY CANDIDIASIS ECTODERMAL D
; TITLE OF INVENTION: (APBCED)
; FILE REFERENCE: VOSS1130
; CURRENT APPLICATION NUMBER: US/09/509,595B
; PRIOR FILING DATE: 2000-07-05
; PRIOR APPLICATION NUMBER: EP 97117154.1
; PRIOR FILING DATE: 1997-10-02
; PRIOR APPLICATION NUMBER: EP 97117398.4
; PRIOR FILING DATE: 1997-10-08
; PRIOR APPLICATION NUMBER: EP 97119810.6
; PRIOR FILING DATE: 1997-11-12
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 20
; LENGTH: 14
; TYPE: PRT

ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide
US-09-509-595B-20

Query Match 28.6% Score 30; DB 2; Length 14;
Best Local Similarity 62.5% Pred. No. 2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9
DB 3 PRKGRKP 10

RESULT 36
US-08-990-888-25
Sequence 25, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 25
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-25

Query Match 28.6% Score 30; DB 2; Length 18;
Best Local Similarity 50.0% Pred. No. 2.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14
DB 6 GVSYPGWLNG 15

RESULT 37
US-08-990-888-65
Sequence 65, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 65
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-65

Query Match 28.6% Score 30; DB 2; Length 18;
Best Local Similarity 50.0% Pred. No. 2.7e+02;

Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14
DB 6 GVSYPGWLNG 15

RESULT 38
US-09-010-999-9
Sequence 9, Application US/09010999
Patent No. 6132976
GENERAL INFORMATION:
APPLICANT: Poole, Anthony R.
APPLICANT: Hollander, Anthony P.
APPLICANT: Billingshurst, R. C.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,999
FILING DATE: 22-JAN-1998
CLASSIFICATION: 4335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/448,501
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,123
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 032931/0212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-010-999-9

Query Match 28.6% Score 30; DB 2; Length 19;
Best Local Similarity 41.2% Pred. No. 2.9e+02;
Matches 7; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 3 AKGSPGIVG 19
DB 2 APGTPGDIAGORGIV 18

RESULT 39
US-09-470-830A-27
Sequence 27, Application US/09470830A
Patent No. 6677139
GENERAL INFORMATION:
APPLICANT: Genencor International, Inc.
TITLE OF INVENTION: Methods for Production of Proteins in

MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/721,761A
FILING DATE: 19910626
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Laessen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-721-761A-17

Query Match 28.1% Score 29.5; DB 1; Length 14;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GPRVGR-EGVL 19
DB 2 GFVWGEGAGVL 12

RESULT 43
US-07-978-687-17
Sequence 17, Application US/07978687
Patent No. 5510255
GENERAL INFORMATION:
APPLICANT: Vic. C. Knauf
TITLE OF INVENTION: Plant Fatty Acid Synthases
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/978,687
FILING DATE: FEBRUARY 1, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05801
FILING DATE: 15-AUGUST-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,761
FILING DATE: 26-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Laessen

REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-978-687-17

Query Match 28.1% Score 29.5; DB 1; Length 14;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GPRVGR-EGVL 19
DB 2 GFVWGEGAGVL 12

RESULT 44
PCT-US91-05801-17
Sequence 17, Application PC/TUS9105801
GENERAL INFORMATION:
APPLICANT: Vic. C. Knauf
TITLE OF INVENTION: Plant Fatty Acid Synthases
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05801
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,761
FILING DATE: 26-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Laessen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US91-05801-17

Query Match 28.1% Score 29.5; DB 4; Length 14;
Best Local Similarity 63.6%; Pred. No. 2.4e+02;

Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRVGE-EGVL 19
Db 2 GFVMEGAGVL 12

RESULT 45

US-07-721-761A-10
Sequence 10, Application US/07721761A
Patent No. 5475099
GENERAL INFORMATION:
APPLICANT: VIC. C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: Plant Fatty Acid Synthases
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07721,761A
FILING DATE: 19910626
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna B. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-721-761A-10

Query Match 28.1%; Score 29.5; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRVGE-EGVL 19
Db 2 GFVMEGAGVL 12

RESULT 46

US-07-978-687-10
Sequence 10, Application US/07978687
Patent No. 5510255
GENERAL INFORMATION:
APPLICANT: VIC. C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: Plant Fatty Acid Synthases
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street

CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07978,687
FILING DATE: FEBRUARY 1, 1993
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05801
FILING DATE: 15-AUGUST-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/721,761
FILING DATE: 26-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Lassen
REGISTRATION NUMBER: 31,845
NAME: Donna B. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-978-687-10

Query Match 28.1%; Score 29.5; DB 1; Length 17;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRVGE-EGVL 19
Db 2 GFVMEGAGVL 12

RESULT 47

PCT-US91-05801-10
Sequence 10, Application PC/TUS9105801
GENERAL INFORMATION:
APPLICANT: VIC. C. Knauf
APPLICANT: Gregory A. Thompson
TITLE OF INVENTION: Plant Fatty Acid Synthases
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calgene, Inc.
STREET: 1920 Fifth Street
CITY: Davis
STATE: CA
COUNTRY: USA
ZIP: 95616
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.0 MB
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.7
SOFTWARE: Microsoft Word 4.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/05801
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/568,493
FILING DATE: 15-AUGUST-1990
PRIOR APPLICATION DATA: 07/721,761
APPLICATION NUMBER: 07/721,761
FILING DATE: 26-JUNE-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elizabeth Laessen
REGISTRATION NUMBER: 31,845
NAME: Donna E. Scherer
REGISTRATION NUMBER: 34,719
REFERENCE/DOCKET NUMBER: CGNE 76-2 WO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (916) 753-6313
TELEFAX: (916) 753-1510
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US91-05801-10

Query Match 28.1%; Score 29.5; DB 4; Length 17;
Best Local Similarity 63.6%; Pred. No. 3.1e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 10 GRTVE-EGVL 19
DB 2 GFVMEGAGVL 12

RESULT 48
US-08-160-604-1
Sequence 1, Application US/08160604
Patent No. 6232522
GENERAL INFORMATION:
APPLICANT: Harley, John
APPLICANT: James, Judith A.
TITLE OF INVENTION: PEPTIDE INDUCTION OF AUTOIMMUNITY AND CLINICAL SYMPTOMATOLOGY
NUMBER OF SEQUENCES: 127
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabat
STREET: 1100 Peachtree Street, Suite 2800
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30309-4530
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/160,604
FILING DATE: 30-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/867,819
FILING DATE: 13-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/648,205
FILING DATE: 31-JAN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/472,947
FILING DATE: 31-JAN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(3)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-815-6508
TELEFAX: (404)-815-6555

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-08-160-604-1

Query Match 27.6%; Score 29; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PPPGMRPP 8

RESULT 49
US-08-475-955-123
Sequence 123, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabat
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-123

Query Match 27.6%; Score 29; DB 2; Length 8;

Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
| | | |
Db 1 PPPGMRPP 8

RESULT 50

US-09-718-693A-3
; Sequence 3, Application US/09718693A
; Patent No. 6642008
; GENERAL INFORMATION:
; APPLICANT: Oklahoma Medical Research Foundation
; APPLICANT: Harley, John B.
; APPLICANT: James, Judith A.
; APPLICANT: Kautman, Kenneth M.
; TITLE OF INVENTION: Assays and Therapies For Latent Viral Infection
; FILE REFERENCE: OMRP 177
; CURRENT APPLICATION NUMBER: US/09/718,693A
; PRIOR FILING DATE: 2000-11-22
; PRIOR FILING DATE: 1999-11-24
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 3
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
US-09-718-693A-3

Query Match 27.6%; Score 29; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
| | | |
Db 1 PPPGMRPP 8

RESULT 51

US-07-867-819D-147
; Sequence 147, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
; FILE REFERENCE: OMRP 114 CIP (2)
; CURRENT APPLICATION NUMBER: US/07/867,819D
; CURRENT FILING DATE: 1992-04-13
; PRIOR APPLICATION NUMBER: 07/472,947
; PRIOR FILING DATE: 1990-01-31
; PRIOR APPLICATION NUMBER: 07/648,205
; PRIOR FILING DATE: 1991-01-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 147
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-07-867-819D-147

Query Match 27.6%; Score 29; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
| | | |
Db 1 PPPGMRPP 8

RESULT 52

US-07-867-819D-149

; Sequence 149, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
; FILE REFERENCE: OMRP 114 CIP (2)
; CURRENT APPLICATION NUMBER: US/07/867,819D
; CURRENT FILING DATE: 1992-04-13
; PRIOR APPLICATION NUMBER: 07/472,947
; PRIOR FILING DATE: 1990-01-31
; PRIOR APPLICATION NUMBER: 07/648,205
; PRIOR FILING DATE: 1991-01-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 149
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-07-867-819D-149

Query Match 27.6%; Score 29; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
| | | |
Db 1 PPPGMRPP 8

RESULT 53

US-07-867-819D-157
; Sequence 157, Application US/07867819D
; Patent No. 6897287
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
; FILE REFERENCE: OMRP 114 CIP (2)
; CURRENT APPLICATION NUMBER: US/07/867,819D
; CURRENT FILING DATE: 1992-04-13
; PRIOR APPLICATION NUMBER: 07/472,947
; PRIOR FILING DATE: 1990-01-31
; PRIOR APPLICATION NUMBER: 07/648,205
; PRIOR FILING DATE: 1991-01-31
; NUMBER OF SEQ ID NOS: 161
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 157
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Homo sapiens
US-07-867-819D-157

Query Match 27.6%; Score 29; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
| | | |
Db 1 PPPGMRPP 8

RESULT 54

US-08-475-955-10
; Sequence 10, Application US/08475955
; Patent No. 6641813
; GENERAL INFORMATION:
; APPLICANT: Harley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; TITLE OF INVENTION: AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSES: Patrea L. Pabst
; STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
; CITY: Atlanta

STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 3..10
US-08-475-955-10

Query Match 27.6%; Score 29; DB 2; Length 11;
Best local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMRP 9
DB 3 PPGMRP 10

RESULT 55
US-07-867-819D-10
Sequence 10, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRP 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: Patentin version 3.1
SEQ ID NO 10
LENGTH: 11
TYPE: PRT
ORGANISM: homo sapien
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (3)..(10)

OTHER INFORMATION: Binding site
US-07-867-819D-10

Query Match 27.6%; Score 29; DB 2; Length 11;
Best local Similarity 62.5%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMRP 9
DB 3 PPGMRP 10

RESULT 56
US-08-475-955-14
Sequence 14, Application US/08475955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2) DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 3..10
NAME/KEY: Modified-site
LOCATION: 6
OTHER INFORMATION: /note= "The arginine at position 8 can be
OTHER INFORMATION: substituted with F, G, H, I, K, S, T, V,
OTHER INFORMATION: and Y."
US-08-475-955-14

Query Match 27.6%; Score 29; DB 2; Length 12;

Best Local Similarity 62.5%; Pred. No. 2.5e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 4 PPGKMRPP 11

RESULT 57

US-07-994-469A-21
Sequence 21, Application US/07994469A
Patent No. 5519119
GENERAL INFORMATION:
APPLICANT: Yamada, No. 5519119utosh
APPLICANT: Kato, Masanari
APPLICANT: Miyata, Keizo
APPLICANT: Aoyama, Yoshiyuki
APPLICANT: Shikama, Hiroshi
TITLE OF INVENTION: Polypeptide
NUMBER OF SEQUENCES: 101
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
ADDRESS: P.C. Jefferson Davis Highway, Fourth Floor
CITY: Arlington
STATE: Virginia
ZIP: 22202
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/994,469A
FILING DATE: 21-DEC-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Obion, No. 5519119man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 72-085-0 FWC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)413-3000
TELEFAX: (703)413-2220
TELEX: 248855 OPAT UR
INFORMATION FOR SEQ ID NO: 21:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-994-469A-21

Query Match 27.6%; Score 29; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 3.4e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMSPP 8
DB 1 DPGKMRPP 8

RESULT 58

US-08-482-142-186
Sequence 186, Application US/08482142
Patent No. 5820862
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean

APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,142
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/445,307
FILING DATE: 07-June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017.6US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-482-142-186

Query Match 27.6%; Score 29; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYBEGSVLS 20
DB 6 LVGDNGVLA 14

RESULT 59

US-08-478-572-186
Sequence 186, Application US/08478572
Patent No. 5968526
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mei-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLERGENS
FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESS:
ADDRESSEE: IMMULOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,572
FILING DATE: 07-June-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976
REFERENCE/DOCKET NUMBER: 017,605
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-478-572-186

Query Match 27.6%; Score 29; DB 1; Length 16;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYGEQVLS 20
DB 6 LVGDNGVLA 14

RESULT 60
US-08-484-296-186
Sequence 186, Application US/08484296
Patent No. 6268491
GENERAL INFORMATION:
APPLICANT: Garman, Richard
APPLICANT: Greenstein, Julia
APPLICANT: Kuo, Mel-chang
APPLICANT: Rogers, Bruce
APPLICANT: Franzen, Henry
APPLICANT: Chen, Xian
APPLICANT: Evans, Sean
APPLICANT: Shaked, Ze'ev
TITLE OF INVENTION: T CELL EPITOPES OF THE MAJOR ALLEGENS
TITLE OF INVENTION: FROM DERMATOPHAGOIDES (HOUSE DUST MITE)
NUMBER OF SEQUENCES: 207
CORRESPONDENCE ADDRESSES:
ADDRESSEE: IMMUNOLOGIC PHARMACEUTICAL CORPORATION
STREET: 610 LINCOLN STREET
CITY: WALTHAM
STATE: MA
COUNTRY: USA
ZIP: 02154
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII TEXT
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,296
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/445,307
FILING DATE: 07 June 1995
ATTORNEY/AGENT INFORMATION:
NAME: CRAIG, ANNE I.
REGISTRATION NUMBER: 32,976

REFERENCE/DOCKET NUMBER: 017,605
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 466-6000
TELEFAX: (617) 466-6040
INFORMATION FOR SEQ ID NO: 186:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
US-08-484-296-186

Query Match 27.6%; Score 29; DB 2; Length 16;
Best Local Similarity 55.6%; Pred. No. 3.4e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYGEQVLS 20
DB 6 LVGDNGVLA 14

RESULT 61
US-08-990-888-24
Sequence 24, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 24
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-24

Query Match 27.6%; Score 29; DB 2; Length 18;
Best Local Similarity 41.7%; Pred. No. 3.9e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGSPPGFIVG 14
DB 4 ALGVTPRWLAG 15

RESULT 62
US-08-990-888-46
Sequence 46, Application US/08990888B
Patent No. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 46
LENGTH: 18

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-46

Query Match 27.6%; Score 29; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGFIVG 14
DB 6 GVSMPGMLAG 15

RESULT 63
US-08-990-888-62
Sequence 62, Application US/08990888B
Patent No. 6387879

GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Britsette, Renee
APPLICANT: Carcano, Juan
APPLICANT: Mandeckl, Wlodeck S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 62
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-62

Query Match 27.6%; Score 29; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGFIVG 14
DB 6 GVSMPGMLAG 15

RESULT 64
US-09-010-999-8
Sequence 8, Application US/09010999
Patent No. 6132976
GENERAL INFORMATION:
APPLICANT: Poole, Anthony R.
APPLICANT: Hollander, Anthony P.
APPLICANT: Billingshurst, R. C.
TITLE OF INVENTION: IMMUNOASSAYS FOR THE MEASUREMENT OF
TITLE OF INVENTION: COLLAGEN DENATURATION AND CLEAVAGE IN CARTILAGE
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/010,999

FILING DATE: 22-JAN-1998
CLASSIFICATION: 4335
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/448,501
FILING DATE: 17-JUL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,123
FILING DATE: 04-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 032931/0212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 8:

SEQUENCE CHARACTERISTICS:

LENGTH: 19 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:

NAME/KEY: Modified-site

LOCATION: 6

OTHER INFORMATION: /product= "Pro(OH)"

US-09-010-999-8
Query Match 27.6%; Score 29; DB 2; Length 19;
Best Local Similarity 29.4%; Pred. No. 4.2e+02;
Matches 5; Conservative 5; Mismatches 7; Indels 0; Gaps 0;

QY 3 AKGMSPPGIVEBGLV 19
DB 2 AEGPYGQGLAGQGRGIV 18

RESULT 65
US-09-980-177A-77
Sequence 77, Application US/09980177A
Patent No. 6838084
GENERAL INFORMATION:
APPLICANT: Jochmus, Ingrid
APPLICANT: Nieland, John
TITLE OF INVENTION: Cytotoxic T-Cell Epitopes of the
TITLE OF INVENTION: Papilloma Virus L1-Protein and Use Thereof in Diagnosis and
FILE REFERENCE: 50125/036001
CURRENT APPLICATION NUMBER: US/09/980,177A
CURRENT FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: PCT/EP00/05006
PRIOR FILING DATE: 2000-05-31
PRIOR APPLICATION NUMBER: DE 19925199.1
PRIOR FILING DATE: 1999-06-01
NUMBER OF SEQ ID NOS: 77
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 77
LENGTH: 20
TYPE: PRT
ORGANISM: Influenza virus type A
US-09-980-177A-77

Query Match 27.6%; Score 29; DB 2; Length 20;
Best Local Similarity 83.3%; Pred. No. 4.4e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 GREGVL 19
DB 7 GREGVL 12

RESULT 66

US-10-007-700-413
Sequence 413, Application US/10007700
Patent No. 6960570
GENERAL INFORMATION:
APPLICANT: Wang, Tonglong
APPLICANT: Wang, Aljun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Recter, Marc W.
APPLICANT: Durham, Margareta
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darrick
APPLICANT: Matanabe, Yoshihiro
APPLICANT: Peckman, David W.
APPLICANT: Cal, Peng
APPLICANT: Roy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 459
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 413
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-007-700-413

Query Match 27.6%; Score 29; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GPVGGEG 17
DB 9 GATIGREG 16

RESULT 67
US-10-394-980-140
Sequence 140, Application US/10394980
Patent No. 6908740
GENERAL INFORMATION:
APPLICANT: Vandekerckhove, Joel
APPLICANT: Gevaert, Kris
TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USES THEREFOR
FILE REFERENCE: VBV-001
CURRENT APPLICATION NUMBER: US/10/394,980
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/EP02/03368
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US60/278,171
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US60/318,749
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US60/323,999
PRIOR FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 473
SOFTWARE: Patentin version 3.1
SEQ ID NO 140
LENGTH: 18
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: part of KPCL_HUMAN (P05771, protein kinase C, beta-I type)
US-10-394-980-140

Query Match 27.1%; Score 28.5; DB 2; Length 18;
Best Local Similarity 47.4%; Pred. No. 4.7e+02;
Matches 9; Conservative 1; Mismatches 6; Indels 3; Gaps 2;

QY 1 DPAKMSPPGFIIVEGCVL 19
DB 2 DPAAG-PPPS-EGESTV 17

RESULT 68
US-08-488-470A-7
Sequence 7, Application US/08488470A
Patent No. 5708153
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gallop, Mark A.
TITLE OF INVENTION: Method of Synthesizing Diverse
TITLE OF INVENTION: Collections of Oligomers
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSER: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,470A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/762,522
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1007E
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-812-8803
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-488-470A-7

Query Match 26.7%; Score 28; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
DB 1 PPGFI 5

RESULT 69
US-07-946-239-15
Sequence 15, Application US/07946239
Patent No. 5770358
GENERAL INFORMATION:
APPLICANT: DOWER, WILLIAM J
APPLICANT: BARRETT, RONALD W
APPLICANT: GALLOP, MARK A

APPLICANT: NEEDLES, MICHAEL C
TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
COLLECTIONS OF OLIGOMERS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: TOWNSEND AND TOWNSEND
STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
CITY: SAN FRANCISCO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/946,239
FILING DATE: 19920916
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Smith, William M.
REGISTRATION NUMBER: 30,223
REFERENCE/DOCKET NUMBER: 11509-36-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-543-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-07-946-239-15

Query Match 26.7%; Score 28; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12
DB 1 PGF1 5

RESULT 70
US-08-484-505A-7
Sequence 7, Application US/08484505A
Patent No. 5789162
GENERAL INFORMATION:
APPLICANT: Dower, William J.
APPLICANT: Barrett, Ronald W.
APPLICANT: Gallop, Mark A.
TITLE OF INVENTION: Method of Synthesizing Diverse
COLLECTIONS OF OLIGOMERS
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESS: Affymax Technologies, N.V.
STREET: 4001 Miranda Ave.
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,505A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,085

FILING DATE: 07-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/762,522
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1007B
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-496-2300
TELEFAX: 415-424-0832
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-505A-7

Query Match 26.7%; Score 28; DB 1; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12
DB 1 PGF1 5

RESULT 71
US-08-383-766-3
Sequence 3, Application US/08383766
Patent No. 6087186
GENERAL INFORMATION:
APPLICANT: Cargill, John
APPLICANT: Armstrong, Robert W.
TITLE OF INVENTION: METHODS AND APPARATUS FOR SYNTHESIZING
LABELED COMBINATORIAL CHEMISTRY LIBRARIES
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESS: Pennle and Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/383,766
FILING DATE: 01-FEB-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Halluin, Albert P.
REGISTRATION NUMBER: 25,227
REFERENCE/DOCKET NUMBER: 8140-009
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-854-3660
TELEFAX: 415-854-3694
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-383-766-3

Query Match 26.7%; Score 28; DB 2; Length 5;

Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12
1 PGF1 5

RESULT 72
US-09-151-467-15
; Sequence 15, Application US/09151467
; Patent No. 6140493
; GENERAL INFORMATION:
; APPLICANT: DOWER, WILLIAM J
; APPLICANT: BARRETT, RONALD W
; APPLICANT: GALLOP, MARK A
; TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
; TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND
; STREET: 1 MARKET PLAZA, STEWART TOWER, SUITE 2000
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151,467
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/07/946,239
; FILING DATE: 1992-09-16
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11509-36-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-543-9600
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-151-467-15

Query Match 26.7%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12
1 PGF1 5

RESULT 73
US-09-078-403A-7
; Sequence 7, Application US/09078403A
; Patent No. 6165717
; GENERAL INFORMATION:
; APPLICANT: DOWER, WILLIAM
; APPLICANT: BARRETT, RONALD
; APPLICANT: GALLOP, MARK
; TITLE OF INVENTION: Method of synthesizing diverse
; TITLE OF INVENTION: collections of compounds

NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Atiyah Research Institute
STREET: 4001 Miranda Avenue
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94034

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/078,403A
FILING DATE: 13-MAY-1998
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/484,505
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: 07/762,522
FILING DATE: 18-SEP-1991
ATTORNEY/AGENT INFORMATION:
NAME: Stevens, Lauren L.
REGISTRATION NUMBER: 36,691
REFERENCE/DOCKET NUMBER: 1007F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650 812 8803
TELEFAX: 650 424 0832
TELEX:
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-078-403A-7

Query Match 26.7%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF1 12
1 PGF1 5

RESULT 74
US-09-256-838-15
; Sequence 15, Application US/09256838
; Patent No. 6416949
; GENERAL INFORMATION:
; APPLICANT: DOWER, WILLIAM J
; APPLICANT: BARRETT, RONALD W
; APPLICANT: GALLOP, MARK A
; APPLICANT: NEEDLE, MICHAEL C
; TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
; TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND AND TOWNSEND
; STREET: 1 MARKET PLAZA, STEWART TOWER, SUITE 2000
; CITY: SAN FRANCISCO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:

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/ APPLICATION NUMBER: US/09/256,838
/ FILING DATE: 24-Feb-1999
/ CLASSIFICATION: <Unknown>
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US/07/946,239
/ FILING DATE: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-543-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ SEQUENCE DESCRIPTION: SEQ ID NO: 15:
US-09-256-838-15

Query Match          26.7%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPFFT 12
       ||||:
       1 PPFFT 5
Db

RESULT 75
US-09-261-718-3
/ Sequence 3, Application US/09261718
/ Patent No. 6417010
/ GENERAL INFORMATION:
/ APPLICANT: Cargill, John
/ APPLICANT: Armstrong, Robert W
/ TITLE OF INVENTION: Methods and Apparatus for Synthesizing Labeled
/ TITLE OF INVENTION: Combinatorial Chemistry Libraries
/ FILE REFERENCE: 7638-PA02C
/ CURRENT APPLICATION NUMBER: US/09/261,718
/ CURRENT FILING DATE: 1999-03-03
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 3
/ LENGTH: 5
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Peptide
US-09-261-718-3

Query Match          26.7%; Score 28; DB 2; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPFFT 12
       ||||:
       1 PPFFT 5
Db

RESULT 76
PCT-US92-07815-15
/ Sequence 15, Application PC/TUS9207815
/ GENERAL INFORMATION:
/ APPLICANT: DOWER, WILLIAM J
/ APPLICANT: BARRETT, RONALD W
/ APPLICANT: GALLOP, MARK A
/ APPLICANT: NEEDLES, MICHAEL C
/ TITLE OF INVENTION: METHOD OF SYNTHESIZING DIVERSE
/ TITLE OF INVENTION: COLLECTIONS OF OLIGOMERS
/ NUMBER OF SEQUENCES: 16
```

```
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: TOWNSEND AND TOWNSEND
/ STREET: 1 MARKET PLAZA, STEUART TOWER, SUITE 2000
/ CITY: SAN FRANCISCO
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94105
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: PCT/US92/07815
/ FILING DATE: 19920916
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Smith, William M.
/ REGISTRATION NUMBER: 30,223
/ REFERENCE/DOCKET NUMBER: 11509-36-1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 415-543-9600
/ TELEFAX: 415-543-5043
/ INFORMATION FOR SEQ ID NO: 15:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 5 amino acids
/ TYPE: AMINO ACID
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
PCT-US92-07815-15

Query Match          26.7%; Score 28; DB 4; Length 5;
Best Local Similarity 80.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPFFT 12
       ||||:
       1 PPFFT 5
Db

RESULT 77
US-08-475-955-117
/ Sequence 117, Application US/08475955
/ Patent No. 6641813
/ GENERAL INFORMATION:
/ APPLICANT: Harley, John
/ TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
/ TITLE OF INVENTION: AUTOANTIBODIES
/ NUMBER OF SEQUENCES: 218
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Patrea L. Pabst
/ STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
/ CITY: Atlanta
/ STATE: GA
/ COUNTRY: USA
/ ZIP: 30309-3450
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/475,955
/ FILING DATE: June 7, 1995
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/667,819
/ FILING DATE: April 13, 1992
/ CLASSIFICATION: 424
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 07/648,205
/ FILING DATE: January 31, 1991
/ PRIOR APPLICATION DATA:
```

APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795
INFORMATION FOR SEQ ID NO: 117:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-117

Query Match 26.7%; Score 28; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PPGMWTP 8

RESULT 78
US-07-867-819D-117
Sequence 117, Application US/07867819D
Patent No. 6897287
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: Methods and Reagents for Diagnosis of Autoantibodies
FILE REFERENCE: OMRP 114 CIP (2)
CURRENT APPLICATION NUMBER: US/07/867,819D
CURRENT FILING DATE: 1992-04-13
PRIOR APPLICATION NUMBER: 07/472,947
PRIOR FILING DATE: 1990-01-31
PRIOR APPLICATION NUMBER: 07/648,205
PRIOR FILING DATE: 1991-01-31
NUMBER OF SEQ ID NOS: 161
SOFTWARE: PatentIn version 3.1
SEQ ID NO 117
LENGTH: 8
TYPE: PRT
ORGANISM: homo sapien
US-07-867-819D-117

Query Match 26.7%; Score 28; DB 2; Length 8;
Best Local Similarity 62.5%; Pred. No. 4.6e+05;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PPGMWTP 8

RESULT 79
US-09-769-180-31
Sequence 31, Application US/09769180
Patent No. 6680173
GENERAL INFORMATION:
APPLICANT: VanMechelen, Eugene
APPLICANT: Vanderstichelen, Hugo
TITLE OF INVENTION: Diagnosis of Tauopathies
FILE REFERENCE: US 112,1181
CURRENT APPLICATION NUMBER: US/09/769,180
CURRENT FILING DATE: 2001-01-24
PRIOR APPLICATION NUMBER: EP 00870008.8
PRIOR FILING DATE: 2000-01-24
PRIOR APPLICATION NUMBER: EP 00870280.5
PRIOR FILING DATE: 2000-11-22

PRIOR APPLICATION NUMBER: US 60/178,391
PRIOR FILING DATE: 2000-01-27
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.0
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
US-09-769-180-31

Query Match 26.7%; Score 28; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 KGMSPPG 10
DB 1 RGAAPPG 7

RESULT 80
US-08-476-509B-30
Sequence 30, Application US/08476509B
Patent No. 6034212
GENERAL INFORMATION:
APPLICANT: SUDOL, MARIUS
APPLICANT: PEER, BORK
APPLICANT: HENRY, CHEN
TITLE OF INVENTION: A SH2 DOMAIN ASSOCIATED PROTEIN, A
TITLE OF INVENTION: SIGNALING DOMAIN THEREIN, NUCLEIC ACIDS ENCODING THE
TITLE OF INVENTION: PROTEIN AND THE DOMAIN, AND DIAGNOSTIC AND THERAPEUTICS
NUMBER OF SEQUENCES: 50
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,509B
FILING DATE: 01-DEC-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Bsq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-101 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521

INFORMATION FOR SEQ ID NO: 30:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: Peptide
HYPOTHETICAL: NO
US-08-476-509B-30

Query Match 26.7%; Score 28; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGTVG 14
DB 1 GTPPPYTVG 10

RESULT 81
US-08-915-498B-22
Sequence 22, Application US/08915498B
Patent No. 6132954
GENERAL INFORMATION:
APPLICANT: James R. Lupski, Robert A. Britton, Donald L.
APPLICANT: Court and Bradford S. Powell
TITLE OF INVENTION: Methods of Screening for Agents that
TITLE OF INVENTION: Delay a Cell Cycle and Compositions Comprising ERA and an Anal
TITLE OF INVENTION: of Wild-Type ERA
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodburn Kurtz Mackiewicz
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE, 3.5 INCH, 1.44 Mb STORAGE
COMPUTER: IBM PS/2
OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPERFECT for WINDOWS 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/915,498B
FILING DATE: August 20, 1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/023,353
FILING DATE: August 20, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Lori Y. Beardsell
REGISTRATION NUMBER: 34,293
REFERENCE/DOCKET NUMBER: BYLR-0037
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 11
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-915-498B-22

Query Match 26.7%; Score 28; DB 2; Length 11;
Best Local Similarity 36.4%; Pred. No. 3.3e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 SPFGPIVBEQ 17
DB 1 SOKGIVIGKKG 11

RESULT 82
US-10-394-980-15
Sequence 15, Application US/10394980
Patent No. 6908740
GENERAL INFORMATION:
APPLICANT: Vandekerckhove, Joel
APPLICANT: Gevaert, Kris
TITLE OF INVENTION: METHODS AND APPARATUS FOR GEL-FREE QUALITATIVE AND
TITLE OF INVENTION: QUANTITATIVE PROTEOME ANALYSIS, AND USBS THEREFOR
FILE REFERENCE: VBV-001
CURRENT APPLICATION NUMBER: US/10/394,980
CURRENT FILING DATE: 2003-03-21
PRIOR APPLICATION NUMBER: PCT/EP02/03368
PRIOR FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: US60/278,171
PRIOR FILING DATE: 2001-03-22

PRIOR APPLICATION NUMBER: US60/318,749
PRIOR FILING DATE: 2001-09-12
PRIOR APPLICATION NUMBER: US60/323,999
PRIOR FILING DATE: 2001-09-20
NUMBER OF SEQ ID NOS: 473
SOFTWARE: PatentIn version 3.1
SEQ ID NO 15
LENGTH: 12
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
OTHER INFORMATION: part of GSHR_HUMAN ((P22352) plasma glutathione peroxidase precur
US-10-394-980-15

Query Match 26.7%; Score 28; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 PIVGEGV 18
DB 1 FLVGPDI 8

RESULT 83
US-08-630-916A-6
Sequence 6, Application US/08630916A
Patent No. 6011137
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-6

Query Match 26.7%; Score 28; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGIVG 14

Db 3 GTPEPPYTVG 12

RESULT 84
US-08-630-916A-85
Sequence 85, Application US/08630916A
Patent No. 601137
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
INFORMATION FOR SEQ ID NO: 85:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-85

Query Match 26.7%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPGFIVG 14
Db 2 GTPEPPYTVG 11

RESULT 85
US-08-630-915A-141
Sequence 141, Application US/08630915A
Patent No. 6309820
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6309820h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas

CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/630,915A
FILING DATE: 03-APR-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-915A-141

Query Match 26.7%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 GMSPPGFIVG 14
Db 2 GTPEPPYTVG 11

RESULT 86
US-09-879-957-141
Sequence 141, Application US/09879957
Patent No. 6709821
GENERAL INFORMATION:
APPLICANT: SPARKS, Andrew B.
APPLICANT: HOFFMAN, No. 6709821h
APPLICANT: KAY, Brian K.
APPLICANT: FOWLKES, Dana M.
APPLICANT: MCCONNELL, Stephen J.
TITLE OF INVENTION: POLYPEPTIDES HAVING A FUNCTIONAL
DOMAIN OF INTEREST AND METHODS OF IDENTIFYING AND
USING SAME
NUMBER OF SEQUENCES: 227
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/879,957
FILING DATE: 13-Jun-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,915
FILING DATE: 03-APR-1996
ATTORNEY/AGENT INFORMATION:

NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-174
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 141:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-09-879-957-141

Query Match 26.7%; Score 28; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14
DB 2 GTPPPPTVG 11

RESULT 87
5187078-4
PATENT NO. 5187078
APPLICANT: OHYA, MASAMI;MIZOGUCHI, JUNZO;ONOZAWA, TAKASHI
TITLE OF INVENTION: PLASMA-TYPE GLUTATHIONE PEROXIDASE GENE
AND APPLICATION OF THE SAME
NUMBER OF SEQUENCES: 24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/540,115
FILING DATE: 19-JUN-1990
SEQ ID NO: 4;
LENGTH: 15
5187078-4

Query Match 26.7%; Score 28; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 FIVGEGV 18
DB 5 FLVGPQGI 12

RESULT 88
US-08-630-916A-9
SEQUENCE 9, Application US/08630916A
PATENT NO. 6011137
GENERAL INFORMATION:
APPLICANT: Pitozzi, Gregorio
APPLICANT: Kay, Brian K.
APPLICANT: Fowlkes, Dana W.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
TITLE OF INVENTION: POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Penile & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: United States
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/630,916A
FILING DATE: 03-APR-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MISTROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-203
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 896-8864/9741
TELEFAX: (212) 896-8864/9741
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-630-916A-9

Query Match 26.7%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14
DB 6 GTPPPPTVG 15

RESULT 89
US-08-990-888-30
SEQUENCE 30, Application US/08990888B
PATENT NO. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002
CURRENT APPLICATION NUMBER: US/08/990,888B
CURRENT FILING DATE: 1997-12-15
NUMBER OF SEQ ID NOS: 81
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 30
LENGTH: 18
TYPE: PPT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-30

Query Match 26.7%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 5.7e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGPIVG 14
DB 6 GLTPGWLIG 15

RESULT 90
US-08-990-888-69
SEQUENCE 69, Application US/08990888B
PATENT NO. 6387879
GENERAL INFORMATION:
APPLICANT: Blume, Arthur J.
APPLICANT: Brissette, Renee
APPLICANT: Carcamo, Juan
APPLICANT: Mandeckl, Wlodeck S.
APPLICANT: Tang, Pauline M.
TITLE OF INVENTION: Assays For Compounds Which Bind Growth Hormone Receptor
FILE REFERENCE: 2598-4002

/ CURRENT APPLICATION NUMBER: US/08/990,888B
/ CURRENT FILING DATE: 1997-12-15
/ NUMBER OF SEQ ID NOS: 81
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 69
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: H5 peptide secondary library sequence
US-08-990-888-69

Query Match 26.7%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGFIVG 14
DB 6 GVTWPGMIG 15

RESULT 91
US-09-292-225-12
/ Sequence 12, Application US/09292225
/ Patent No. 6455686
/ GENERAL INFORMATION:
/ APPLICANT: McCall, Catherine A.
/ APPLICANT: Hunter, Shirley Wu
/ APPLICANT: Weber, Eric R.
/ TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
/ FILE REFERENCE: AL-2-C3
/ CURRENT APPLICATION NUMBER: US/09/292,225
/ EARLIER FILING DATE: 1999-04-15
/ EARLIER APPLICATION NUMBER: 60/098,909
/ EARLIER FILING DATE: 1998-09-02
/ EARLIER APPLICATION NUMBER: 60/085,295
/ EARLIER FILING DATE: 1998-05-13
/ EARLIER APPLICATION NUMBER: 60/098,565
/ EARLIER FILING DATE: 1998-04-17
/ EARLIER APPLICATION NUMBER: 09/062,013
/ EARLIER FILING DATE: 1998-04-17
/ NUMBER OF SEQ ID NOS: 49
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 12
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Dermatophagoides farinae
US-09-292-225-12

Query Match 26.7%; Score 28; DB 2; Length 18;
Best Local Similarity 85.7%; Pred. No. 5.7e+02;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYGESEV 18
DB 12 IYGESEV 18

RESULT 92
US-09-570-022-12
/ Sequence 12, Application US/09570022
/ Patent No. 6573244
/ GENERAL INFORMATION:
/ APPLICANT: MOORAD, RICHARD K.
/ APPLICANT: MOORAD, DEBORAH R.
/ APPLICANT: DOCTOR, BHUPENDRA P.
/ APPLICANT: GARCIA, GREGORY E.
/ TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
/ TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
/ FILE REFERENCE: 38644-170531
/ CURRENT APPLICATION NUMBER: US/09/570,022
/ CURRENT FILING DATE: 2000-05-12

/ PRIOR APPLICATION NUMBER: 60/134,446
/ PRIOR FILING DATE: 1999-05-17
/ NUMBER OF SEQ ID NOS: 26
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-09-570-022-12

Query Match 26.7%; Score 28; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 5.7e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGFI 12
DB 5 AKGLQPPGIL 14

RESULT 93
US-09-068-624-2
/ Sequence 2, Application US/09068624
/ Patent No. 6184346
/ GENERAL INFORMATION:
/ APPLICANT: KANG, KE-WON
/ APPLICANT: KIN, DONG-RYOUNG
/ TITLE OF INVENTION: NOVEL PROTEASE INHIBITORS
/ TITLE OF INVENTION: DERIVED FROM GUANERIN
/ NUMBER OF SEQUENCES: 3
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Knobbe, Martens, Olson & Bear
/ STREET: 620 Newport Center Drive 16th Floor
/ CITY: Newport Beach
/ STATE: CA
/ COUNTRY: U.S.A.
/ ZIP: 92660
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ COMPUTER: IBM Compatible
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FastSeq Version 1.5
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/068,624
/ FILING DATE:
/ CLASSIFICATION: 514
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER:
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Altman, Daniel B
/ REGISTRATION NUMBER: 34,115
/ REFERENCE/DOCKET NUMBER: HYLEB16.001APC
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 714-760-0404
/ TELEFAX: 714-760-9502
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 19 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
US-09-068-624-2

Query Match 26.7%; Score 28; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGLIVGEG 17

Db 10 PNGFKVDENG 19

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RESULT 94
US-09-068-624-3
; Sequence 3, Application US/09068624
; Patent No. 6184346
; GENERAL INFORMATION:
; APPLICANT: KANG, KE-MON
; TITLE OF INVENTION: NOVEL PROTEASE INHIBITORS
; TITLE OF INVENTION: DERIVED FROM GUAMERIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Knobbe, Martens, Olson & Bear
; STREET: 620 Newport Center Drive 16th Floor
; CITY: Newport Beach
; STATE: CA
; COUNTRY: U.S.A.
; ZIP: 92660
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/068,624
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; NAME: Altman, Daniel E
; REGISTRATION NUMBER: 34,115
; REFERENCE/DOCKET NUMBER: HYDEB16.001APC
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 714-760-0404
; TELEFAX: 714-760-9502
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; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-09-068-624-3
Query Match 26.7%; Score 28; DB 2; Length 19;
Best Local Similarity 60.0%; Pred. No. 6.1e+02;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 8 PPGFVGEEG 17
Db 10 PNGFKVDENG 19
RESULT 95
US-07-956-848A-17
; Sequence 17, Application US/07956848A
; Patent No. 5447914
; GENERAL INFORMATION:
; APPLICANT: Travels, James
; APPLICANT: Shafer, William M.
; APPLICANT: Bangalore, Neellesh
; APPLICANT: Pohl, Jan
; TITLE OF INVENTION: Antimicrobial Peptides
; NUMBER OF SEQUENCES: 59
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Greenlee and Winner, P.C.
; STREET: 5370 Manhattan Circle, Suite 201

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; CITY: Boulder
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80303
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/956,848A
; FILING DATE: 02-OCT-1992
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Peiber, Donna M.
; REGISTRATION NUMBER: 33,878
; REFERENCE/DOCKET NUMBER: 3-90B
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (303) 499-8080
; TELEFAX: (303) 499-8089
;
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
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US-07-956-848A-17
Query Match 26.7%; Score 28; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
Qy 10 GPVGESEVL 19
Db 11 GFLVREDPEVL 20

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RESULT 96
US-08-468-514-7
; Sequence 7, Application US/08468514
; Patent No. 5576296
; GENERAL INFORMATION:
; APPLICANT: Bartfai, Tomas
; APPLICANT: Hofkfelt, Tomas
; APPLICANT: Langell, Ulo
; APPLICANT: Ahren, Bo
; APPLICANT: Lindskog, Stefan
; APPLICANT: Console, Silvana
; APPLICANT: Land, Tilt
; APPLICANT: Wiesenfeld-Hallin, Zuzsanna
; TITLE OF INVENTION: GALANIN ANTAGONIST
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: White & Case
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: NY
; COUNTRY: USA
; ZIP: 10036-2787
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,514
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/146,139
; FILING DATE: 12-NOV-1993

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APPLICATION NUMBER: PCT/SE92/00316
FILING DATE: 14-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: SE 9104472-0
FILING DATE: 15-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Steiner Ph.D., Richard J.
REGISTRATION NUMBER: 35,372
REFERENCE/DOCKET NUMBER: 1103326-074
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-819-8783
TELEFAX: 212-354-8113
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
FEATURE:
NAME/KEY: Modified-site
LOCATION: 20
OTHER INFORMATION: /note= "amide or free acid"
US-08-468-514-7

Query Match 26.7%; Score 28; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 6.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 MSPPGF 11
Db 11 LGPPGF 16

RESULT 97
US-08-471-956-17
Sequence 17, Application US/08471956
Patent No. 5798336
GENERAL INFORMATION:
APPLICANT: Travel, James
APPLICANT: Shafer, William M.
APPLICANT: Bangalore, Neelesh
APPLICANT: Pohl, Jan
TITLE OF INVENTION: Antimicrobial Peptides
NUMBER OF SEQUENCES: 59
CORRESPONDENCE ADDRESS:
ADDRESSER: Greenlee and Winner, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: USA
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/471,956
FILING DATE: 06-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/956,848
FILING DATE: 02-OCT-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/541,635
FILING DATE: 21-JUN-1990
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 3-90D
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080

TELEFAX: (303) 499-8089
TELEX: 43617824
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-471-956-17

Query Match 26.7%; Score 28; DB 1; Length 20;
Best Local Similarity 60.0%; Pred. No. 6.5e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFIVGEGVL 19
Db 11 GFLVRDPLV 20

RESULT 98
US-08-786-455B-2
Sequence 2, Application US/08786455B
Patent No. 6193971
GENERAL INFORMATION:
APPLICANT: HORMANN, Joachim
APPLICANT: SCHMID, Karlheinz
TITLE OF INVENTION: DICTYOCALUS VIVIPARUS ANTIGEN FOR
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Foley & Lardner
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,455B
FILING DATE: 21-JAN-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 196 01 754.8
FILING DATE: 19-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: GRANDOS, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 18748/327
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-786-455B-2

Query Match 26.7%; Score 28; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 6.5e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DPAKGMSP 9
Db 5 DPASGVLDP 13

RESULT 99
US-09-715-838A-6
Sequence 6, Application US/09715838A
Patent No. 6846907
GENERAL INFORMATION:
APPLICANT: Shaugnessy, S.
APPLICANT: Austin, R.
TITLE OF INVENTION: OSTROPOROSIS TREATMENT
FILE REFERENCE: MDSP-P03-180
CURRENT APPLICATION NUMBER: US/09/715,838A
CURRENT FILING DATE: 2000-11-17
PRIOR APPLICATION NUMBER: PCT/CA99/00516
PRIOR FILING DATE: 1999-05-19
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin version 3.1
SEQ ID NO 6
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-715-838A-6

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Best Local Similarity 42.9%; Pred. No. 7.8e+02;
Matches 6; Conservative 3; Mismatches 2; Indels 3; Gaps 1;

QY 1 DPAKGM---SPGPF 11
DB 6 DPGGLRVESVPGY 19

RESULT 100
US-08-475-955-195
Sequence 195, Application US/084755955
Patent No. 6641813
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
TITLE OF INVENTION: AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patrea L. Pabat
STREET: 2800 One Atlantic Center, 1250 West Peachtree Street
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3450
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/475,955
FILING DATE: June 7, 1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP14CIP(2)DIV
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-873-8794
TELEFAX: (404)-873-8795

INFORMATION FOR SEQ ID NO: 195:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-475-955-195

Query Match 25.7%; Score 27; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSP 9
DB 1 PCKGTTP 8

Search completed: January 20, 2006, 19:14:13
Job time : 21.9615 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 20, 2006, 19:11:21 ; Search time 72.1154 Seconds
(without alignments)
115.878 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105

Sequence: 1 DPAKGMSPGFIVGEEGVLS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

Published Applications AA Main:*

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2: /cgn2_6/prodata/1/pubppa/US08_PUBCOMB.pep:*

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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4	34	32.4	8	4 US-10-012-756-6	Sequence 6, Appl1
5	34	32.4	8	4 US-10-376-121A-116	Sequence 116, Appl1
6	34	32.4	9	4 US-10-376-121A-100	Sequence 100, Appl1
7	33	31.4	15	3 US-09-953-510-67	Sequence 67, Appl1
8	33	31.4	15	3 US-09-953-413-67	Sequence 67, Appl1
9	33	31.4	15	5 US-10-147-255-67	Sequence 67, Appl1
10	33	31.4	15	5 US-10-695-155-67	Sequence 67, Appl1
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17	33	31.4	20	5 US-10-860-790-603	Sequence 603, Appl1
18	33	31.4	20	5 US-10-661-156-146	Sequence 146, Appl1
19	32	30.5	16	3 US-09-838-785-26	Sequence 26, Appl1
20	32	30.5	16	5 US-10-953-901-593	Sequence 593, Appl1
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22	31	29.5	14	4 US-10-307-956-25	Sequence 25, Appl1
23	31	29.5	17	5 US-10-211-088-356	Sequence 356, Appl1
24	31	29.5	17	5 US-10-950-163-8	Sequence 8, Appl1
25	31	29.5	18	3 US-09-999-781-10	Sequence 10, Appl1
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27	31	29.5	18	5 US-10-854-646-13	Sequence 13, Appl1

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29	31	29.5	20	3 US-09-897-778-463	Sequence 463, Appl1
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33	31	29.5	20	4 US-10-313-986-541	Sequence 541, Appl1
34	31	29.5	20	5 US-10-775-972-463	Sequence 463, Appl1
35	31	29.5	20	5 US-10-775-972-541	Sequence 541, Appl1
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45	30	28.6	13	5 US-10-972-236A-27	Sequence 27, Appl1
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50	30	28.6	16	4 US-10-285-394-376	Sequence 376, Appl1
51	30	28.6	18	4 US-10-029-386-32096	Sequence 32096, A
52	30	28.6	18	5 US-10-862-195-907	Sequence 907, Appl1
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54	29.5	28.1	7	3 US-10-307-956-24	Sequence 24, Appl1
55	29	27.6	7	3 US-09-990-832C-57	Sequence 57, Appl1
56	29	27.6	8	4 US-10-012-756-4	Sequence 4, Appl1
57	29	27.6	8	5 US-10-646-132-3	Sequence 3, Appl1
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91	29	27.6	15	4 US-10-224-999A-2949	Sequence 2949, Appl1
92	29	27.6	15	4 US-10-128-520-38	Sequence 38, Appl1
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ALIGNMENTS

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RESULT 1
US-10-218-743-4
; Sequence 4, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-4

Query Match          100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFIVGEGVLS 20
| | | | | | | | | | | | | | | | | | | | | |
DB 1 DPAKMSPPGFIVGEGVLS 20

RESULT 2
US-10-218-743-13
; Sequence 13, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
```

```
; ORGANISM: Dermatophagoides farinae
US-10-218-743-13

Query Match          100.0%; Score 105; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.1e-08;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFIVGEGVLS 20
| | | | | | | | | | | | | | | | | | | | | |
DB 1 DPAKMSPPGFIVGEGVLS 20

RESULT 3
US-10-280-066-302
; Sequence 302, Application US/10280066
; Publication No. US20030180718A1
; GENERAL INFORMATION:
; APPLICANT: Pillutla, Renuka C.
; APPLICANT: Brissette, Renee
; APPLICANT: Spruyt, Michael
; APPLICANT: Dedova, Olga
; APPLICANT: Blume, Arthur J.
; APPLICANT: Prendergast, John
; APPLICANT: Goldstein, Neil I.
; TITLE OF INVENTION: TARGET SPECIFIC SCREENING AND ITS USE FOR IDENTIFYING TARGET BIND
; FILE REFERENCE: 2598-4009US1
; CURRENT APPLICATION NUMBER: US/10/280,066
; CURRENT FILING DATE: 2002-10-24
; PRIOR APPLICATION NUMBER: 60/345,471
; PRIOR FILING DATE: 2001-10-24
; NUMBER OF SEQ ID NOS: 537
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 302
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Escherichia coli
; FEATURE:
; NAME/KEY: MISC FEATURE
; OTHER INFORMATION: DGIS-20M-4-E4
US-10-280-066-302

Query Match          33.3%; Score 35; DB 4; Length 20;
Best Local Similarity 53.3%; Pred. No. 3.7e+02;
Matches 8; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 5 GKSPGPFIVGEGVL 19
| | | | | | | | | | | | | | | | | |
DB 2 GRLPPMGLVGERGGL 16

RESULT 4
US-10-012-756-6
; Sequence 6, Application US/10012756
; Publication No. US20020164355A1
; GENERAL INFORMATION:
; APPLICANT: John B. Harley and Judith A. James
; TITLE OF INVENTION: Diagnostics And Therapy Of Epstein-Barr
; TITLE OF INVENTION: Virus In Autoimmune Disorders
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Patricia L. Pabst
; STREET: 2800 One Atlantic Center
; CITY: Atlanta
; STATE: Georgia
; COUNTRY: USA
; ZIP: 30306-3450
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
```

APPLICATION NUMBER: US/10/012,756
FILING DATE: 24-Oct-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/81,296
FILING DATE: 13-JAN-1997
APPLICATION NUMBER: 60/019,053
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: 08/160,604
FILING DATE: 30-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-10-012-756-6

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PAKGMRPP 8

RESULT 5
US-10-376-121A-116
Sequence 116, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 116:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 116:
US-10-376-121A-116

Query Match 32.4%; Score 34; DB 4; Length 8;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PAKGMRPP 8

RESULT 6
US-10-376-121A-100
Sequence 100, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 100:
SEQUENCE CHARACTERISTICS:
LENGTH: 9 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURES:
NAME/KEY: Binding-site
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 100:

US-10-376-121A-100

Query Match 32.4%; Score 34; DB 4; Length 9;
Best Local Similarity 75.0%; Pred. No. 1.7e+06;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 9
2 PAKGMP 9
2 PAKGMP 9

RESULT 7
US-09-953-510-67

; Sequence 67, Application US/09953510
; Patent No. US20020131975A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,510

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:

TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-510-67

Query Match 31.4%; Score 33; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMP 8
1 DPAKMP 8
1 DPAKMP 8

Db 4 DPGQMP 11

RESULT 8
US-09-953-413-67
; Sequence 67, Application US/09953413
; Publication No. US20040018209A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.

TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use

NUMBER OF SEQUENCES: 91

CORRESPONDENCE ADDRESS:

ADDRESSEE: Kurt A. Maclean

STREET: 2029 Century Park East, Suite 3800

CITY: Los Angeles

STATE: California

COUNTRY: U.S.A.

ZIP: 90067

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0,
Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/953,413

FILING DATE: 14-Sep-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/447,398

FILING DATE: 23-MAY-1995

APPLICATION NUMBER: US 08/289,667

FILING DATE: 12-AUG-1994

APPLICATION NUMBER: US 08/156,358

FILING DATE: 23-NOV-1993

ATTORNEY/AGENT INFORMATION:

NAME: Maclean, Kurt A.

REGISTRATION NUMBER: 31,118

REFERENCE/DOCKET NUMBER: 112-272

TELECOMMUNICATION INFORMATION:

TELEPHONE: (310) 788-5000

TELEFAX: (310) 277-1297

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 15 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

MOLECULE TYPE: linear

HYPOTHETICAL: NO

ANTI-SENSE: NO

FRAGMENT TYPE: Internal

ORIGINAL SOURCE:

ORGANISM: Mycobacterium tuberculosis

STRAIN: Erdman

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-953-413-67

Query Match 31.4%; Score 33; DB 3; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKMP 8
1 DPAKMP 8
4 DPGQMP 11

RESULT 9

US-10-147-255-67

; Sequence 67, Application US/10147255
; Publication No. US20030152584A1

GENERAL INFORMATION:

APPLICANT: Horwitz, Marcus A.
TITLE OF INVENTION: Abundant Extracellular
Products and Methods for Their Production and Use
NUMBER OF SEQUENCES: 91
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kurt A. Maclean
STREET: 2029 Century Park East, Suite 3800
CITY: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90067
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/147,255
FILING DATE: 15-May-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/226,539A
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/447,398
FILING DATE: 23-MAY-1995
APPLICATION NUMBER: US 08/289,667
FILING DATE: 12-AUG-1994
APPLICATION NUMBER: US 08/156,358
FILING DATE: 23-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Maclean, Kurt A.
REGISTRATION NUMBER: 31,118
REFERENCE/DOCKET NUMBER: 112-272
TELECOMMUNICATION INFORMATION:
TELEPHONE: (310) 788-5000
TELEFAX: (310) 277-1297
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHEICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Mycobacterium tuberculosis
STRAIN: Erdman
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-10-147-255-67
Query Match 31.4%; Score 33; DB 4; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DPAKMSF 8
DB 4 DPGQMGF 11
RESULT 10
US-10-695-155-67
Sequence 67, Application US/10695155
Publication No. US2004022873A1
GENERAL INFORMATION:
APPLICANT: HORWITZ, MARCUS A.
APPLICANT: HARTH, GUNTER
APPLICANT: LEE, BAI-YU
TITLE OF INVENTION: ABUNDANT EXTRACELLULAR PRODUCTS AND METHODS FOR THEIR PRODUCTION
AND USE
FILE REFERENCE: 51326-00004

CURRENT APPLICATION NUMBER: US/10/695,155
CURRENT FILING DATE: 2003-10-27
PRIOR APPLICATION NUMBER: 08/652,842
PRIOR FILING DATE: 1996-03-23
PRIOR APPLICATION NUMBER: 08/568,357
PRIOR FILING DATE: 1995-12-06
PRIOR APPLICATION NUMBER: 08/551,149
PRIOR FILING DATE: 1995-10-31
PRIOR APPLICATION NUMBER: 08/447,398
PRIOR FILING DATE: 1995-05-23
PRIOR APPLICATION NUMBER: 08/289,667
PRIOR FILING DATE: 1994-08-12
PRIOR APPLICATION NUMBER: 08/156,358
PRIOR FILING DATE: 1993-11-23
PRIOR APPLICATION NUMBER: 08/545,926
PRIOR FILING DATE: 1995-10-20
NUMBER OF SEQ ID NOS: 167
SOFTWARE: Patentin version 3.2
SEQ ID NO 67
LENGTH: 15
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-695-155-67
Query Match 31.4%; Score 33; DB 5; Length 15;
Best Local Similarity 62.5%; Pred. No. 5.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 1 DPAKMSF 8
DB 4 DPGQMGF 11
RESULT 11
US-09-884-441-397
Sequence 397, Application US/09884441
Patent No. US20020119158A1
GENERAL INFORMATION:
APPLICANT: Algate, Paul A.
APPLICANT: Carter, Darlick
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
DIAGNOSIS OF OVARIAN CANCER
FILE REFERENCE: 210121.462c7
CURRENT APPLICATION NUMBER: US/09/884,441
CURRENT FILING DATE: 2001-06-18
NUMBER OF SEQ ID NOS: 489
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 397
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-884-441-397
Query Match 31.4%; Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
QY 13 VGESEGVLS 20
DB 3 IGEDGILS 10
RESULT 12
US-09-907-969-397
Sequence 397, Application US/09907969
Publication No. US20030091580A1
GENERAL INFORMATION:
APPLICANT: Mitcham, Jennifer L.
APPLICANT: King, Gordon B.
APPLICANT: Algate, Paul A.
APPLICANT: Fling, Steven P.
APPLICANT: Retter, Marc W.
APPLICANT: Fanger, Gary Richard

```
/ APPLICANT: Reed, Steven G.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Hill, Paul
/ APPLICANT: Albane, Earl
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C8
/ CURRENT APPLICATION NUMBER: US/09/907,969
/ CURRENT FILING DATE: 2001-07-17
/ NUMBER OF SEQ ID NOS: 596
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-907-969-397
```

```
Query Match      31.4%; Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 VGEBCVLS 20
       :||:|:|
Db      3 IGEDGILS 10
```

```
RESULT 13
US-09-827-271-397
/ Sequence 397, Application US/09827271
/ Publication No. US20030165504A1
/ GENERAL INFORMATION:
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
/ FILE REFERENCE: 210121.462C6
/ CURRENT APPLICATION NUMBER: US/09/827,271
/ CURRENT FILING DATE: 2001-04-04
/ NUMBER OF SEQ ID NOS: 461
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-827-271-397
```

```
Query Match      31.4%; Score 33; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 VGEBCVLS 20
       :||:|:|
Db      3 IGEDGILS 10
```

```
RESULT 14
US-10-198-053-397
/ Sequence 397, Application US/10198053
/ Publication No. US20030124140A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C9
/ CURRENT APPLICATION NUMBER: US/10/198,053
/ CURRENT FILING DATE: 2002-07-17
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
```

```
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-198-053-397
```

```
Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 VGEBCVLS 20
       :||:|:|
Db      3 IGEDGILS 10
```

```
RESULT 15
US-10-198-053-603
/ Sequence 603, Application US/10198053
/ Publication No. US20030124140A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C9
/ CURRENT APPLICATION NUMBER: US/10/198,053
/ CURRENT FILING DATE: 2002-07-17
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 603
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-198-053-603
```

```
Query Match      31.4%; Score 33; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 VGEBCVLS 20
       :||:|:|
Db      3 IGEDGILS 10
```

```
RESULT 16
US-10-860-790-397
/ Sequence 397, Application US/10860790
/ Publication No. US20050031634A1
/ GENERAL INFORMATION:
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ APPLICANT: Hill, Paul
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.462C11
/ CURRENT APPLICATION NUMBER: US/10/860,790
/ CURRENT FILING DATE: 2004-06-02
/ NUMBER OF SEQ ID NOS: 624
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 397
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-860-790-397
```

```
Query Match      31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 VGEBCVLS 20
       :||:|:|
```


Db 3 IGEDGILS 10

RESULT 17
US-10-860-790-603
Sequence 603, Application US/10860790
Publication No. US20050031634A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaitanya S.
APPLICANT: Retter, Marc W.
APPLICANT: Ronger, Gary R.
APPLICANT: Hill, Paul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.462C11
CURRENT APPLICATION NUMBER: US/10/860.790
PRIORITY FILING DATE: 2004-06-02
NUMBER OF SEQ ID NOS: 624
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 603
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-860-790-603

Query Match 31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 7.4e+02;
Matches 5; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY 13 VGESEGVLS 20
:|:|:|:
Db 3 IGEDGILS 10

RESULT 18
US-10-661-156-146
Sequence 146, Application US/10661156
Publication No. US20050100963A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussac, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khuzana, Sucha
APPLICANT: Linder, Karen E.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappan, Palenappa
APPLICANT: Nunn, Adrian
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylla
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
FILE REFERENCE: D0617.70012U500
CURRENT APPLICATION NUMBER: US/10/661.156
PRIORITY FILING DATE: 2003-09-11
CURRENT APPLICATION NUMBER: US 10/382.082
PRIORITY FILING DATE: 2003-03-03
PRIORITY FILING DATE: 2003-03-03
PRIORITY FILING DATE: 2003-03-03
PRIORITY FILING DATE: 2003-01-15
PRIORITY FILING DATE: 2003-01-15
PRIORITY FILING DATE: 2002-03-01
PRIORITY FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 617
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 146
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-661-156-146

Query Match 31.4%; Score 33; DB 5; Length 20;
Best Local Similarity 58.3%; Pred. No. 7.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 PGEFVGESEGV 19
|||:|:
Db 2 PGEFVGESEGV 13

RESULT 19
US-10-328-916-58
Sequence 58, Application US/10328916
Publication No. US20040002114A1
GENERAL INFORMATION:
APPLICANT: Gregoire, Francine M.
APPLICANT: Johnson, Jeffrey D.
APPLICANT: Blume, John E.
APPLICANT: Metabolix, Inc.
TITLE OF INVENTION: Nucleic Acids Encoding a G-Protein Coupled Receptor
FILE REFERENCE: 016325-007210US
CURRENT APPLICATION NUMBER: US/10/328.916
PRIORITY FILING DATE: 2003-01-06
PRIORITY FILING DATE: 2002-01-04
PRIORITY FILING DATE: 2002-01-04
NUMBER OF SEQ ID NOS: 59
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 58
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:C-terminal
US-10-328-916-58

Query Match 30.5%; Score 32; DB 4; Length 15;
Best Local Similarity 54.5%; Pred. No. 7.6e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 6 MPPPGVGESE 16
|||:|:
Db 4 MPPPGVGESE 14

RESULT 20
US-09-838-785-26
Sequence 26, Application US/09838785
Patent No. US20020009455A1
GENERAL INFORMATION:
APPLICANT: Lau, Ted
APPLICANT: Lin, Rick
APPLICANT: Parkes, Debbie
APPLICANT: Parry, Gordon
APPLICANT: Schneider, Douglas
APPLICANT: Steindricher, Renate
APPLICANT: Van Heult, Pam T
APPLICANT: Wu, John
TITLE OF INVENTION: DNA Encoding a No. US20020009455A1 PROST 03
FILE REFERENCE: 51831AUSM1
CURRENT APPLICATION NUMBER: US/09/838.785
PRIORITY FILING DATE: 2001-04-20
PRIORITY FILING DATE: 2000-04-27
PRIORITY FILING DATE: 2000-04-27
NUMBER OF SEQ ID NOS: 26

/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 26
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-838-785-26

Query Match 30.5%; Score 32; DB 3; Length 16;
Best Local Similarity 55.6%; Pred. No. 8.2e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DPAKMSPP 9
: |||: |
Db 3 BPAEGHSAP 11

RESULT 21
US-10-953-901-593
/ Sequence 593, Application US/10953901
/ Publication No. US20050181464A1
/ GENERAL INFORMATION:
/ APPLICANT: EDWARDS, ALED
/ APPLICANT: DHARMASI, AKIL
/ APPLICANT: VEDADI, MASOUD
/ APPLICANT: ALAM, MUHAMMAD ZAHOR
/ APPLICANT: ARROWSMITH, CHERYL
/ APPLICANT: AMREY, DONALD E.
/ APPLICANT: BEATTIE, BRYAN
/ APPLICANT: BUZADZITA, KRISTINA
/ APPLICANT: CLARKE, TERESA
/ APPLICANT: DOMAGALA, MEGAN
/ APPLICANT: HOUSTON, SIMON
/ APPLICANT: KANAGARAJAH, DHUSHY
/ APPLICANT: LI, QIN
/ APPLICANT: MANSOURY, KAMRAN
/ APPLICANT: McDONALD, MERRY-LYNN
/ APPLICANT: NETHERY, KATHLEEN
/ APPLICANT: NG, IVY
/ APPLICANT: OUYANG, HUI
/ APPLICANT: RICHARDS, DAMN
/ APPLICANT: VALLEE, FRANCOIS
/ APPLICANT: VIRAG, CRISTINA
/ TITLE OF INVENTION: NOVEL PURIFIED POLYPEPTIDES FROM BACTERIA
/ FILE REFERENCE: IPT-207.01
/ CURRENT APPLICATION NUMBER: US/10/953,901
/ PRIOR FILING DATE: 2004-09-29
/ PRIOR APPLICATION NUMBER: PCT/CA03/00465
/ PRIOR FILING DATE: 2003-04-04
/ PRIOR APPLICATION NUMBER: 60/370,060
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: 60/369,831
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: 60/369,819
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: 60/369,826
/ PRIOR FILING DATE: 2002-04-04
/ PRIOR APPLICATION NUMBER: 60/370,852
/ PRIOR FILING DATE: 2002-04-08
/ PRIOR APPLICATION NUMBER: 60/370,681
/ PRIOR FILING DATE: 2002-04-08
/ PRIOR APPLICATION NUMBER: 60/371,014
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/371,180
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/371,008
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/371,008
/ PRIOR FILING DATE: 2002-04-09
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 901
/ SOFTWARE: Patentin Ver. 3.3
/ SEQ ID NO 593
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Staphylococcus aureus

US-10-953-901-593

Query Match 30.5%; Score 32; DB 5; Length 16;
Best Local Similarity 70.0%; Pred. No. 8.2e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GRIVGESEVYL 19
: ||| |||:
Db 5 GDIVGESEVYM 14

RESULT 22
US-10-661-156-170
/ Sequence 170, Application US/10661156
/ Publication No. US20050100963A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buesat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappa, Palaniappa
/ APPLICANT: Nunn, Adrian
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
/ TITLE OF INVENTION: Their Use in Diagnosis and Therapy
/ FILE REFERENCE: D0617.70012US00
/ CURRENT APPLICATION NUMBER: US/10/661,156
/ CURRENT FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 617
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 170
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-661-156-170

Query Match 30.5%; Score 32; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 1e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 PGGFVGESEVYL 19
: ||| |||: |
Db 2 PGGFSEYEQDAL 13

RESULT 23
US-10-307-956-25
/ Sequence 25, Application US/10307956
/ Publication No. US20030119072A1
/ GENERAL INFORMATION:
/ APPLICANT: Hoekstra, Merl F.

```
/ APPLICANT: Xie, Weilin
/ APPLICANT: Murray, Brian
/ APPLICANT: Mercutio, Frank
/ TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
/ FILE REFERENCE: 860098.433
/ CURRENT APPLICATION NUMBER: US/10/307,956
/ PRIOR FILING DATE: 2002-12-02
/ PRIOR APPLICATION NUMBER: US/09/385,918
/ PRIOR FILING DATE: 1999-08-30
/ NUMBER OF SEQ ID NOS: 32
/ SOFTWARE: PaetSeq for Windows Version 3.0
/ SEQ ID NO 25
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-307-956-25
```

Query Match 29.5%; Score 31; DB 4; Length 14;
Best Local Similarity 38.5%; Pred. No. 1e+03;
Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

```
QY 5 GMSPPGVGSEEG 17
DB 2 GLTPPGVLSBDG 14
```

```
RESULT 24
US-10-211-088-356
/ Sequence 356, Application US/10211088
/ Publication No. US20030104479A1
/ GENERAL INFORMATION:
/ APPLICANT: Bright, Gary R.
/ APPLICANT: Premkumar, D. David
/ APPLICANT: Chen, Yih-Tai
/ TITLE OF INVENTION: NO. US20030104479A1 Fusion Proteins And Assays For Molecular B
/ FILE REFERENCE: 01-1022-US
/ CURRENT APPLICATION NUMBER: US/10/211,088
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: 60/309,395
/ PRIOR FILING DATE: 2001-08-01
/ PRIOR APPLICATION NUMBER: 60/341,589
/ PRIOR FILING DATE: 2001-12-13
/ NUMBER OF SEQ ID NOS: 366
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 356
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Post-translational modification site
US-10-211-088-356
```

Query Match 29.5%; Score 31; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

```
QY 2 PAKGMSPPG 10
DB 2 PGKGVKSPG 10
```

```
RESULT 25
US-10-950-163-8
/ Sequence 8, Application US/10950163
/ Publication No. US20050152911A1
/ GENERAL INFORMATION:
/ APPLICANT: Hardy, Michele
/ TITLE OF INVENTION: NOROVIRUS MONOCLONAL ANTIBODIES AND PEPTIDES
/ FILE REFERENCE: 33576/US/2
/ CURRENT APPLICATION NUMBER: US/10/950,163
/ CURRENT FILING DATE: 2004-09-24
/ PRIOR APPLICATION NUMBER: US 60/508,262
```

```
/ PRIOR FILING DATE: 2003-09-24
/ NUMBER OF SEQ ID NOS: 159
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 8
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Grimsby virus
US-10-950-163-8
```

Query Match 29.5%; Score 31; DB 5; Length 17;
Best Local Similarity 71.4%; Pred. No. 1.2e+03;
Matches 5; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```
QY 2 PAKGMSPPG 8
DB 7 PAKGLSP 13
```

```
RESULT 26
US-09-999-781-10
/ Sequence 10, Application US/09999781
/ Publication No. US20040082456A1
/ GENERAL INFORMATION:
/ APPLICANT: ACTON, SUSAN L.
/ APPLICANT: OCCAIN, TIMOTHY D.
/ APPLICANT: GOULD, ALEXANDRA
/ APPLICANT: DALES, NATALIE A.
/ APPLICANT: GUAN, BING
/ APPLICANT: BROWN, JAMES A.
/ APPLICANT: PATANE, MICHAEL
/ APPLICANT: KADAMBI, VIVEK J.
/ APPLICANT: SOLOMON, MICHAEL
/ APPLICANT: STRICKER-KRONGRAD, ALAIN
/ TITLE OF INVENTION: ACE-2 MODULATING COMPOUNDS AND METHODS
/ FILE REFERENCE: MEI-082CP4
/ CURRENT APPLICATION NUMBER: US/09/999,781
/ CURRENT FILING DATE: 2001-10-31
/ PRIOR APPLICATION NUMBER: 09/870,382
/ PRIOR FILING DATE: 2001-05-29
/ PRIOR APPLICATION NUMBER: 09/704,216
/ PRIOR FILING DATE: 2000-11-01
/ PRIOR APPLICATION NUMBER: 60/XXX,XXX
/ PRIOR FILING DATE: 2001-10-19
/ NUMBER OF SEQ ID NOS: 34
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 10
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-999-781-10
```

Query Match 29.5%; Score 31; DB 3; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

```
QY 1 DPAKMSPPGF 11
DB 1 DISKGNPNPGF 11
```

```
RESULT 27
US-10-854-646-13
/ Sequence 13, Application US/10854646
/ Publication No. US20050113304A1
/ GENERAL INFORMATION:
/ APPLICANT: GORDON, RICHARD K.
/ APPLICANT: MOORAD, DEBORAH R.
/ APPLICANT: DOCTOR, BHUPENDRA P.
/ APPLICANT: GARCIA, GREGORY B.
/ TITLE OF INVENTION: PREVINS AS SPECIFIC INHIBITORS AND THERAPEUTIC AGENTS
/ TITLE OF INVENTION: FOR BOTULINUM TOXIN B AND TETANUS NEUROTOXINS
/ FILE REFERENCE: 38644-202822
```

```
/ CURRENT APPLICATION NUMBER: US/10/854,646
/ CURRENT FILING DATE: 2004-05-27
/ PRIOR APPLICATION NUMBER: 60/134,446
/ PRIOR FILING DATE: 1999-05-17
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-854-646-13

Query Match      29.5%; Score 31; DB 5; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      3 AKGMSPPGFIV 13
      |||: |||: |
Db      5 AKGLOPGLMV 15

RESULT 28
US-11-059-218-29
/ Sequence 29, Application US/11059218
/ Publication No. US20050147600A1
/ GENERAL INFORMATION:
/ APPLICANT: Acton, Susan L. et al.
/ TITLE OF INVENTION: ANGIOTENSIN CONVERTING ENZYME HOMOLOG AND THERAPEUTIC
/ FILE REFERENCE: NMT-132CP3
/ CURRENT APPLICATION NUMBER: US/11/059,218
/ CURRENT FILING DATE: 2005-02-16
/ PRIOR APPLICATION NUMBER: US/09/635,501
/ PRIOR FILING DATE: 2000-08-09
/ PRIOR APPLICATION NUMBER: 09/407,427
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 09/163,648
/ PRIOR FILING DATE: 1998-09-30
/ PRIOR APPLICATION NUMBER: 08/989,299
/ PRIOR FILING DATE: 1997-12-11
/ NUMBER OF SEQ ID NOS: 107
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 29
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: motifs
US-11-059-218-29

Query Match      29.5%; Score 31; DB 6; Length 18;
Best Local Similarity 54.5%; Pred. No. 1.3e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      1 DPAKMSPPGPF 11
      |::|::|::|
Db      1 DISKGNNGPF 11

RESULT 29
US-09-897-778-463
/ Sequence 463, Application US/09897778
/ Patent No. US20020147143A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Marnerakis, Margarita
/ APPLICANT: Ranger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Watanabe, Yoshihiro
```

```
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: Peckham, David W.
/ APPLICANT: Ranger, Neil
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C16
/ CURRENT APPLICATION NUMBER: US/09/897,778
/ CURRENT FILING DATE: 2001-06-28
/ NUMBER OF SEQ ID NOS: 467
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-897-778-463

Query Match      29.5%; Score 31; DB 3; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      |||: |||: |
Db      9 PTSGMPP 16

RESULT 30
US-10-007-700-463
/ Sequence 463, Application US/10007700
/ Publication No. US20030064947A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Wang, Aijun
/ APPLICANT: Skeiky, Yasir A.W.
/ APPLICANT: Li, Samuel X.
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Henderson, Robert A.
/ APPLICANT: McNeill, Patricia D.
/ APPLICANT: Ranger, Neil
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Durham, Margarita
/ APPLICANT: Ranger, Gary R.
/ APPLICANT: Vedvick, Thomas S.
/ APPLICANT: Carter, Darrick
/ APPLICANT: Watanabe, Yoshihiro
/ APPLICANT: Peckham, David W.
/ APPLICANT: Cai, Feng
/ APPLICANT: Foy, Teresa M.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C17
/ CURRENT APPLICATION NUMBER: US/10/007,700
/ CURRENT FILING DATE: 2001-11-30
/ NUMBER OF SEQ ID NOS: 469
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-007-700-463

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSPP 9
      |||: |||: |
Db      9 PTSGMPP 16

RESULT 31
US-10-117-982-463
/ Sequence 463, Application US/10117982
/ Publication No. US20030138438A1
```

```

; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darick
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Kelos, Michael D.
; APPLICANT: Meticle, Barbara
; APPLICANT: Spies, Gregory A.
; APPLICANT: Fan, Liqun
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C18
; CURRENT APPLICATION NUMBER: US/10/117,982
; CURRENT FILING DATE: 2002-04-05
; NUMBER OF SEQ ID NOS: 484
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-117-982-463

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSP 9
Db      9 PTSGMPP 16

RESULT 32
US-10-313-986-463
; Sequence 463, Application US/10313986
; Publication No. US20030236209A1
; GENERAL INFORMATION:
; APPLICANT: Foy, Teresa M.
; APPLICANT: McNabb, Andria
; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-463

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSP 9
Db      9 PTSGMPP 16

```

```

; APPLICANT: Matanabe, Yoshihiro
; APPLICANT: Reed, Steven G.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C19
; CURRENT APPLICATION NUMBER: US/10/313,986
; CURRENT FILING DATE: 2002-12-04
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-313-986-541

Query Match      29.5%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSP 9
Db      9 PTSGMPP 16

RESULT 34
US-10-775-972-463
; Sequence 463, Application US/10775972
; Publication No. US20040235072A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C21
; CURRENT APPLICATION NUMBER: US/10/775,972
; CURRENT FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 563
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 463
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-775-972-463

Query Match      29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY      2 PAKGMSP 9
Db      9 PTSGMPP 16

RESULT 35
US-10-775-972-541
; Sequence 541, Application US/10775972
; Publication No. US20040235072A1
; GENERAL INFORMATION:
; APPLICANT: Henderson, Robert A.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C21
; CURRENT APPLICATION NUMBER: US/10/775,972
; CURRENT FILING DATE: 2004-02-10
; NUMBER OF SEQ ID NOS: 563
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 20
; TYPE: PRT

```

ORGANISM: Homo sapiens
US-10-922-972-541

Query Match 29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 36

US-10-922-124-463
Sequence 463, Application US/10922124
Publication No. US20050142620A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaltanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C22
CURRENT APPLICATION NUMBER: US/10/922,124
PRIOR FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 10/775,972
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 10/623,155
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 10/313,986
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 10/007,700
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/897,778
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 09/850,716
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: 09/735,705
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 09/685,696
PRIOR FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: 09/662,786
PRIOR FILING DATE: 2000-09-15
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 563
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 463
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-922-124-463

Query Match 29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 37

US-10-922-124-541
Sequence 541, Application US/10922124
Publication No. US20050142620A1
GENERAL INFORMATION:
APPLICANT: Bangur, Chaltanya S.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C22
CURRENT APPLICATION NUMBER: US/10/922,124

CURRENT FILING DATE: 2004-08-18
PRIOR APPLICATION NUMBER: 10/775,972
PRIOR FILING DATE: 2004-02-10
PRIOR APPLICATION NUMBER: 10/623,155
PRIOR FILING DATE: 2003-07-17
PRIOR APPLICATION NUMBER: 10/313,986
PRIOR FILING DATE: 2002-12-04
PRIOR APPLICATION NUMBER: 10/117,982
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 10/007,700
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: 09/897,778
PRIOR FILING DATE: 2001-06-28
PRIOR APPLICATION NUMBER: 09/850,716
PRIOR FILING DATE: 2001-05-07
PRIOR APPLICATION NUMBER: 09/735,705
PRIOR FILING DATE: 2000-12-12
PRIOR APPLICATION NUMBER: 09/685,696
PRIOR FILING DATE: 2000-10-09
PRIOR APPLICATION NUMBER: 09/662,786
PRIOR FILING DATE: 2000-09-15
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 563
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 541
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-922-124-541

Query Match 29.5%; Score 31; DB 5; Length 20;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 9 PTSGMPP 16

RESULT 38

US-10-376-121A-12
Sequence 12, Application US/10376121A
Publication No. US2003021654A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESS:
ADDRESSER: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 1..8
SEQUENCE DESCRIPTION: SEQ ID NO: 12:
US-10-376-121A-12

Query Match 28.6%; Score 30; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 3 GMSPPG 8

RESULT 39
US-10-376-121A-123
Sequence 123, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 123:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: Misc Feature
LOCATION: 6
OTHER INFORMATION: /note= "The Xaa at position 6 can be
R, F, G, H, I, K, S, T, V,
and Y."
SEQUENCE DESCRIPTION: SEQ ID NO: 123:
US-10-376-121A-123

Query Match 28.6%; Score 30; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9
DB 1 PPKMKP 8

RESULT 40
US-10-376-121A-205
Sequence 205, Application US/10376121A
Publication No. US20030216544A1
GENERAL INFORMATION:
APPLICANT: Harley, John
TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTOANTIBODIES
NUMBER OF SEQUENCES: 218
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Patrea L. Pabst
STREET: Suite 2000, 1201 West Peachtree Street, N.E.
CITY: Atlanta
STATE: GA
COUNTRY: USA
ZIP: 30309-3400
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/376,121A
FILING DATE: 27-Mar-2003
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 205:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 205:
US-10-376-121A-205

Query Match 28.6%; Score 30; DB 4; Length 8;
Best Local Similarity 83.3%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10
DB 1 PPKMKP 8

Db 2 GMPPG 7

RESULT 41

US-10-376-121A-206

Sequence 206, Application US/10376121A
Publication No. US2003021654A1

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTANTIBODIES

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Patrea L. Pabst

STREET: Suite 2000, 1201 West Peachtree Street, N.E.

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/376,121A

FILING DATE: 27-Mar-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/867,819

FILING DATE: April 13, 1992

APPLICATION NUMBER: 07/648,205

FILING DATE: January 31, 1991

APPLICATION NUMBER: 07/472,947

FILING DATE: January 31, 1990

ATTORNEY/AGENT INFORMATION:

NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284

REFERENCE/DOCKET NUMBER: OMRF14CIP(2)DIV(2)

TELEPHONE: (404)-817-8473

TELEFAX: (404)-817-8588

INFORMATION FOR SEQ ID NO: 206:

SEQUENCE CHARACTERISTICS:

LENGTH: 8 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 206:

US-10-376-121A-206

Query Match 28.6%; Score 30; DB 4; Length 8;

Best Local Similarity 83.3%; Pred. No. 1.7e+06;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPPG 10

Db 1 GMPPG 6

RESULT 42

US-09-572-404B-272

Sequence 272, Application US/09572404B

Publication No. US2003007837A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 272

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: sequence located in RGS12 at 1275-1284 and may interact with Sequ

US-09-572-404B-272

Query Match 28.6%; Score 30; DB 3; Length 10;

Best Local Similarity 55.6%; Pred. No. 9.8e+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGSPPG 10

Db 1 PGSASPPG 9

RESULT 43

US-09-572-404B-274

Sequence 274, Application US/09572404B

Publication No. US2003007837A1

GENERAL INFORMATION:

APPLICANT: Proteom Ltd

TITLE OF INVENTION: Complementary peptide ligands from the human genome

FILE REFERENCE: Human patent

CURRENT APPLICATION NUMBER: US/09/572,404B

CURRENT FILING DATE: 2000-05-17

NUMBER OF SEQ ID NOS: 4203

SOFTWARE: ProtPatent version 1.0

SEQ ID NO 274

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapiens

FEATURE:

OTHER INFORMATION: sequence located in RGS12 at 1274-1283 and may interact with Sequ

US-09-572-404B-274

Query Match 28.6%; Score 30; DB 3; Length 10;

Best Local Similarity 55.6%; Pred. No. 9.8e+02;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGSPPG 10

Db 2 PGSASPPG 10

RESULT 44

US-10-376-121A-14

Sequence 14, Application US/10376121A

Publication No. US2003021654A1

GENERAL INFORMATION:

APPLICANT: Harley, John

TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
AUTANTIBODIES

NUMBER OF SEQUENCES: 218

CORRESPONDENCE ADDRESSES:

ADDRESSEE: Patrea L. Pabst

STREET: Suite 2000, 1201 West Peachtree Street, N.E.

CITY: Atlanta

STATE: GA

COUNTRY: USA

ZIP: 30309-3400

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/376,121A

FILING DATE: 27-Mar-2003

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/867,819
FILING DATE: April 13, 1992
APPLICATION NUMBER: 07/648,205
FILING DATE: January 31, 1991
APPLICATION NUMBER: 07/472,947
FILING DATE: January 31, 1990
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMR114CIP(2)DIV(2)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)-817-8473
TELEFAX: (404)-817-8588
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 3..10
LOCATION: 9
OTHER INFORMATION: /note= "The Xaa at position 9 can be
R, P, G, H, I, K, S, T, V,
and Y."

US-10-376-121A-14

SEQUENCE DESCRIPTION: SEQ ID NO: 14:
US-10-376-121A-14

Query Match 28.6%; Score 30; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.2e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKMSPP 9
DB 4 PPKMKPP 11

RESULT 45
US-10-972-236A-27
Sequence 27, Application US/10972236A
GENERAL INFORMATION:
APPLICANT: NG, Gordon
APPLICANT: LI, Yue-Sheng
APPLICANT: Gegg, Colin
APPLICANT: Askew, Jr., Benny
APPLICANT: Storz, Thomas
APPLICANT: Lu, Yuelie
APPLICANT: D'Amico, Derin
TITLE OF INVENTION: ANTAGONISTS OF THE BRADYKININ B1 RECEPTOR
FILE REFERENCE: A-836B
CURRENT APPLICATION NUMBER: US/10/972,236A
CURRENT FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: 60/538,929
PRIOR FILING DATE: 2004-01-24
PRIOR APPLICATION NUMBER: 60/513,913
PRIOR FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.2
SEQ ID NO 27
LENGTH: 13
TYPE: PRT
ORGANISM: ARTIFICIAL
FEATURES:
OTHER INFORMATION: SYNTHETICALLY PRODUCED
US-10-972-236A-27

Query Match 28.6%; Score 30; DB 5; Length 13;

Best Local Similarity 71.4%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPGF 11
DB 4 GKRPFGP 10

RESULT 46
US-10-185-050-53
Sequence 53, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.
TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-185-050-53

Query Match 28.6%; Score 30; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPGF 14
DB 2 GTAPPEYTVG 11

RESULT 47
US-10-185-050-54
Sequence 54, Application US/10185050
Publication No. US20030077577A1
GENERAL INFORMATION:
APPLICANT: Pirozzi, Gregorio
Kay, Brian K.
Fowlkes, Dana M.

TITLE OF INVENTION: IDENTIFICATION AND ISOLATION OF NOVEL
POLYPEPTIDES HAVING WW DOMAINS AND METHODS OF USING SAME
NUMBER OF SEQUENCES: 233
CORRESPONDENCE ADDRESS:
ADDRESSEE: PENNIE & EDMONDS LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/185,050
FILING DATE: 28-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/826,516
FILING DATE: 03-Apr-1997
ATTORNEY/AGENT INFORMATION:
NAME: MISROCK, S. LESLIE
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-208-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9990
TELEFAX: (212) 896-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 54:
SEQUENCE CHARACTERISTICS:
LENGTH: 14 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-185-050-54
Query Match 28.6%; Score 30; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 5 GMSPPGTVG 14
DB 2 GTPEPPATVVG 11
RESULT 48
US-10-434-906-3
Sequence 3, Application US/10434906
Publication No. US20030212000A1
GENERAL INFORMATION:
APPLICANT: William P. Van Antwerp
TITLE OF INVENTION: IMMUNOPROTECTIVE METHODS FOR BETA CELL
FILE REFERENCE: 130.59-US-01
CURRENT APPLICATION NUMBER: US/10/434,906
CURRENT FILING DATE: 2003-05-09
PRIOR APPLICATION NUMBER: 60/379,202
PRIOR FILING DATE: 2002-05-09
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 15
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-434-906-3
Query Match 28.6%; Score 30; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSPG 10
DB 5 DPTOSTERNG 14
RESULT 49
US-10-972-236A-28
Sequence 28, Application US/10972236A
Publication No. US20050215470A1
GENERAL INFORMATION:
APPLICANT: Ng, Gordon
APPLICANT: Li, Yue-Sheng
APPLICANT: Gegg, Colin
APPLICANT: Askew, Jr., Benny
APPLICANT: Storz, Thomas
APPLICANT: Lu, Yuelie
APPLICANT: D'Amico, Derin
TITLE OF INVENTION: ANTAGONISTS OF THE BRADYKININ B1 RECEPTOR
FILE REFERENCE: A-836B
CURRENT APPLICATION NUMBER: US/10/972,236A
CURRENT FILING DATE: 2004-10-21
PRIOR APPLICATION NUMBER: 60/538,929
PRIOR FILING DATE: 2004-01-24
PRIOR APPLICATION NUMBER: 60/513,913
PRIOR FILING DATE: 2003-10-22
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn version 3.2
SEQ ID NO 28
LENGTH: 15
TYPE: PRT
ORGANISM: ARTIFICIAL
FEATURE:
OTHER INFORMATION: SYNTHETICALLY PRODUCED
US-10-972-236A-28
Query Match 28.6%; Score 30; DB 5; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5 GMSPPGF 11
DB 6 GKRPPGF 12
RESULT 50
US-10-285-394-376
Sequence 376, Application US/10285394
Publication No. US20030228583A1
GENERAL INFORMATION:
APPLICANT: AMACHER, DAVID E.
APPLICANT: PASILO, LISA M.
APPLICANT: HERATH, HERATH MODIYANSELAGE ATHULA CHANDRASIRI
APPLICANT: HOLT, GORDON DUANE
APPLICANT: STIGER, THOMAS R.
TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
FILE REFERENCE: POA-003.01
CURRENT APPLICATION NUMBER: US/10/285,394
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,964
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 412
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 376
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-285-394-376
Query Match 28.6%; Score 30; DB 4; Length 16;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGFVGBGV 18
 |||||
 Db 6 PGASGTGGL 15

RESULT 51
 US-10-029-386-32096
 ; Sequence 32096, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR C
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
 ; FILE REFERENCE: AEMICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 32096
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; OTHER INFORMATION: MAP TO AH005332.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 2.2
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 2
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.4
 US-10-029-386-32096

Query Match 28.6%; Score 30; DB 4; Length 18;
 Best Local Similarity 55.6%; Pred. No. 1.9e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMSPPGF 11
 :|||
 Db 2 SSGTLPPGF 10

RESULT 52
 US-10-862-195-907
 ; Sequence 907, Application US/10862195
 ; Publication No. US20050164324A1
 ; GENERAL INFORMATION:
 ; APPLICANT: GIGI, STEVEN P.
 ; TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
 ; FILE REFERENCE: 58890(70207)
 ; CURRENT APPLICATION NUMBER: US/10/862,195
 ; CURRENT FILING DATE: 2004-06-04
 ; PRIOR APPLICATION NUMBER: 60/476,010
 ; PRIOR FILING DATE: 2003-06-04
 ; NUMBER OF SEQ ID NOS: 2245
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 907
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURES:
 ; OTHER INFORMATION: See specification as filed for preferred embodiments
 ; OTHER INFORMATION: and description of phosphorylation sites
 US-10-862-195-907

Query Match 28.6%; Score 30; DB 5; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1.9e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGSP 9
 |||||
 Db 10 PAKSLSP 17

RESULT 53

US-10-714-212-27
 ; Sequence 27, Application US/10714212
 ; Publication No. US20040077038A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Genencor International, Inc.
 ; TITLE OF INVENTION: Methods for Production of Proteins in
 ; TITLE OF INVENTION: Host Cells
 ; FILE REFERENCE: GC559-PCT
 ; CURRENT APPLICATION NUMBER: US/10/714,212
 ; CURRENT FILING DATE: 2003-11-13
 ; PRIOR APPLICATION NUMBER: US 09/470,830
 ; PRIOR FILING DATE: 1999-12-23
 ; NUMBER OF SEQ ID NOS: 44
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 27
 ; LENGTH: 19
 ; TYPE: PRT
 ; ORGANISM: Mycobacterium leprae
 US-10-714-212-27

Query Match 28.6%; Score 30; DB 4; Length 19;
 Best Local Similarity 38.5%; Pred. No. 2e+03;
 Matches 5; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKGMSPPGF 15
 :|||
 Db 2 AETTPSGLVIP 14

RESULT 54
 US-10-307-956-24
 ; Sequence 24, Application US/10307956
 ; Publication No. US20030119072A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Hoeckstra, Merl F.
 ; APPLICANT: Xie, Weilin
 ; APPLICANT: Murray, Brian
 ; APPLICANT: Mercurio, Frank
 ; TITLE OF INVENTION: METHODS FOR MODULATING SIGNAL
 ; TITLE OF INVENTION: TRANSDUCTION MEDIATED BY TGF-BETA AND RELATED PROTEINS
 ; FILE REFERENCE: 860098.433
 ; CURRENT APPLICATION NUMBER: US/10/307,956
 ; CURRENT FILING DATE: 2002-12-02
 ; PRIOR APPLICATION NUMBER: US/09/385,918
 ; PRIOR FILING DATE: 1999-08-30
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 24
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-307-956-24

Query Match 28.1%; Score 29.5; DB 4; Length 14;
 Best Local Similarity 60.0%; Pred. No. 1.7e+03;
 Matches 6; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 8 PGFVGBGV 17
 |||||
 Db 6 PGVYT-SDG 14

RESULT 55
 US-09-990-832C-57
 ; Sequence 57, Application US/09990832C
 ; Publication No. US20030149235A1
 ; GENERAL INFORMATION:
 ; APPLICANT: University Court of the University of Glasgow
 ; TITLE OF INVENTION: Targeting peptides
 ; FILE REFERENCE: PC/MC/JM/P11910US
 ; CURRENT APPLICATION NUMBER: US/09/990,832C
 ; CURRENT FILING DATE: 2003-01-27
 ; NUMBER OF SEQ ID NOS: 127

SOFTWARE: PatentIn version 3.1
SEQ ID NO 57
LENGTH: 7
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Targeting peptide sequence
US-09-990-832C-57

Query Match 27.6%; Score 29; DB 3; Length 7;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSPPG 10
DB 1 MSPPG 5

RESULT 56
US-10-012-756-4
Sequence 4, Application US/10012756
Publication No. US20020164355A1
GENERAL INFORMATION:
APPLICANT: John B. Harley and Judith A. James
TITLE OF INVENTION: Diagnostic And Therapy Of Epstein-Barr
Virus In Autoimmune Disorders
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Patricia L. Peabec
STREET: 2800 One Atlantic Center
1201 West Peachtree Street
CITY: Atlanta
STATE: Georgia
COUNTRY: USA
ZIP: 30306-3450

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/012,756
FILING DATE: 24-Oct-2001
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/781,296
FILING DATE: 13-JAN-1997
APPLICATION NUMBER: 60/019,053
FILING DATE: 16-MAY-1996
APPLICATION NUMBER: 08/160,604
FILING DATE: 30-NOV-1996

ATTORNEY/AGENT INFORMATION:
NAME: Peabec, Patricia L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF161
TELECOMMUNICATION INFORMATION:
TELEPHONE: (404)873-8794
TELEFAX: (404)873-8795
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 4
US-10-012-756-4

Query Match 27.6%; Score 29; DB 4; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PPPGMRPP 8

RESULT 57
US-10-646-132-3
Sequence 3, Application US/10646132
Publication No. US20050074751A1
GENERAL INFORMATION:
APPLICANT: Oklahoma Medical Research Foundation
APPLICANT: Harley, John B.
APPLICANT: Kaufman, Kenneth M.
TITLE OF INVENTION: Assays and Therapies For Latent Viral Infection
FILE REFERENCE: OMRF 177
CURRENT APPLICATION NUMBER: US/10/646,132
CURRENT FILING DATE: 2003-08-22
PRIOR APPLICATION NUMBER: US/09/718,693A
PRIOR FILING DATE: 2000-11-22
PRIOR APPLICATION NUMBER: US 60/167,212
PRIOR FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.1
SEQ ID NO 3
LENGTH: 8
TYPE: PRT
ORGANISM: Human herpesvirus 4
US-10-646-132-3

Query Match 27.6%; Score 29; DB 5; Length 8;
Best Local Similarity 62.5%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
DB 1 PPPGMRPP 8

RESULT 58
US-10-224-999A-2893
Sequence 2893, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2893
LENGTH: 9
TYPE: PRT
ORGANISM: Hepatitis G virus
US-10-224-999A-2893

Query Match 27.6%; Score 29; DB 4; Length 9;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPPFI 12
DB 1 PPPFV 5

RESULT 59

```

Query Match          27.6%  Score 29; DB 3; Length 10,
Best local similarity 55.6%  Pred. No. 1.4e+03,
Matches      5; Conservative      1; Mismatches      3; Indels      0; Gaps      0;

QY      2 PAKGMSPPG 10
      ||| : ||
Db      2 PAKAVKAPG 10

RESULT 61
US-09-573-822C-684
/ Sequence 684, Application US/09573822C
/ Publication No. US20030199011A1
/ GENERAL INFORMATION:
/ APPLICANT: Proteom Ltd
/ TITLE OF INVENTION: Complementary peptide ligands generated from microbial genome seq
/ FILE REFERENCE: Microbe patent
/ CURRENT APPLICATION NUMBER: US/09/573,822C
/ CURRENT FILING DATE: 2000-05-18
/ NUMBER OF SEQ. ID NOS: 804
/ SOFTWARE: ProCpatent version 1.0
/ SEQ ID NO 684
/ LENGTH: 10

```

Query Match	27.6%;	Score 29;	DB 4;	Length 10,
Best Local Similarity	80.0%;	Pred. No. 1.4e+03;		

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
Qy 8 PGFPI 12
|||:
Db 1 PGFV 5

RESULT 64
US-10-224-999A-2906
; Sequence 2906, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2906
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2906

Query Match 27.6%; Score 29; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFPI 12
|||:
Db 3 PGFV 7

RESULT 65
US-10-224-999A-2907
; Sequence 2907, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2907
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2907

Query Match 27.6%; Score 29; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFPI 12
|||:
Db 2 PGFV 6

RESULT 66
US-10-224-999A-2908

; Sequence 2908, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2908
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2908

Query Match 27.6%; Score 29; DB 4; Length 11;
Best Local Similarity 80.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PGFPI 12
|||:
Db 1 PGFV 5

RESULT 67
US-10-376-121A-10
; Sequence 10, Application US/10376121A
; Publication No. US20030216544A1
; GENERAL INFORMATION:
; APPLICANT: Hatley, John
; TITLE OF INVENTION: METHODS AND REAGENTS FOR DIAGNOSIS OF
; AUTOANTIBODIES
; NUMBER OF SEQUENCES: 218
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Patricia L. Pabst
; STREET: Suite 2000, 1201 West Peachtree Street, N.E.
; CITY: Atlanta
; STATE: GA
; COUNTRY: USA
; ZIP: 30309-3400
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/376,121A
; FILING DATE: 27-Mar-2003
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/867,819
; FILING DATE: April 13, 1992
; APPLICATION NUMBER: 07/648,205
; FILING DATE: January 31, 1991
; APPLICATION NUMBER: 07/472,947
; FILING DATE: January 31, 1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Pabst, Patricia L.
; REGISTRATION NUMBER: 31,284
; REFERENCE/DOCKET NUMBER: OMRP114CIP(2)DIV(2)
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (404)-817-8473
; TELEFAX: (404)-817-8588
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Binding-site
LOCATION: 3..10
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-10-376-121A-10

Query Match 27.6%; Score 29; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
Db 3 PPGMRPP 10

RESULT 68
US-10-285-394-140
Sequence 140; Application US/10285394
Publication No. US20030228583A1
GENERAL INFORMATION:
APPLICANT: AMACHER, DAVID E.
APPLICANT: PASULO, LISA M.
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATTULA CHANDRASIRI
APPLICANT: HOLT, GORDON DUANE
APPLICANT: STIGER, THOMAS R.
TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
FILE REFERENCE: POA-003.01
CURRENT APPLICATION NUMBER: US/10/285,394
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,964
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 412
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 140
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-285-394-140

Query Match 27.6%; Score 29; DB 4; Length 11;
Best Local Similarity 62.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 11 FIVEGEGV 18
Db 1 FLVGPDGV 8

RESULT 69
US-10-286-457-50
Sequence 50; Application US/10286457
Publication No. US20030166004A1
GENERAL INFORMATION:
APPLICANT: JENO CYRUS et al.
TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
FILE REFERENCE: GPCI-P01-178
CURRENT APPLICATION NUMBER: US/10/286,457
CURRENT FILING DATE: 2002-11-01
PRIOR APPLICATION NUMBER: 60/334822
PRIOR FILING DATE: 2001-11-01
NUMBER OF SEQ ID NOS: 684
SOFTWARE: PatentIn version 3.1
SEQ ID NO 50
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
US-10-286-457-50

Query Match 27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 62.5%; Pred. No. 1.7e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 AKGMSPPG 10
Db 1 ATGTNPPG 8

RESULT 70
US-10-224-999A-2914
Sequence 2914; Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2914
LENGTH: 12
TYPE: PRT
ORGANISM: Hepatitis G virus
US-10-224-999A-2914

Query Match 27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPGFI 12
Db 4 PPGFV 8

RESULT 71
US-10-224-999A-2915
Sequence 2915; Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2915
LENGTH: 12
TYPE: PRT
ORGANISM: Hepatitis G virus
US-10-224-999A-2915

Query Match 27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPGFI 12
Db 3 PPGFV 7

```
RESULT 72
US-10-224-999A-2916
; Sequence 2916, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2916
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2916

Query Match      27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      2 PPGFV 6

RESULT 73
US-10-224-999A-2917
; Sequence 2917, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2917
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2917

Query Match      27.6%; Score 29; DB 4; Length 12;
Best Local Similarity 80.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      2 PPGFV 6

RESULT 74
US-10-224-999A-2923
; Sequence 2923, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
```

```
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2923
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2923

Query Match      27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      5 PPGFV 9

RESULT 75
US-10-224-999A-2924
; Sequence 2924, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2924
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2924

Query Match      27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGFI 12
      ||||:
Db      4 PPGFV 8

RESULT 76
US-10-224-999A-2925
; Sequence 2925, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
```


/ SEQ ID NO 2925
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2925

Query Match 27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFPI 12
DB 3 PGFV 7

RESULT 77
US-10-224-999A-2926
/ Sequence 2926, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2926
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2926

Query Match 27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFPI 12
DB 2 PGFV 6

RESULT 78
US-10-224-999A-2927
/ Sequence 2927, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2927
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2927

Query Match 27.6%; Score 29; DB 4; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGFPI 12
DB 1 PGFV 5

RESULT 79
US-10-948-707-1350
/ Sequence 1350, Application US/10948707
/ Publication No. US20050187147A1
/ GENERAL INFORMATION:
/ APPLICANT: Ballatore, Carlo
/ APPLICANT: Castellino, Angelo
/ APPLICANT: Desharnais, Joel
/ APPLICANT: Guo, Zifan
/ APPLICANT: Li, Qing
/ APPLICANT: Newman, Michael James
/ APPLICANT: Sun, Chengzao
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
/ FILE REFERENCE: 17967-003001
/ CURRENT APPLICATION NUMBER: US/10/948,707
/ PRIOR FILING DATE: 2004-09-22
/ PRIOR APPLICATION NUMBER: 60/505,325
/ PRIOR FILING DATE: 2003-09-22
/ PRIOR APPLICATION NUMBER: 60/568,340
/ PRIOR FILING DATE: 2004-05-04
/ PRIOR APPLICATION NUMBER: 60/581,835
/ PRIOR FILING DATE: 2004-06-22
/ NUMBER OF SEQ ID NOS: 1422
/ SOFTWARE: PastSeq for Windows Version 4.0
/ SEQ ID NO 1350
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-948-707-1350

Query Match 27.6%; Score 29; DB 5; Length 13;
Best Local Similarity 83.3%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 KGMSP 9
DB 1 KGMMP 6

RESULT 80
US-10-224-999A-2933
/ Sequence 2933, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2933
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2933

Query Match 27.6%; Score 29; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPgFI 12
 ||||:
 Db 6 PPgFV 10

RESULT 81

US-10-224-999A-2934
 ; Sequence 2934, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2934
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Hepatitis G virus
 US-10-224-999A-2934

Query Match 27.6%; Score 29; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPgFI 12
 ||||:
 Db 5 PPgFV 9

RESULT 82

US-10-224-999A-2935
 ; Sequence 2935, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2935
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Hepatitis G virus
 US-10-224-999A-2935

Query Match 27.6%; Score 29; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPgFI 12
 ||||:
 Db 4 PPgFV 8

RESULT 83

US-10-224-999A-2936
 ; Sequence 2936, Application US/10224999A
 ; Publication No. US20030171318A1

; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2936
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Hepatitis G virus
 US-10-224-999A-2936

Query Match 27.6%; Score 29; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPgFI 12
 ||||:
 Db 3 PPgFV 7

RESULT 84

US-10-224-999A-2937
 ; Sequence 2937, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; PRIOR FILING DATE: 2003-03-03
 ; PRIOR APPLICATION NUMBER: US 60/313,695
 ; PRIOR FILING DATE: 2001-08-20
 ; NUMBER OF SEQ ID NOS: 3484
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 2937
 ; LENGTH: 14
 ; TYPE: PRT
 ; ORGANISM: Hepatitis G virus
 US-10-224-999A-2937

Query Match 27.6%; Score 29; DB 4; Length 14;
 Best Local Similarity 80.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 PPgFI 12
 ||||:
 Db 2 PPgFV 6

RESULT 85

US-10-224-999A-2938
 ; Sequence 2938, Application US/10224999A
 ; Publication No. US20030171318A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Myriad Genetics, Inc.
 ; APPLICANT: Morham, Scott
 ; APPLICANT: Zavitz, Kenton
 ; APPLICANT: Hobden, Adrian
 ; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
 ; FILE REFERENCE: 5004.01
 ; CURRENT APPLICATION NUMBER: US/10/224,999A
 ; CURRENT FILING DATE: 2003-03-03

/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2938
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2938

Query Match 27.6%; Score 29; DB 4; Length 14;
Best Local Similarity 80.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 1 PPGFV 5

RESULT 86
US-10-149-240-12
/ Sequence 12, Application US/10149240
/ Publication No. US20030211589A1
/ GENERAL INFORMATION:
/ APPLICANT: Children's Medical Center
/ APPLICANT: Viasum Research Development
/ APPLICANT: Shmuel A. Ben-Sasson
/ TITLE OF INVENTION: Short peptides from the B4 and B5 Regions of Protein Kinases Whic
/ FILE REFERENCE: 1242.2001002
/ CURRENT APPLICATION NUMBER: US/10/149,240
/ PRIOR FILING DATE: 2002-06-10
/ PRIOR APPLICATION NUMBER: US 09/458,491
/ PRIOR FILING DATE: 1999-12-09
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: unknown
/ FEATURE:
/ OTHER INFORMATION: BMPR-II
US-10-149-240-12

Query Match 27.6%; Score 29; DB 4; Length 14;
Best Local Similarity 75.0%; Pred. No. 2e+03;
Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 11 FIVGEGV 18
Db 1 FIVGDERV 8

RESULT 87
US-10-224-999A-2944
/ Sequence 2944, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2944
/ LENGTH: 15
/ TYPE: PRT

/ ORGANISM: Hepatitis G virus
US-10-224-999A-2944

Query Match 27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 7 PPGFV 11

RESULT 88
US-10-224-999A-2945
/ Sequence 2945, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2945
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2945

Query Match 27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 6 PPGFV 10

RESULT 89
US-10-224-999A-2946
/ Sequence 2946, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 2946
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2946

Query Match 27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 1 PPGFV 5

```
Db          5 PPGFV 9

RESULT 90
US-10-224-999A-2947
; Sequence 2947, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2947
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2947

Query Match          27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          8 PPGFI 12
          ||||:
          4 PPGFV 8

RESULT 91
US-10-224-999A-2948
; Sequence 2948, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2948
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2948

Query Match          27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          8 PPGFI 12
          ||||:
          3 PPGFV 7

RESULT 92
US-10-224-999A-2949
; Sequence 2949, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.

Db          5 PPGFV 9

; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2949
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2949

Query Match          27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          8 PPGFI 12
          ||||:
          2 PPGFV 6

RESULT 93
US-10-224-999A-2950
; Sequence 2950, Application US/10224999A
; Publication No. US20030171318A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Composition and Method for Treating Viral Infection
; FILE REFERENCE: 5004.01
; CURRENT APPLICATION NUMBER: US/10/224,999A
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/313,695
; PRIOR FILING DATE: 2001-08-20
; NUMBER OF SEQ ID NOS: 3484
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2950
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Hepatitis G virus
US-10-224-999A-2950

Query Match          27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.2e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY          8 PPGFI 12
          ||||:
          1 PPGFV 5

RESULT 94
US-10-128-520-38
; Sequence 38, Application US/10128520
; Publication No. US20040105862A1
; GENERAL INFORMATION:
; APPLICANT: PAN et al.
; TITLE OF INVENTION: Human TIMP-1 Antibodies
; FILE REFERENCE: 02973.00073
; CURRENT APPLICATION NUMBER: US/10/128,520
; CURRENT FILING DATE: 2002-04-24
; PRIOR APPLICATION NUMBER: US 60/285,683
; PRIOR FILING DATE: 2001-04-24
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 38
```

LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
US-10-128-520-38

Query Match 27.6%; Score 29; DB 4; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGFVIG 14
Db 2 MTPPGHYG 10

RESULT 95
US-10-225-567A-1513

Sequence 1513, Application US/10225567A
Publication No. US20030113798A1
GENERAL INFORMATION:
APPLICANT: Lifespan Biosciences
APPLICANT: Brown, Joseph P.
APPLICANT: Burner, Glenn C.
APPLICANT: Roush, Christine L.
TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
FILE REFERENCE: 1920-4-4
CURRENT APPLICATION NUMBER: US/10/225,567A
CURRENT FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 60/257,144
PRIOR FILING DATE: 2000-12-19
NUMBER OF SEQ ID NOS: 2392
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1513
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-10-225-567A-1513

Query Match 27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.3e+03;

Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKMSPPGFI 12
Db 4 NPTKDLTNGMV 15

RESULT 96

US-10-224-999A-2956
Sequence 2956, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2956
LENGTH: 16
TYPE: PRT
ORGANISM: Hepatitis G virus
US-10-224-999A-2956

Query Match 27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 8 PPGFV 12

RESULT 97
US-10-224-999A-2957
Sequence 2957, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2957
LENGTH: 16
TYPE: PRT
ORGANISM: Hepatitis G virus
US-10-224-999A-2957

Query Match 27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 7 PPGFV 11

RESULT 98
US-10-224-999A-2958
Sequence 2958, Application US/10224999A
Publication No. US20030171318A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Inc.
APPLICANT: Morham, Scott
APPLICANT: Zavitz, Kenton
APPLICANT: Hobden, Adrian
TITLE OF INVENTION: Composition and Method for Treating Viral Infection
FILE REFERENCE: 5004.01
CURRENT APPLICATION NUMBER: US/10/224,999A
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/313,695
PRIOR FILING DATE: 2001-08-20
NUMBER OF SEQ ID NOS: 3484
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2958
LENGTH: 16
TYPE: PRT
ORGANISM: Hepatitis G virus
US-10-224-999A-2958

Query Match 27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGFI 12
Db 6 PPGFV 10

RESULT 99
US-10-224-999A-2959
Sequence 2959, Application US/10224999A
Publication No. US20030171318A1

```

/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2959
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2959

```

```

Query Match      27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 PPGFI 12
      ||||:
Db      5 PPGFV 9

```

```

RESULT 100
US-10-224-999A-2960
/ Sequence 2960, Application US/10224999A
/ Publication No. US20030171318A1
/ GENERAL INFORMATION:
/ APPLICANT: Myriad Genetics, Inc.
/ APPLICANT: Morham, Scott
/ APPLICANT: Zavitz, Kenton
/ APPLICANT: Hobden, Adrian
/ TITLE OF INVENTION: Composition and Method for Treating Viral Infection
/ FILE REFERENCE: 5004.01
/ CURRENT APPLICATION NUMBER: US/10/224,999A
/ CURRENT FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/313,695
/ PRIOR FILING DATE: 2001-08-20
/ NUMBER OF SEQ ID NOS: 3484
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 2960
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Hepatitis G virus
US-10-224-999A-2960

```

```

Query Match      27.6%; Score 29; DB 4; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      8 PPGFI 12
      ||||:
Db      4 PPGFV 8

```

Search completed: January 20, 2006, 19:45:40
 Job time : 74.1154 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 : Search time 8.07692 Seconds
(without alignments)
25.093 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105
Sequence: 1 DPAKMSPPGFIYGEVGLS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Maximum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

Published Applications AA New:*
1: /cgn2_6/prodata/1/pubppa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
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8: /cgn2_6/prodata/1/pubppa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	33	31.4	20	6	US-10-939-890-146
2	32	30.5	20	6	US-10-939-890-170
3	31	29.5	20	6	US-10-623-155-463
4	31	29.5	20	6	US-10-623-155-541
5	29	27.6	20	6	US-10-623-155-413
6	29	27.6	20	6	US-10-623-155-524
7	29	27.6	20	7	US-11-094-142-16
8	28	26.7	15	6	US-10-889-197-25
9	28	26.7	15	6	US-10-839-890-203
10	28	26.7	16	7	US-11-054-515-3003
11	28	26.7	20	6	US-10-893-584-212
12	27	25.7	15	6	US-10-516-676-1
13	27	25.7	15	6	US-10-532-426-2
14	27	25.7	16	7	US-11-054-515-2153
15	27	25.7	16	7	US-11-054-515-2780
16	27	25.7	16	7	US-11-054-515-2783
17	27	25.7	20	7	US-11-053-100-18
18	26.5	25.2	20	6	US-10-485-788A-598
19	26	24.8	9	7	US-11-178-269-27
20	26	24.8	15	6	US-10-839-890-193
21	26	24.8	17	6	US-10-893-584-206
22	26	24.8	18	6	US-10-842-206-26
23	26	24.8	18	6	US-10-980-459-12
24	26	24.8	19	6	US-10-503-575-131
25	26	24.8	20	6	US-10-97-201A-31

26	26	24.8	20	6	US-10-623-155-532	Sequence 532, App
27	26	24.8	20	6	US-10-623-155-542	Sequence 542, App
28	26	24.8	20	6	US-10-623-155-543	Sequence 543, App
29	25	23.8	8	6	US-10-989-226-81	Sequence 81, App1
30	25	23.8	9	7	US-11-053-100-9	Sequence 9, App1
31	25	23.8	11	7	US-11-045-024-1467	Sequence 1467, App
32	25	23.8	11	7	US-11-045-024-6285	Sequence 6285, App
33	25	23.8	14	7	US-11-116-144-285	Sequence 285, App
34	25	23.8	16	7	US-11-060-646-5	Sequence 5, App1
35	25	23.8	17	7	US-11-193-512-47	Sequence 47, App1
36	25	23.8	19	6	US-10-893-584-233	Sequence 233, App
37	25	23.8	20	6	US-10-623-155-414	Sequence 414, App
38	25	23.8	20	6	US-10-623-155-525	Sequence 525, App
39	24.5	23.3	11	7	US-11-105-708-11	Sequence 11, App1
40	24	22.9	7	6	US-10-986-501-338	Sequence 338, App
41	24	22.9	9	7	US-11-045-024-1247	Sequence 1247, App
42	24	22.9	9	7	US-11-045-024-8847	Sequence 8847, App
43	24	22.9	10	6	US-10-919-492-35	Sequence 35, App1
44	24	22.9	10	7	US-11-045-024-5221	Sequence 5221, App
45	24	22.9	10	7	US-11-129-104-61	Sequence 61, App1
46	24	22.9	10	7	US-11-129-104-62	Sequence 62, App1
47	24	22.9	14	7	US-11-129-104-7	Sequence 7, App1
48	24	22.9	15	6	US-10-866-120-4	Sequence 4, App1
49	24	22.9	15	6	US-10-919-492-6	Sequence 6, App1
50	24	22.9	15	6	US-10-919-492-13	Sequence 13, App1
51	24	22.9	19	6	US-10-503-575-119	Sequence 119, App
52	24	22.9	20	7	US-11-022-562-145	Sequence 145, App
53	24	22.9	20	7	US-11-022-562-146	Sequence 146, App
54	23	21.9	7	6	US-10-485-788A-79	Sequence 79, App1
55	23	21.9	8	6	US-10-485-788A-80	Sequence 80, App1
56	23	21.9	9	6	US-10-850-635-26	Sequence 26, App1
57	23	21.9	9	7	US-11-010-748A-617	Sequence 617, App
58	23	21.9	9	7	US-11-010-748A-618	Sequence 618, App
59	23	21.9	9	7	US-11-010-748A-620	Sequence 620, App
60	23	21.9	9	7	US-11-010-748A-621	Sequence 621, App
61	23	21.9	9	7	US-11-010-748A-625	Sequence 625, App
62	23	21.9	9	7	US-11-010-748A-635	Sequence 635, App
63	23	21.9	9	7	US-11-055-557-28	Sequence 28, App1
64	23	21.9	11	7	US-11-033-365-22	Sequence 22, App1
65	23	21.9	12	6	US-10-893-584-102	Sequence 102, App
66	23	21.9	14	6	US-10-893-584-198	Sequence 198, App
67	23	21.9	14	6	US-10-746-959C-5	Sequence 5, App1
68	23	21.9	15	6	US-10-939-890-200	Sequence 200, App
69	23	21.9	15	6	US-10-939-890-202	Sequence 202, App
70	23	21.9	15	6	US-10-893-584-247	Sequence 247, App
71	23	21.9	15	7	US-11-187-558-3	Sequence 4, App1
72	23	21.9	16	6	US-10-919-492-3	Sequence 3, App1
73	23	21.9	16	6	US-10-919-492-10	Sequence 10, App1
74	23	21.9	16	7	US-11-108-185-42	Sequence 42, App1
75	23	21.9	17	6	US-10-880-238-107	Sequence 107, App
76	23	21.9	17	6	US-10-880-238-109	Sequence 109, App
77	23	21.9	17	7	US-11-010-748A-405	Sequence 405, App
78	23	21.9	18	7	US-11-033-093-1324	Sequence 1324, App
79	23	21.9	19	6	US-10-503-575-224	Sequence 224, App
80	23	21.9	19	6	US-10-503-575-302	Sequence 302, App
81	23	21.9	19	6	US-10-503-575-303	Sequence 303, App
82	23	21.9	20	6	US-10-623-155-533	Sequence 533, App
83	23	21.9	20	7	US-11-106-415-182	Sequence 192, App
84	23	21.9	20	7	US-11-041-893-198	Sequence 198, App
85	22.5	21.4	17	7	US-11-107-029-11	Sequence 11, App1
86	22	21.0	8	6	US-10-485-788A-120	Sequence 120, App
87	22	21.0	8	7	US-11-045-024-5161	Sequence 5161, App
88	22	21.0	8	7	US-11-045-024-7282	Sequence 7282, App
89	22	21.0	9	7	US-11-045-024-11708	Sequence 13708, App
90	22	21.0	9	7	US-11-033-039-24	Sequence 24, App1
91	22	21.0	9	7	US-11-033-039-24	Sequence 292, App
92	22	21.0	10	7	US-11-045-024-1211	Sequence 1311, App
93	22	21.0	10	7	US-11-045-024-6377	Sequence 6377, App
94	22	21.0	10	7	US-11-045-024-9066	Sequence 9066, App
95	22	21.0	10	7	US-11-045-024-11266	Sequence 11266, App
96	22	21.0	10	7	US-11-208-541-11	Sequence 11, App1
97	22	21.0	11	7	US-11-033-365-5	Sequence 5, App1
98	22	21.0	11	7	US-11-045-024-3056	Sequence 3056, App

99 22 21.0 11 7 US-11-045-024-5702
100 22 21.0 11 7 US-11-045-024-9026

Sequence 5702, Ap
Sequence 9026, Ap

ALIGNMENTS

RESULT 1
US-10-939-890-146

/ Sequence 146, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogaast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 146
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-146

Query Match 31.4% Score 33; DB 6; Length 20;
Best Local Similarity 58.3%; Pred. No. 18;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 8 PPGFVGEQVLT 19
Db 2 PPGFVGEQVLT 13

RESULT 2
US-10-939-890-170

/ Sequence 170, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.

/ APPLICANT: Arbogaast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 170
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-170

Query Match 30.5% Score 32; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 25;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 8 PPGFVGEQVLT 19
Db 2 PPGFVGEQVLT 13

RESULT 3
US-10-623-155-463

/ Sequence 463, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 463
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-463

Query Match 29.5% Score 31; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
| : : :
Db 9 PTSGMPP 16

RESULT 4

US-10-623-155-541
; Sequence 541, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 541
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-541

Query Match 29.5%; Score 31; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
| : : :
Db 9 PTSGMPP 16

RESULT 5

US-10-623-155-413
; Sequence 413, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 413
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-413

Query Match 27.6%; Score 29; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIYGEQ 17
| : : :
Db 9 GAIIGKEG 16

RESULT 6
US-10-623-155-524
; Sequence 524, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; CURRENT FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 524
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-524

Query Match 27.6%; Score 29; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFIYGEQ 17
| : : :
Db 9 GAIIGKEG 16

RESULT 7

US-11-094-142-16
; Sequence 16, Application US/11094142
; Publication No. US2005026070A1
; GENERAL INFORMATION:
; APPLICANT: Cohen, Irun R.
; APPLICANT: Quintana, Francisco Javier
; APPLICANT: Domany, Eytan
; APPLICANT: Blizur, Gad
; APPLICANT: Hagedorn, Peter H.
; TITLE OF INVENTION: ANTIGEN ARRAY AND DIAGNOSTIC USES THEREOF
; FILE REFERENCE: 29462
; CURRENT APPLICATION NUMBER: US/11/094,142
; CURRENT FILING DATE: 2005-03-31
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 16
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-11-094-142-16

Query Match 27.6%; Score 29; DB 7; Length 20;
Best Local Similarity 55.6%; Pred. No. 74;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 GFIYGEQ 18
| : : :
Db 7 GAVFGEGL 15

RESULT 8

US-10-889-197-25
; Sequence 25, Application US/10889197
; Publication No. US20050271689A1
; GENERAL INFORMATION:
; APPLICANT: HUANG, CHUN-MING
; APPLICANT: ZHANG, JIANFENG
; APPLICANT: TANG, DE-CHU
; TITLE OF INVENTION: NOVEL TARGETS AND COMPOSITIONS FOR USE IN
; TITLE OF INVENTION: DECONTAMINATION, IMMUNOPROPHYLAXIS, AND POST-EXPOSURE
; FILE REFERENCE: 858610-2006.1
; CURRENT APPLICATION NUMBER: US/10/889,197
; CURRENT FILING DATE: 2004-07-12

/ PRIOR APPLICATION NUMBER: 60/486,369
/ PRIOR FILING DATE: 2003-07-11
/ NUMBER OF SEQ ID NOS: 44
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 25
/ LENGTH: 12
/ TYPE: PRF
/ ORGANISM: Bacillus anthracis
US-10-889-197-25

Query Match 26.7%; Score 28; DB 6; Length 12;
Best Local Similarity 55.6%; Pred. No. 59;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 PRGFTVGR 16
DB 4 PAGEFTGRK 12

RESULT 9

US-10-939-890-203
/ Sequence 203, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanisappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddi
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617, 70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 203
/ LENGTH: 15
/ TYPE: PRF
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Library Isolate
US-10-939-890-203

Query Match 26.7%; Score 28; DB 6; Length 15;
Best Local Similarity 71.4%; Pred. No. 76;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8
DB 4 PAGEFTGRK 12

DB 3 PCKGMLP 9

RESULT 10

US-11-054-515-3003
/ Sequence 3003, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PR523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3003
/ LENGTH: 16
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-11-054-515-3003

Query Match 26.7%; Score 28; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11
DB 4 DPLTGVSLDGF 14

RESULT 11

US-10-893-584-212
/ Sequence 212, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Adam
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ CURRENT FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 212

/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: E. coli
US-10-893-584-212

Query Match 26.7% Score 28; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.1e+02;
Matches 5; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 2 PAKGMSPPGIVG 14
DB 2 PGRVGGPGRVVG 14

RESULT 12
US-10-516-676-1
/ Sequence 1, Application US/10516676
/ Publication No. US20050244393A1
/ GENERAL INFORMATION:
/ APPLICANT: Philippart, Pierre
/ TITLE OF INVENTION: SEALANT OR TISSUE GENERATING PRODUCT
/ FILE REFERENCE: 232037
/ CURRENT APPLICATION NUMBER: US/10/516,676
/ CURRENT FILING DATE: 2004-12-03
/ PRIOR APPLICATION NUMBER: 10/176,401
/ PRIOR FILING DATE: 2002-06-21
/ NUMBER OF SEQ ID NOS: 1
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthesized
/ FEATURE:
/ OTHER INFORMATION: PEPGEN P15 (TM) SYNTHETIC PEPTIDE
US-10-516-676-1

Query Match 25.7% Score 27; DB 6; Length 15;
Best Local Similarity 40.0%; Pred. No. 1.1e+02;
Matches 6; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 5 GMSPPGIVGSEGV 19
DB 1 GTPGPGIAGQREV 15

RESULT 13
US-10-532-426-2
/ Sequence 2, Application US/10532426
/ Publication No. US2006009516A1
/ GENERAL INFORMATION:
/ APPLICANT: Rosenberg, Lawrence
/ TITLE OF INVENTION: USE OF INGP FOR REVERSING DIABETES
/ FILE REFERENCE: 1912-0308PUS1
/ CURRENT APPLICATION NUMBER: US/10/532,426
/ CURRENT FILING DATE: 2005-04-22
/ PRIOR APPLICATION NUMBER: US 60/420,677
/ PRIOR FILING DATE: 2002-10-24
/ NUMBER OF SEQ ID NOS: 2
/ SOFTWARE: PasteSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: INGP peptide
US-10-532-426-2

Query Match 25.7% Score 27; DB 6; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKMSPPG 10
DB 4 DPLGTGVSFDGF 13

RESULT 14
US-11-054-515-2153
/ Sequence 2153, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2153
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2153

Query Match 25.7% Score 27; DB 7; Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11
DB 4 DPLGTGVSFDGF 14

RESULT 15
US-11-054-515-2780
/ Sequence 2780, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19

```
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2780
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2780
```

```
Query Match      25.7% Score 27, DB 7, Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 DPAKMSPPGF 11
      |||
Db      4 DPLTGYSPDF 14
```

RESULT 16
US-11-054-515-2783

```
/ Sequence 2783, Application US/11054515
/ Publication No. US20050255532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
/ FILE REFERENCE: PFS23P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2783
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2783
```

```
Query Match      25.7% Score 27, DB 7, Length 16;
Best Local Similarity 54.5%; Pred. No. 1.2e+02;
Matches 6; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
```

```
Qy      1 DPAKMSPPGF 11
      |||
Db      4 DPLTGYSPDF 14
```

```
RESULT 17
US-11-053-100-18
/ Sequence 18, Application US/11053100
/ Publication No. US20050255554A1
/ GENERAL INFORMATION:
/ APPLICANT: CHILKOTI, Ashutosh
/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
/ FILE REFERENCE: 4176-101 CIP
/ CURRENT APPLICATION NUMBER: US/11/053,100
/ CURRENT FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: US 09/812,382
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,659
/ PRIOR FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 18
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial
/ OTHER INFORMATION: Synthetic Construct
/ FEATURE:
/ NAME/KEY: REPEAT
/ LOCATION: (1)..(20)
/ OTHER INFORMATION: BLP1 [K1V2P1-4]
US-11-053-100-18
```

```
Query Match      25.7% Score 27, DB 7, Length 20;
Best Local Similarity 52.9%; Pred. No. 1.5e+02;
Matches 9; Conservative 1; Mismatches 3; Indels 4; Gaps 2;
```

```
Qy      2 PAKGSPGFVGEKV 18
      |||
Db      2 PEGV--PG--VGVPV 14
```

```
RESULT 18
US-10-485-788A-598
/ Sequence 598, Application US/10485788A
/ Publication No. US20050282743A1
/ GENERAL INFORMATION:
/ APPLICANT: Lu, Peter S.
/ APPLICANT: Rabinowitz, Joshua D.
/ APPLICANT: Schweitzer, Johannes
/ APPLICANT: Carrick, Deanna Marie
/ APPLICANT: Arbor Vita Corporation
/ TITLE OF INVENTION: Molecular Interactions in Cells
/ FILE REFERENCE: 20054-003320US
/ CURRENT APPLICATION NUMBER: US/10/485,788A
/ CURRENT FILING DATE: 2004-02-03
/ PRIOR APPLICATION NUMBER: US 60/309,841
/ PRIOR FILING DATE: 2001-08-03
/ PRIOR APPLICATION NUMBER: US 60/360,061
/ PRIOR FILING DATE: 2002-02-25
/ PRIOR APPLICATION NUMBER: WO PCT/US02/24655
/ PRIOR FILING DATE: 2002-08-02
/ NUMBER OF SEQ ID NOS: 841
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 598
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-485-788A-598
```

```
Query Match      25.2% Score 26.5, DB 6, Length 20;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
Qy      1 DPAKMSPP 9
      |||
Db      10 DPGV-MSPP 17
```

```

RESULT 19
US-11-178-269-27
/ Sequence 27, Application US/11178269
/ Publication No. US20050272661A1
/ GENERAL INFORMATION:
/ APPLICANT: Richeleau, Elliott
/ APPLICANT: Cusack, Bernadette Marie
/ APPLICANT: Pang, Yuan-Ping
/ APPLICANT: McCormick, Daniel J.
/ APPLICANT: Faug, Abdul
/ APPLICANT: Tyler, Beth Marie
/ APPLICANT: Boules, Mona
/ TITLE OF INVENTION: NEO-TRYPTOPHAN
/ FILE REFERENCE: 07039/141001
/ CURRENT APPLICATION NUMBER: US/11/178,269
/ CURRENT FILING DATE: 2005-07-08
/ PRIOR APPLICATION NUMBER: US/10/858,226
/ PRIOR FILING DATE: 2004-06-01
/ PRIOR APPLICATION NUMBER: US/10/265,099
/ PRIOR FILING DATE: 2002-10-04
/ PRIOR APPLICATION NUMBER: US/09/755,638
/ PRIOR FILING DATE: 2001-01-05
/ PRIOR APPLICATION NUMBER: 09/289,693
/ PRIOR FILING DATE: 2001-01-18
/ PRIOR APPLICATION NUMBER: US 60/098,119
/ PRIOR FILING DATE: 1998-08-27
/ PRIOR APPLICATION NUMBER: US 60/092,195
/ PRIOR FILING DATE: 1998-07-09
/ PRIOR APPLICATION NUMBER: US 60/081,356
/ PRIOR FILING DATE: 1998-04-10
/ NUMBER OF SEQ ID NOS: 30
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 27
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetically generated peptide
US-11-178-269-27

Query Match          24.8%; Score 26; DB 7; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      8 PPGF 11
Db      2 PPGF 5

RESULT 20
US-10-939-890-193
/ Sequence 193, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussert, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibyllie
/ APPLICANT: Ramalingam, Kondareddar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo

```

```

/ APPLICANT: Swenson, Rolf B.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 193
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-193

Query Match          24.8%; Score 26; DB 6; Length 15;
Best Local Similarity 62.5%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY      1 DPAKMS 8
Db      2 DPAKMS 9

RESULT 21
US-10-893-584-240
/ Sequence 240, Application US/10893584
/ Publication No. US20050272048A1
/ GENERAL INFORMATION:
/ APPLICANT: Borgford, Thor
/ APPLICANT: Braun, Curtis
/ APPLICANT: Purac, Admir
/ APPLICANT: Stoll, Dominik
/ TITLE OF INVENTION: Ricin-Like Toxin Variants for Treatment of Cancer,
/ FILE REFERENCE: 10447-025
/ CURRENT APPLICATION NUMBER: US/10/893,584
/ CURRENT FILING DATE: 2004-07-19
/ PRIOR APPLICATION NUMBER: US 09/551,151
/ PRIOR FILING DATE: 2000-04-14
/ PRIOR APPLICATION NUMBER: US 09/403,752
/ PRIOR FILING DATE: 1999-10-29
/ PRIOR APPLICATION NUMBER: US 10/089,058
/ PRIOR FILING DATE: 2000-10-04
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 240
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: E. coli
US-10-893-584-240

Query Match          24.8%; Score 26; DB 6; Length 17;
Best Local Similarity 45.5%; Pred. No. 1.8e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY      9 PGFVGBGV 19
Db      4 PGFVGBGV 14

RESULT 22

```

US-10-842-206-26
; Sequence 26, Application US/10842206
; Publication No. US20050256039A1
; GENERAL INFORMATION:
; APPLICANT: Peterson, Jeffrey D
; APPLICANT: Sciore, Paul J
; TITLE OF INVENTION: NOVEL FIBROBLAST GROWTH FACTORS AND METHODS OF USE THEREOF
; FILE REFERENCE: Cura 570A
; CURRENT APPLICATION NUMBER: US/10/842,206
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 26
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-842-206-26

Query Match 24.8%; Score 26; DB 6; Length 18;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFVGBEGV 18
||: ||:
Db 9 GFLGGLEGL 17

RESULT 23

US-10-980-459-12
; Sequence 12, Application US/10980459
; Publication No. US20050256042A1
; GENERAL INFORMATION:
; APPLICANT: Alvarez, Enrique
; APPLICANT: Chilikuru, Rajeev A.
; APPLICANT: Jeffers, Michael E.
; APPLICANT: Larocheille, William J.
; APPLICANT: Lichenstein, Henri
; APPLICANT: Nandev, Pradyumna Kumar
; APPLICANT: Valac, Pascal
; APPLICANT: Yim, Zachary
; APPLICANT: Hahne, William
; TITLE OF INVENTION: Methods of Preventing and Treating Alimentary Mucositis
; FILE REFERENCE: Cura-57 AM
; CURRENT APPLICATION NUMBER: US/10/980,459
; CURRENT FILING DATE: 2004-11-03
; PRIOR APPLICATION NUMBER: 10/435,087
; PRIOR FILING DATE: 2003-5-9
; PRIOR APPLICATION NUMBER: 10/842,179
; PRIOR FILING DATE: 2004-5-10
; PRIOR APPLICATION NUMBER: 60/541,728
; PRIOR FILING DATE: 2004-2-4
; PRIOR APPLICATION NUMBER: 60/545,278
; PRIOR FILING DATE: 2004-2-18
; PRIOR APPLICATION NUMBER: 60/_____
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: CuraSeqList version 0.1
; SEQ ID NO 12
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-980-459-12

Query Match 24.8%; Score 26; DB 6; Length 18;
Best Local Similarity 55.6%; Pred. No. 1.9e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 10 GFVGBEGV 18
||: ||:
Db 9 GFLGGLEGL 17

RESULT 24

US-10-503-575-131
; Sequence 131, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drijfhout, Jan Mouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 131
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-131

Query Match 24.8%; Score 26; DB 6; Length 19;
Best Local Similarity 35.7%; Pred. No. 2e+02;
Matches 5; Conservative 4; Mismatches 3; Indels 2; Gaps 1;

Qy 8 PPGG-FVGBEGVL 19
||| : ||:
Db 1 PPGGGLAGGORGIV 14

RESULT 25

US-10-997-201A-31
; Sequence 31, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sul, Jianhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; CURRENT FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-31

Query Match 24.8%; Score 26; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 6 MSPGGFVGB 15
: ||| ||
Db 9 LGPPGGPPGE 18

RESULT 26
US-10-623-155-532
; Sequence 532, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY

/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 532
/ LENGTH: 20
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-623-155-532

Query Match 24.8%; Score 26; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRIVSEB 17
| :| :| :|
Db 10 GRIKKEG 17

RESULT 27
US-10-623-155-542
/ Sequence 542, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 542
/ LENGTH: 20
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-623-155-542

Query Match 24.8%; Score 26; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9
| :| :| :|
Db 10 PPSAMTPP 17

RESULT 28
US-10-623-155-545
/ Sequence 545, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 545
/ LENGTH: 20
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-623-155-545

Query Match 24.8%; Score 26; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 GRIVSEB 17
| :| :| :|
Db 9 GRIKKEG 16

RESULT 29
US-10-989-226-81
/ Sequence 81, Application US/10989226
/ Publication No. US20050255491A1
/ GENERAL INFORMATION:
/ APPLICANT: Lee, Frank D.
/ APPLICANT: Meng, Xun
/ APPLICANT: Afeyan, Noubat B.
/ APPLICANT: Gordon, Neal F.
/ TITLE OF INVENTION: SMALL MOLECULE AND PEPTIDE ARRAYS AND
/ TITLE OF INVENTION: USES THEREOF
/ FILE REFERENCE: EPTM-P01-005
/ CURRENT APPLICATION NUMBER: US/10/989,226
/ CURRENT FILING DATE: 2004-11-15
/ PRIOR APPLICATION NUMBER: US 60/519,530
/ PRIOR FILING DATE: 2003-11-13
/ PRIOR APPLICATION NUMBER: US 60/532,687
/ PRIOR FILING DATE: 2003-12-24
/ NUMBER OF SEQ ID NOS: 84
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 81
/ LENGTH: 8
/ TYPE: PRF
/ ORGANISM: Homo sapiens
US-10-989-226-81

Query Match 23.8%; Score 25; DB 6; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSPPG 10
| :| :| :|
Db 4 VSPPG 8

RESULT 30
US-11-053-100-9
/ Sequence 9, Application US/11053100
/ Publication No. US20050255554A1
/ GENERAL INFORMATION:
/ APPLICANT: CHILKOTI, Ashutosh
/ TITLE OF INVENTION: FUSION PEPTIDES ISOLATABLE BY PHASE TRANSITION
/ FILE REFERENCE: 4176-101 CIP
/ CURRENT APPLICATION NUMBER: US/11/053,100
/ CURRENT FILING DATE: 2005-02-08
/ PRIOR APPLICATION NUMBER: US 09/812,382
/ PRIOR FILING DATE: 2001-03-20
/ PRIOR APPLICATION NUMBER: US 60/190,659
/ PRIOR FILING DATE: 2000-03-20
/ NUMBER OF SEQ ID NOS: 58
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 9
/ LENGTH: 9
/ TYPE: PRF
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic Construct
US-11-053-100-9

Query Match 23.8%; Score 25; DB 7; Length 9;
Best Local Similarity 83.3%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGRVIG 14
|||
DB 2 PGRVIG 7

```
RESULT 31
US-11-045-024-1467
; Sequence 1467, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Bstedan
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1467
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1467

Query Match 23.8%; Score 25; DB 7; Length 11;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6285
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6285

Query Match 23.8%; Score 25; DB 7; Length 11;
Best Local Similarity 45.5%; Pred. No. 1.6e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
RESULT 33
US-11-116-144-285
; Sequence 285, Application US/11116144
; Publication No. US20050277181A1
; GENERAL INFORMATION:
; APPLICANT: BERTHET, FRANCOIS XAVIER
; APPLICANT: CASADEVAL, FRANCESC VAYREDA
; APPLICANT: SANZ MARIA, MARIA CRUZ
; APPLICANT: GARCIA, TERESA LLOP
; APPLICANT: OLE, ANGELS MOR
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
; TITLE OF INVENTION: INFECTION
; FILE REFERENCE: INT-084
; CURRENT FILING DATE: US/11/116,144
; CURRENT FILING DATE: 2005-04-27
; PRIOR APPLICATION NUMBER: PCT/ES04/000581
; PRIOR FILING DATE: 2004-12-23
; PRIOR APPLICATION NUMBER: EP 03380307.3
; PRIOR FILING DATE: 2003-12-23
; NUMBER OF SEQ ID NOS: 301
; SOFTWARE: Patentin Ver. 3.3
; SEQ ID NO 285
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Trypanosoma cruzi
US-11-116-144-285

Query Match 23.8%; Score 25; DB 7; Length 14;
Best Local Similarity 40.0%; Pred. No. 2e+02;
Matches 4; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 11 PVRGEGVLS 20
::|||:
DB 2 YVCGEKGHIA 11
```


RESULT 34
US-11-060-646-5
Sequence 5, Application US/11060646
Publication No. US2005025555A1
GENERAL INFORMATION:
APPLICANT: Johns, Terrance Grant
APPLICANT: Scott, Andrew Mark
APPLICANT: Burgess, Anthony Wilks
APPLICANT: Old, Lloyd J.
APPLICANT: Adams, Timothy E.
APPLICANT: Wiltup, K. Dane
APPLICANT: Chao, Ginger
TITLE OF INVENTION: EGF Receptor Epitope Peptides and Uses
TITLE OF INVENTION: Thereof
FILE REFERENCE: 2332-1-011N
CURRENT APPLICATION NUMBER: US/11/060,646
CURRENT FILING DATE: 2005-02-17
PRIOR APPLICATION NUMBER: 60/546,602
PRIOR FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/584,623
PRIOR FILING DATE: 2004-07-01
NUMBER OF SEQ ID NOS: 17
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: epitope peptide
US-11-060-646-5

Query Match 23.8%; Score 25; DB 7; Length 16;
Best Local Similarity 45.5%; Pred. No. 2.4e+02;
Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
QY 8 PGPVGEBCV 18
DB 3 PDSYEVBCV 13

RESULT 35
US-11-193-512-47
Sequence 47, Application US/1193512
Publication No. US20050272918A1
GENERAL INFORMATION:
APPLICANT: KOIKE, Masaichi
FURUYA, Akiho
NAKAMURA, Kazuyasu
IIDA, Akihiko
ANAZAWA, Hideharu
HANAI, Nobuo
TAKATSU, Kiyoshi
TITLE OF INVENTION: Antibody Against Human Interleukin-5
Receptor Alpha Chain
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Pennie & Edmonds LLP
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10036
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11/193,512
FILING DATE: 01-Aug-2005
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/10/283,349
FILING DATE: 29-Oct-2002
APPLICATION NUMBER: US/08/836,561
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: JP 232384/95
FILING DATE: 11-SEP-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lawrence, III, Stanton T
REGISTRATION NUMBER: 25,736
REFERENCE/DOCKET NUMBER: 7005-115-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 47:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 47:
US-11-193-512-47

Query Match 23.8%; Score 25; DB 7; Length 17;
Best Local Similarity 53.8%; Pred. No. 2.5e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 2; Gaps 1;
QY 1 DPAKG--MSPPGF 11
DB 3 DPANGTKSDPKF 15

RESULT 36
US-10-893-584-233
Sequence 233, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Adam
APPLICANT: Scoll, Donald
TITLE OF INVENTION: Richin-Like Toxin Variants for Treatment of Cancer,
Viral or Parasitic Infections
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 233
LENGTH: 19
TYPE: PRT
ORGANISM: E. coli
US-10-893-584-233

Query Match 23.8%; Score 25; DB 6; Length 19;
Best Local Similarity 55.6%; Pred. No. 2.9e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGPVGEBCV 17
DB 5 PGRVGGG 13

RESULT 37
US-10-623-155-414
Sequence 414, Application US/10623155

```
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Reiter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 414
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-414
```

```
Query Match      23.8%; Score 25; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 IVGEG 17
|:|:|
Db      1 IIGKEG 6
```

```
RESULT 38
US-10-623-155-525
/ Sequence 525, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Reiter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ CURRENT FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 525
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-525
```

```
Query Match      23.8%; Score 25; DB 6; Length 20;
Best Local Similarity 66.7%; Pred. No. 3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      12 IVGEG 17
|:|:|
Db      1 IIGKEG 6
```

```
RESULT 39
US-11-105-708-11
/ Sequence 11, Application US/11105708
/ Publication No. US20050281821A1
/ GENERAL INFORMATION:
/ APPLICANT: Pernaaseth, Flavia
/ APPLICANT: Freimark, Bruce
/ APPLICANT: Van Epps, Dennis
/ APPLICANT: Brooks, Peter C
/ TITLE OF INVENTION: Method and Composition for Angiogenesis Inhibition
/ FILE REFERENCE: 30797-704.501
/ CURRENT APPLICATION NUMBER: US/11/105, 708
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: 09/478, 977
```

```
/ PRIOR FILING DATE: 2000-01-06
/ PRIOR APPLICATION NUMBER: 60/152,496
/ PRIOR FILING DATE: 1999-09-02
/ PRIOR APPLICATION NUMBER: 60/143,534
/ PRIOR FILING DATE: 1999-09-02
/ PRIOR APPLICATION NUMBER: 60/114,878
/ PRIOR FILING DATE: 1999-01-06
/ PRIOR APPLICATION NUMBER: 60/114,877
/ PRIOR FILING DATE: 1998-01-06
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 11
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-105-708-11
```

```
Query Match      23.3%; Score 24.5; DB 7; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 6; Conservative 1; Mismatches 1; Indels 1; Gaps 1;
```

```
Qy      9 PGFIVGEG 17
|:|:|
Db      2 PGF-RGDEG 9
```

```
RESULT 40
US-10-986-501-338
/ Sequence 338, Application US/10986501
/ Publication No. US2005024845A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2C1
/ CURRENT APPLICATION NUMBER: US/10/986,501
/ CURRENT FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: US/10/621,363
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 338
/ LENGTH: 7
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-338
```

```
Query Match      22.9%; Score 24; DB 6; Length 7;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      1 DPAKG 5
|:|:|
Db      2 DPAKG 6
```

```
RESULT 41
US-11-045-024-1247
/ Sequence 1247, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ SEQUENCE FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1247
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1247

Query Match      22.9%; Score 24; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 PAKMSPP 9
      ||: ||
Db      1 PABPTAP 8

RESULT 42
US-11-045-024-8847
/ Sequence 8847, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bateban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
```

```

/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 8847
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8847

Query Match      22.9%; Score 24; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      2 PAKMSPP 9
      ||: ||
Db      1 PABPTAP 8

RESULT 43
US-10-919-492-35
/ Sequence 35, Application US/10919492
/ Publication No. US2005028249A1
/ GENERAL INFORMATION:
/ APPLICANT: STOUGAARD, PETER
/ APPLICANT: HANSEN, OLE CAI
/ TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE. A METHOD OF PRODUCING
/ FILE REFERENCE: 14923.0014
/ CURRENT APPLICATION NUMBER: US/10/919,492
/ CURRENT FILING DATE: 2004-08-17
/ PRIOR APPLICATION NUMBER: 09/824,053
/ PRIOR FILING DATE: 2001-04-03
/ PRIOR APPLICATION NUMBER: 08/669,304
/ PRIOR FILING DATE: 1996-07-12
/ PRIOR APPLICATION NUMBER: PCT/DK96/00238
/ PRIOR FILING DATE: 1996-06-04
/ PRIOR APPLICATION NUMBER: 08/476,910
/ PRIOR FILING DATE: 1995-06-07
/ NUMBER OF SEQ ID NOS: 37
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 35
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
US-10-919-492-35

Query Match      22.9%; Score 24; DB 6; Length 10;
Best Local Similarity 80.0%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      9 PGRTV 13
      ||: ||
Db      2 PGRTV 6
```

```
RESULT 44
US-11-045-024-5221
; Sequence 5221, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celsis, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 5221
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5221

Query Match          22.9%; Score 24; DB 7; Length 10;
Best Local Similarity 50.0%; Pred. No. 2e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-129-104-61

Query Match          22.9%; Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      5 GMSPPG 10
DB      3 GAPPPG 8

RESULT 45
US-11-129-104-61
; Sequence 61, Application US/11129104
; Publication No. US20050287644A1
; GENERAL INFORMATION:
; APPLICANT: CHIU, YI-FANG
; APPLICANT: CHEN, LEE-HSIUAN
; APPLICANT: HUANG, JEN-PIN
; TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
; TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
; TITLE OF INVENTION: RABBIT-MOUSE HYBRIDOMAS
; FILE REFERENCE: 09468.0005-00000
; CURRENT APPLICATION NUMBER: US/11/129,104
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/571,440
; PRIOR FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
US-11-129-104-7

Query Match          22.9%; Score 24; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      8 PPGKIV 13
DB      2 PPGKIV 7

RESULT 47
US-11-129-104-7
; Sequence 7, Application US/11129104
; Publication No. US20050287644A1
; GENERAL INFORMATION:
; APPLICANT: CHIU, YI-FANG
; APPLICANT: CHEN, LEE-HSIUAN
; APPLICANT: HUANG, JEN-PIN
; TITLE OF INVENTION: METHODS FOR PRODUCING AND CULTURING RABBIT-MOUSE
; TITLE OF INVENTION: HYBRIDOMAS AND MONOCLONAL ANTIBODIES SECRETED BY
; TITLE OF INVENTION: RABBIT-MOUSE HYBRIDOMAS
; FILE REFERENCE: 09468.0005-00000
; CURRENT APPLICATION NUMBER: US/11/129,104
; CURRENT FILING DATE: 2005-05-13
; PRIOR APPLICATION NUMBER: 60/571,440
; PRIOR FILING DATE: 2004-05-14
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 3.3
; SEQ ID NO 7
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Unknown Organism
; FEATURE:
; OTHER INFORMATION: Description of Unknown Organism: Human, Mouse, or
US-11-129-104-7
```

Query Match 22.9%; Score 24; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 PGPIV 13
DB 2 PGPIV 7

RESULT 48

US-10-866-120-4
Sequence 4, Application US/10866120
Publication No. US20050271173A1
GENERAL INFORMATION:
APPLICANT: Chin, Li-Te
APPLICANT: Heu, Shu-Ching
TITLE OF INVENTION: METHOD FOR PRODUCING HUMAN ANTIBODIES OF AGONIST, ANTAGONIST, OR
FILE REFERENCE: P7226/0600
CURRENT APPLICATION NUMBER: US/10/866,120
CURRENT FILING DATE: 2004-06-14
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn version 3.3
SEQ ID NO 4
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(15)
US-10-866-120-4

Query Match 22.9%; Score 24; DB 6; Length 15;
Best Local Similarity 44.4%; Pred. No. 3.1e+02;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGPIV 14
DB 5 MYPPPYLG 13

RESULT 49

US-10-919-492-6
Sequence 6, Application US/10919492
Publication No. US20050282249A1
GENERAL INFORMATION:
APPLICANT: STOUGAARD, PETER
APPLICANT: HANSEN, OLE CAI
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING
FILE REFERENCE: 14923.0014
CURRENT APPLICATION NUMBER: US/10/919,492
CURRENT FILING DATE: 2004-08-17
PRIOR APPLICATION NUMBER: 09/824,053
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 08/669,304
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: PCT/DK96/00238
PRIOR FILING DATE: 1996-06-04
PRIOR APPLICATION NUMBER: 08/476,910
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 6
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
FEATURE:
NAME/KEY: MOD_RES

LOCATION: (14)
OTHER INFORMATION: any naturally occurring amino acid, Asx or Glx
US-10-919-492-6

Query Match 22.9%; Score 24; DB 6; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGPIV 13
DB 2 PGPIV 6

RESULT 50

US-10-919-492-13
Sequence 13, Application US/10919492
Publication No. US20050282249A1
GENERAL INFORMATION:
APPLICANT: STOUGAARD, PETER
APPLICANT: HANSEN, OLE CAI
TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING
FILE REFERENCE: 14923.0014
CURRENT APPLICATION NUMBER: US/10/919,492
CURRENT FILING DATE: 2004-08-17
PRIOR APPLICATION NUMBER: 09/824,053
PRIOR FILING DATE: 2001-04-03
PRIOR APPLICATION NUMBER: 08/669,304
PRIOR FILING DATE: 1996-07-12
PRIOR APPLICATION NUMBER: PCT/DK96/00238
PRIOR FILING DATE: 1996-06-04
PRIOR APPLICATION NUMBER: 08/476,910
PRIOR FILING DATE: 1995-06-07
NUMBER OF SEQ ID NOS: 37
SOFTWARE: PatentIn Ver. 3.2
SEQ ID NO 13
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-919-492-13

Query Match 22.9%; Score 24; DB 6; Length 15;
Best Local Similarity 80.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 PGPIV 13
DB 2 PGPIV 6

RESULT 51

US-10-503-575-119
Sequence 119, Application US/10503575
Publication No. US20050244823A1
GENERAL INFORMATION:
APPLICANT: Drifhout, Jan Wouter
APPLICANT: van Veele, Petrus Antonius
APPLICANT: Koning, Frits
TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
FILE REFERENCE: 2799/72843-PCT-US
CURRENT APPLICATION NUMBER: US/10/503,575
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: PCT/NL03/00077
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: EP 02075456.0
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.1
SEQ ID NO 119

LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-575-119

Query Match 22.9%; Score 24; DB 6; Length 19;
Best Local Similarity 42.9%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 KMSPPGRTVREG 17
DB 4 KGPSPGQGPAGEG 17

RESULT 52
US-11-022-562-145

Sequence 145, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Rupprecht, Ruth M.
APPLICANT: Shieng, Jlang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 145
LENGTH: 20
TYPE: PRT
ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-145

Query Match 22.9%; Score 24; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPPGF 11
DB 14 APPGY 18

RESULT 53
US-11-022-562-146

Sequence 146, Application US/11022562
Publication No. US20050249742A1
GENERAL INFORMATION:
APPLICANT: Rupprecht, Ruth M.
APPLICANT: Shieng, Jlang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562
CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 146
LENGTH: 20
TYPE: PRT
ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-146

Query Match 22.9%; Score 24; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 4.4e+02;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 7 SPPGF 11
DB 4 APPGY 8

RESULT 54
US-10-485-788A-79

Sequence 79, Application US/10485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-00320US
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79
LENGTH: 7
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-79

Query Match 21.9%; Score 23; DB 6; Length 7;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSP 9
DB 1 MSP 4

RESULT 55
US-10-485-788A-80

Sequence 80, Application US/10485788A
Publication No. US20050282743A1
GENERAL INFORMATION:
APPLICANT: Lu, Peter S.
APPLICANT: Rabinowitz, Joshua D.
APPLICANT: Schweizer, Johannes
APPLICANT: Carrick, Deanna Marie
TITLE OF INVENTION: Molecular Interactions in Cells
FILE REFERENCE: 20054-00320US
CURRENT APPLICATION NUMBER: US/10/485,788A
CURRENT FILING DATE: 2004-02-03
PRIOR APPLICATION NUMBER: US 60/309,841
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 60/360,061
PRIOR FILING DATE: 2002-02-25
PRIOR APPLICATION NUMBER: WO PCT/US02/24655
PRIOR FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 841
SOFTWARE: PatentIn version 3.1
SEQ ID NO 80
LENGTH: 8
TYPE: PRT
ORGANISM: Homo sapiens
US-10-485-788A-80

Query Match 21.9%; Score 23; DB 6; Length 8;

Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 MSPP 9
|||
Db 2 MSPP 5

RESULT 56

US-10-850-635-26
; Sequence 26; Application US/10850635
; Publication No. US20050287149A1
; GENERAL INFORMATION:
; APPLICANT: Keiler, Tibor
; APPLICANT: Lowy, Israel
; APPLICANT: Vitale, Laura
; APPLICANT: Blaneset, Diane
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES AGAINST
; FILE REFERENCE: MXI-305
; CURRENT APPLICATION NUMBER: US/10/850,635
; CURRENT FILING DATE: 2004-05-21
; PRIOR APPLICATION NUMBER: 60/472636
; PRIOR FILING DATE: 2003-05-21
; PRIOR APPLICATION NUMBER: 60/512336
; PRIOR FILING DATE: 2003-10-16
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 26
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-850-635-26

Query Match 21.9%; Score 23; DB 6; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 GMSPP 9
|||
Db 4 GMSPP 8

RESULT 57

US-11-010-748A-617
; Sequence 617; Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 617
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-617

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFPLG 14
|||
Db 1 PGFPLG 6

RESULT 58

US-11-010-748A-618
; Sequence 618; Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 618
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-618

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFPLG 14
|||
Db 3 PGFPLG 8

RESULT 59

US-11-010-748A-620
; Sequence 620; Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: WOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; CURRENT FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 620
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-620

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14
||| : |
Db 4 PGFPIG 9

RESULT 60
US-11-010-748A-621
; Sequence 621, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 621
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-621

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14
||| : |
Db 2 PGFPIG 7

RESULT 61
US-11-010-748A-625
; Sequence 625, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 625
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-625

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Db 4 PGFPIG 9
||| : |

RESULT 62
US-11-010-748A-635
; Sequence 635, Application US/11010748A
; Publication No. US20050244421A1
; GENERAL INFORMATION:
; APPLICANT: Merck Patent GmbH
; APPLICANT: STRITTMAYER, Wolfgang
; APPLICANT: MOLL, Heidrun
; APPLICANT: SCHARM, Burkhard
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
; FILE REFERENCE: MER-136
; CURRENT APPLICATION NUMBER: US/11/010,748A
; PRIOR FILING DATE: 2004-12-13
; PRIOR APPLICATION NUMBER: PCT/EP03/06251
; PRIOR FILING DATE: 2003-06-13
; PRIOR APPLICATION NUMBER: EP02013423.5
; PRIOR FILING DATE: 2002-06-13
; NUMBER OF SEQ ID NOS: 926
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 635
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HLA-binding peptide of Seq. No. 611
US-11-010-748A-635

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 9 PGFIVG 14
||| : |
Db 1 PGFPIG 6

RESULT 63
US-11-055-557-28
; Sequence 28, Application US/11055557
; Publication No. US20050255083A1
; GENERAL INFORMATION:
; APPLICANT: Leppla, Stephen H.
; APPLICANT: Liu, Shi-Hui
; APPLICANT: Bugge, Thomas H.
; APPLICANT: The Government of the United States of America
; APPLICANT: as represented by the Secretary of the
; APPLICANT: Department of Health and Human Services
; TITLE OF INVENTION: Multimeric Protein Toxins to Target Cells Having
; TITLE OF INVENTION: Multiple Identifying Characteristics
; FILE REFERENCE: 015280-501100US
; CURRENT APPLICATION NUMBER: US/11/055,557
; PRIOR FILING DATE: 2005-02-09
; PRIOR APPLICATION NUMBER: US 60/543,417
; PRIOR FILING DATE: 2004-02-09
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasminogen
; OTHER INFORMATION: activator cleavage site, uPA and tPA physiological
; OTHER INFORMATION: substrate sequence
US-11-055-557-28

Query Match 21.9%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14
||:|
Db 3 PGRVIG 8

RESULT 64

US-11-033-365-22
Sequence 22, Application US/11033365
Publication No. US20050250678A1
GENERAL INFORMATION:
APPLICANT: NeoSeo Technologies Inc.
APPLICANT: Defrees, Shawn
APPLICANT: Zopf, David
APPLICANT: Wang, Zhigang
APPLICANT: Clausen, Henrik
TITLE OF INVENTION: O-Linked Glycosylation of peptides
FILE REFERENCE: 040853-01-5138
CURRENT APPLICATION NUMBER: US/11/033,365
CURRENT FILING DATE: 2005-01-10
PRIOR APPLICATION NUMBER: 60/535,284
PRIOR FILING DATE: 2004-01-08
PRIOR APPLICATION NUMBER: 60/544,411
PRIOR FILING DATE: 2004-02-12
PRIOR APPLICATION NUMBER: 60/546,631
PRIOR FILING DATE: 2004-02-20
PRIOR APPLICATION NUMBER: 60/555,813
PRIOR FILING DATE: 2004-03-23
PRIOR APPLICATION NUMBER: 60/570,891
PRIOR FILING DATE: 2004-05-12
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PatentIn version 3.2
SEQ ID NO 22
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-11-033-365-22

Query Match 21.9%; Score 23; DB 7; Length 11;
Best Local Similarity 42.9%; Pred. No. 3.2e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMSP 8
||:|
Db 3 PTGSLCP 9

RESULT 65

US-10-893-584-102
Sequence 102, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Adam
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 102
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence

FEATURE:
OTHER INFORMATION: Mutant preprotrixin linker region for Urokinase-Type Plasminogen
US-10-893-584-102

Query Match 21.9%; Score 23; DB 6; Length 12;
Best Local Similarity 66.7%; Pred. No. 3.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14
||:|
Db 4 PGRVIG 9

RESULT 66

US-10-893-584-198
Sequence 198, Application US/10893584
Publication No. US20050272048A1
GENERAL INFORMATION:
APPLICANT: Borgford, Thor
APPLICANT: Braun, Curtis
APPLICANT: Purac, Adam
APPLICANT: Stoll, Dominik
TITLE OF INVENTION: Richn-like Toxin Variants for Treatment of Cancer,
FILE REFERENCE: 10447-025
CURRENT APPLICATION NUMBER: US/10/893,584
CURRENT FILING DATE: 2004-07-19
PRIOR APPLICATION NUMBER: US 09/551,151
PRIOR FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: US 09/403,752
PRIOR FILING DATE: 1999-10-29
PRIOR APPLICATION NUMBER: US 10/089,058
PRIOR FILING DATE: 2000-10-04
NUMBER OF SEQ ID NOS: 274
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 198
LENGTH: 13
TYPE: PRT
ORGANISM: E. coli
US-10-893-584-198

Query Match 21.9%; Score 23; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 3.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14
||:|
Db 2 PGRVIG 7

RESULT 67

US-10-746-959C-5
Sequence 5, Application US/10746959C
Publication No. US20050260222A1
GENERAL INFORMATION:
APPLICANT: Los Alamos National Laboratory
APPLICANT: Gupta, Goutam, et al.
TITLE OF INVENTION: STRUCTURE-BASED RECEPTOR MIMICS TARGETED AGAINST BACTERIAL
FILE REFERENCE: S-99,945
CURRENT APPLICATION NUMBER: US/10/746,959C
CURRENT FILING DATE: 2003-12-24
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.2
SEQ ID NO 5
LENGTH: 14
TYPE: PRT
ORGANISM: Homo Sapiens
US-10-746-959C-5

Query Match 21.9%; Score 23; DB 6; Length 14;
Best Local Similarity 50.0%; Pred. No. 4.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Oy 2 PAKGMSPP 9
|||
Db 6 PAKGSTAPP 13

RESULT 68
US-10-939-890-200
; Sequence 200, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palanlappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 200
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-200

Query Match 21.9%; Score 23; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 PAKGMSPP 8
|||
Db 3 PCKGYMP 9

RESULT 69
US-10-939-890-202
; Sequence 202, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe

; APPLICANT: Bussat, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palanlappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 202
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-202

Query Match 21.9%; Score 23; DB 6; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Oy 2 PAKGMSPP 8
|||
Db 3 PCKGYMP 9

RESULT 70
US-10-893-584-247
; Sequence 247, Application US/10893584
; Publication No. US20050272048A1
; GENERAL INFORMATION:
; APPLICANT: Borgford, Thor
; APPLICANT: Braun, Curtis
; APPLICANT: Purac, Adamir
; APPLICANT: Stoll, Dominik
; TITLE OF INVENTION: Rac1-like Toxin Variants for Treatment of Cancer.
; TITLE OF INVENTION: Viral or Parasitic Infections
; FILE REFERENCE: 10447-025
; CURRENT APPLICATION NUMBER: US/10/893,584
; PRIOR FILING DATE: 2004-07-19
; PRIOR APPLICATION NUMBER: US 09/551,151
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: US 09/403,752
; PRIOR FILING DATE: 1999-10-29
; PRIOR APPLICATION NUMBER: US 10/089,058
; PRIOR FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 274
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 247
; LENGTH: 15
; TYPE: PRT
; ORGANISM: E. coli

US-10-893-584-247

Query Match 21.9%; Score 23; DB 6; Length 15;
Best Local Similarity 66.7%; Pred. No. 4.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVVG 14
|||
Db 3 PGFVVG 8

RESULT 71

US-11-187-558-4

Sequence 4, Application US/11187558

Publication No. US20050271655A1

GENERAL INFORMATION:

APPLICANT: Huang, Xin-Yun

TITLE OF INVENTION: METHODS FOR DESIGNING SPECIFIC ION CHANNEL BLOCKERS

FILE REFERENCE: 19603/1454

CURRENT APPLICATION NUMBER: US/11/187,558

CURRENT FILING DATE: 2005-07-22

PRIOR APPLICATION NUMBER: 60/079,268

PRIOR FILING DATE: 1998-03-25

PRIOR APPLICATION NUMBER: 09/273,217

PRIOR FILING DATE: 1999-03-19

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 4

LENGTH: 15

TYPE: PRT

ORGANISM: rat

US-11-187-558-4

Query Match 21.9%; Score 23; DB 7; Length 15;
Best Local Similarity 57.1%; Pred. No. 4.5e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DPAKGS 7
|||
Db 6 DPTSGFS 12

RESULT 72

US-10-919-492-3

Sequence 3, Application US/10919492

Publication No. US20050282249A1

GENERAL INFORMATION:

APPLICANT: STOUGAARD, PETER

TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING

FILE REFERENCE: 14923.0014

CURRENT APPLICATION NUMBER: US/10/919,492

CURRENT FILING DATE: 2004-08-17

PRIOR APPLICATION NUMBER: 09/824,053

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: 08/669,304

PRIOR FILING DATE: 1996-07-12

PRIOR APPLICATION NUMBER: PCT/DK96/00238

PRIOR FILING DATE: 1996-06-04

PRIOR APPLICATION NUMBER: 08/476,910

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 3

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES: Description of Artificial Sequence: Synthetic

OTHER INFORMATION: Peptide

FEATURE: NAME/KEY: MOD_RES

LOCATION: (15)
OTHER INFORMATION: any naturally occurring amino acid, Asx or Glx
US-10-919-492-3

Query Match 21.9%; Score 23; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MSPPGFI 12
|||
Db 4 MSPRGVI 10

RESULT 73

US-10-919-492-10

Sequence 10, Application US/10919492

Publication No. US20050282249A1

GENERAL INFORMATION:

APPLICANT: STOUGAARD, PETER

TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING

FILE REFERENCE: 14923.0014

CURRENT APPLICATION NUMBER: US/10/919,492

CURRENT FILING DATE: 2004-08-17

PRIOR APPLICATION NUMBER: 09/824,053

PRIOR FILING DATE: 2001-04-03

PRIOR APPLICATION NUMBER: 08/669,304

PRIOR FILING DATE: 1996-07-12

PRIOR APPLICATION NUMBER: PCT/DK96/00238

PRIOR FILING DATE: 1996-06-04

PRIOR APPLICATION NUMBER: 08/476,910

PRIOR FILING DATE: 1995-06-07

NUMBER OF SEQ ID NOS: 37

SOFTWARE: PatentIn Ver. 3.2

SEQ ID NO 10

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURES:

OTHER INFORMATION: Description of Artificial Sequence: Synthetic

US-10-919-492-10

Query Match 21.9%; Score 23; DB 6; Length 16;
Best Local Similarity 71.4%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 MSPPGFI 12
|||
Db 4 MSPRGVI 10

RESULT 74

US-11-108-185-42

Sequence 42, Application US/11108185

Publication No. US20050262591A1

GENERAL INFORMATION:

APPLICANT: Debonte, Lorin R.

TITLE OF INVENTION: FATY ACID DESATURASES AND MUTANT SEQUENCES THEREOF

FILE REFERENCE: 07148-063003

CURRENT APPLICATION NUMBER: US/11/108,185

CURRENT FILING DATE: 2005-04-18

PRIOR APPLICATION NUMBER: US/09/771,904

PRIOR FILING DATE: 2001-01-29

PRIOR APPLICATION NUMBER: US 08/874,109

PRIOR FILING DATE: 1997-06-12

NUMBER OF SEQ ID NOS: 70

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 42

LENGTH: 16

TYPE: PRT
ORGANISM: Rictinus communis
US-11-108-185-42

Query Match 21.9%; Score 23; DB 7; Length 16;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SPFGFIV 13
DB 10 NPPGRIM 16

RESULT 75
US-10-880-238-107
Sequence 107, Application US/10880238
Publication No. US20050287538A1
GENERAL INFORMATION:
APPLICANT: Cheng, Ming-Tai
TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
FILE REFERENCE: 17329-003001
CURRENT APPLICATION NUMBER: US/10/880,238
CURRENT FILING DATE: 2004-06-29
NUMBER OF SEQ ID NOS: 214
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 107
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-107

Query Match 21.9%; Score 23; DB 6; Length 17;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5
DB 3 DPAMG 7

RESULT 76
US-10-880-238-109
Sequence 109, Application US/10880238
Publication No. US20050287538A1
GENERAL INFORMATION:
APPLICANT: Cheng, Ming-Tai
TITLE OF INVENTION: FRAME-SHIFTING PCR FOR GERMLINE
FILE REFERENCE: 17329-003001
CURRENT APPLICATION NUMBER: US/10/880,238
CURRENT FILING DATE: 2004-06-29
NUMBER OF SEQ ID NOS: 214
SOFTWARE: PaateSeq for Windows Version 4.0
SEQ ID NO 109
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated peptide
US-10-880-238-109

Query Match 21.9%; Score 23; DB 6; Length 17;
Best Local Similarity 80.0%; Pred. No. 5.2e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5
DB 3 DPAMG 7

RESULT 77
US-11-010-748A-405
Sequence 405, Application US/11010748A
Publication No. US20050244421A1
GENERAL INFORMATION:
APPLICANT: Merck Patent GmbH
APPLICANT: STRITTMAYER, Wolfgang
APPLICANT: MOLL, Heidrun
APPLICANT: SCHARM, Burkhard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
FILE REFERENCE: MER-136
CURRENT APPLICATION NUMBER: US/11/010,748A
PRIOR FILING DATE: 2004-12-13
PRIOR APPLICATION NUMBER: PCT/EP03/06251
PRIOR FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: EP02013423.5
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 926
SOFTWARE: PatentIn version 3.1
SEQ ID NO 405
LENGTH: 17
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: CD42b peptide fragment
US-11-010-748A-405

Query Match 21.9%; Score 23; DB 7; Length 17;
Best Local Similarity 37.5%; Pred. No. 5.2e+02;
Matches 6; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

QY 2 PAKGMSPPGFIVGEERG 17
DB 6 PAKGCP---TLGDEG 17

RESULT 78
US-11-033-039-1324
Sequence 1324, Application US/11033039
Publication No. US20060002947A1
GENERAL INFORMATION:
APPLICANT: HUMPHREYS, ROBERT
APPLICANT: XU, MINZHEN
TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIPTOPE HYBRID PEPTIDE VACCINES
FILE REFERENCE: REH-2017US01
CURRENT APPLICATION NUMBER: US/11/033,039
CURRENT FILING DATE: 2005-01-11
PRIOR FILING DATE: 2002-09-17
PRIOR APPLICATION NUMBER: 10/245,871
PRIOR FILING DATE: 2002-07-17
PRIOR APPLICATION NUMBER: 09/396,813
PRIOR FILING DATE: 1999-09-14
NUMBER OF SEQ ID NOS: 1452
SOFTWARE: PatentIn version 3.3
SEQ ID NO 1324
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: hybrid peptide
NAME/KEY: MOD_RBS
LOCATION: (5)..(5)
OTHER INFORMATION: Ava
US-11-033-039-1324

Query Match 21.9%; Score 23; DB 7; Length 18;
Best Local Similarity 44.4%; Pred. No. 5.5e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 9 PGFVGEVG 17
| | | | |
Db 8 PGLVAGWYG 16

RESULT 79
US-10-503-575-224
; Sequence 224, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Driffhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR FILING DATE: 2002-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 224
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-224

Query Match 21.9%; Score 23; DB 6; Length 19;
Best Local Similarity 45.5%; Pred. No. 5.8e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 10 GFIVGEGVLS 20
| | | | |
Db 4 GYIVTDQKPLS 14

RESULT 80
US-10-503-575-302
; Sequence 302, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Driffhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 302
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-302

Query Match 21.9%; Score 23; DB 6; Length 19;
Best Local Similarity 36.4%; Pred. No. 5.8e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KGMSPPGFVIG 14
| | | | |
Db 8 EGDDPSGLQIG 18

RESULT 81
US-10-503-575-303
; Sequence 303, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Driffhout, Jan Wouter
; APPLICANT: van Veelen, Petrus Antonius
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHO
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; PRIOR FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 303
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-303

Query Match 21.9%; Score 23; DB 6; Length 19;
Best Local Similarity 36.4%; Pred. No. 5.8e+02;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 4 KGMSPPGFVIG 14
| | | | |
Db 2 EGDDPSGLQIG 12

RESULT 82
US-10-623-155-533
; Sequence 533, Application US/10623155
; Publication No. US20050261166A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Peckham, David W.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C20
; CURRENT APPLICATION NUMBER: US/10/623,155
; PRIOR FILING DATE: 2003-07-17
; NUMBER OF SEQ ID NOS: 560
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 533
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-623-155-533

Query Match 21.9%; Score 23; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 6.2e+02;
Matches 3; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 12 IVGEEG 17
| | | | |
Db 2 LIGKEG 7

RESULT 83
US-11-106-415-192
; Sequence 192, Application US/11106415
; Publication No. US20050287153A1
; GENERAL INFORMATION:
; APPLICANT: MARK S. DENNIS
; TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting

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; FILE REFERENCE: P1774R1P2
; CURRENT APPLICATION NUMBER: US/11/106,415
; CURRENT FILING DATE: 2005-04-13
; PRIOR APPLICATION NUMBER: US 10/186,229
; PRIOR FILING DATE: 2002-06-28
; NUMBER OF SEQ ID NOS: 425
; SEQ ID NO 192
; LENGTH: 20
; TYPE: PRN
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: sequence is synthesized
US-11-106-415-192

Query Match
Best Local Similarity 21.9%; Score 23; DB 7; Length 20;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 14 GEEGVL 19
   |||||
Db 2 GEEGDL 7

RESULT 84
US-11-041-893-178
; Sequence 178, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahaitas, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: PaateSeq for Windows Version 4.0
; SEQ ID NO 178
; LENGTH: 20
; TYPE: PRN
; ORGANISM: Toxoplasma gondii
US-11-041-893-178

Query Match
Best Local Similarity 21.9%; Score 23; DB 7; Length 20;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 PGPIVGE 16
   ||:|
Db 3 PGDVIVE 10

RESULT 85
US-11-107-029-11
; Sequence 11, Application US/11107029
; Publication No. US20050271667A1
; GENERAL INFORMATION:
; APPLICANT: NGUYEN, MAI H.
; TITLE OF INVENTION: IDENTIFICATION OF A NOVEL ENDOTHELIAL-DERIVED GENE EG-1
; FILE REFERENCE: 407T-30410US
; CURRENT APPLICATION NUMBER: US/11/107,029
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US10/029,137
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 34
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 11
; LENGTH: 17
; TYPE: PRN
; ORGANISM: Homo sapiens
```

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US-11-107-029-11

Query Match
Best Local Similarity 21.4%; Score 22.5; DB 7; Length 17;
Matches 5; Conservative 4; Mismatches 3; Indels 1; Gaps 1;

QY 7 SPPGPIVGE 19
   |||:|:|
Db 1 APFG-LPGQASL 12

RESULT 86
US-10-485-788A-120
; Sequence 120, Application US/10485788A
; Publication No. US20050282743A1
; GENERAL INFORMATION:
; APPLICANT: Lu, Peter S.
; APPLICANT: Rabinowitz, Joshua D.
; APPLICANT: Schweizer, Johannes
; APPLICANT: Carrick, Deanna Marie
; APPLICANT: Arbor Vita Corporation
; TITLE OF INVENTION: Molecular Interactions in Cells
; FILE REFERENCE: 20054-00320US
; CURRENT APPLICATION NUMBER: US/10/485,788A
; CURRENT FILING DATE: 2004-02-03
; PRIOR APPLICATION NUMBER: US 60/309,841
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 60/360,061
; PRIOR FILING DATE: 2002-02-25
; PRIOR APPLICATION NUMBER: WO PCT/US02/24655
; PRIOR FILING DATE: 2002-08-02
; NUMBER OF SEQ ID NOS: 841
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 120
; LENGTH: 8
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-485-788A-120

Query Match
Best Local Similarity 21.0%; Score 22; DB 6; Length 8;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMS 7
   ||:|
Db 1 DPAKGS 7

RESULT 87
US-11-045-024-5161
; Sequence 5161, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kudo, Ralph
; APPLICANT: Cells, Esteban
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
```

;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 5161
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5161

Query Match 21.0%; Score 22; DB 7; Length 8;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 10
| | | |
Db 1 GPIPFG 6

RESULT 88

US-11-045-024-7282
;; Sequence 7282, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Celis, Steban
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Bpimmune Inc.
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
;; CURRENT FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 7282
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-7282

Query Match 21.0%; Score 22; DB 7; Length 8;

Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 10
| | | |
Db 1 GPIPFG 6

RESULT 89
US-11-045-024-13708
;; Sequence 13708, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Celis, Steban
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Bpimmune Inc.
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
;; CURRENT FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 13708
;; LENGTH: 9
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13708

Query Match 21.0%; Score 22; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 GMSPPG 10
| | | |
Db 4 GPIPFG 9

RESULT 90
US-11-033-039-24
;; Sequence 24, Application US/11033039
;; Publication No. US20060002947A1
;; GENERAL INFORMATION:
;; APPLICANT: HUMPHREYS, ROBERT
;; APPLICANT: XU, MINZHEN
;; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIPTOPE HYBRID PEPTIDE VACCINES
;; FILE REFERENCE: REH-2017US01
;; CURRENT APPLICATION NUMBER: US/11/033,039
;; CURRENT FILING DATE: 2005-01-11
;; PRIOR APPLICATION NUMBER: 10/245,871

```
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 24
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Atacchia hypogaea
US-11-033-039-24
```

```
Query Match      21.0%; Score 22; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      8 PGPGI 12
DB      4 PGGFI 8
```

```
RESULT 91
US-11-033-039-292
/ Sequence 292, Application US/11033039
/ Publication No. US2006002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPI TOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: REH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ PRIOR FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO: 292
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-033-039-292
```

```
Query Match      21.0%; Score 22; DB 7; Length 9;
Best Local Similarity 28.6%; Pred. No. 5.5e+04;
Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      10 GRIEVER 16
DB      3 GYVIGIQ 9
```

```
RESULT 92
US-11-045-024-1311
/ Sequence 1311, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Estebean
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
```

```
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO: 1311
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1311
```

```
Query Match      21.0%; Score 22; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GMSPPG 10
DB      3 GRIPPG 8
```

```
RESULT 93
US-11-045-024-6377
/ Sequence 6377, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Estebean
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
```



```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6377
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6377
```

```
Query Match          21.0%; Score 22; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GMSPPG 10
      | | | |
Db      3 GPIPPG 8
```

```
RESULT 94
US-11-045-024-9066
/ Sequence 9066, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esben
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 9066
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-9066
```

```
Query Match          21.0%; Score 22; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GMSPPG 10
      | | | |
Db      2 GPIPPG 7
```

```
RESULT 95
US-11-045-024-11266
/ Sequence 11266, Application US/11045024
/ Publication No. US20050271676A1
```

```
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Esben
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11266
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-11266
```

```
Query Match          21.0%; Score 22; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 4e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      5 GMSPPG 10
      | | | |
Db      2 GPIPPG 7
```

```
RESULT 96
US-11-208-541-11
/ Sequence 11, Application US/11208541
/ Publication No. US20050287160A1
/ GENERAL INFORMATION:
/ APPLICANT: Itoh, Kyoto
/ APPLICANT: HARADA, Mamoru
/ TITLE OF INVENTION: HLA-A24 Binding Peptides of Enhancer of Zeste Homolog 2
/ FILE REFERENCE: 541818
/ CURRENT APPLICATION NUMBER: US/11/208,541
/ PRIOR FILING DATE: 2005-08-23
/ NUMBER OF SEQ ID NOS: 18
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 11
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURES:
/ OTHER INFORMATION: E2H2 119-128
US-11-208-541-11
```

```
Query Match          21.0%; Score 22; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 4e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      11 FIVGEEGV L 19
        | : | : | |
Db      2 FMVEDETV L 10
```

RESULT 97

```

US-11-033-365-5
; Sequence 5, Application US/11033365
; Publication No. US20050250678A1
; GENERAL INFORMATION:
; APPLICANT: Neose Technologies Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Wang, ZhiGang
; APPLICANT: Clausen, Henrik
; TITLE OF INVENTION: O-Linked Glycosylation of peptides
; FILE REFERENCE: 040853-01-5138
; CURRENT APPLICATION NUMBER: US/11/033,365
; CURRENT FILING DATE: 2005-01-10
; PRIOR APPLICATION NUMBER: 60/535,284
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 60/544,411
; PRIOR FILING DATE: 2004-02-12
; PRIOR APPLICATION NUMBER: 60/546,631
; PRIOR FILING DATE: 2004-02-20
; PRIOR APPLICATION NUMBER: 60/555,813
; PRIOR FILING DATE: 2004-03-23
; PRIOR APPLICATION NUMBER: 60/570,891
; PRIOR FILING DATE: 2004-05-12
; NUMBER OF SEQ ID NOS: 213
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 11
; TYPE: prt
; ORGANISM: Homo sapiens
US-11-033-365-5

```

Query Match	21.0%;	Score 22;	DB 7;	Length 11;
Best Local Similarity	44.4%;	Pred. No. 4.5e+02;		
Matches	4;	Conservative	1;	Mismatches 4;
			Indels	0;
			Gaps	0

```
QY      2 PAKGMSPPG 10
        | : | |
Db      2 PTQGAMPLG 10
```

RESULT 98

US-11-045-024-3056
Sequence 3056, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Cells, Esteban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2006.0004007
CURRENT APPLICATION NUMBER: US/11/045, 024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412, 863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027, 146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073, 205
PRIOR FILING DATE: 1993-06-04

```

1 PRIOR APPLICATION NUMBER: US 08/103,396
2 PRIOR FILING DATE: 1993-08-06
3 PRIOR APPLICATION NUMBER: US 08/159,184
4 PRIOR FILING DATE: 1993-11-29
5 PRIOR APPLICATION NUMBER: US 08/159,339
6 PRIOR FILING DATE: 1993-11-29
7 PRIOR APPLICATION NUMBER: US 08/205,713
8 PRIOR FILING DATE: 1994-03-04
9 PRIOR APPLICATION NUMBER: US 08/347,610
10 PRIOR FILING DATE: 1994-12-01
11 NUMBER OF SEQ ID NOS: 14528
12 SOFTWARE: FastSeq for Windows Version 4.0
13 SEQ ID NO 3056
14 LENGTH: 11
15 TYPE: prt
16 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
17 US-11-045-024-3056

```

Query Match	21.0%;	Score 22;	DB 7;	Length 11;
Best Local Similarity	66.7%;	Pred. No. 4.5e+02;		
Matches	4;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

QY	5	GMSPPG	10
Db	3	GPIPPG	8

RESULT 95
US-11-045

```

Sequence 5702, Application US/11045024
Publication No. US2005027676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Eserban
APPLICANT: Kudo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: Epimmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 5702
LENGTH: 11
TYPE: PRF
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-5702

```

Query Match	21.0%;	Score 22;	DB 7;	Length 11.
Best Local Similarity	66.7%;	Pred. No. 4.5e+02;		

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 5 GMSPPG 10
 Db 4 GRIPPG 9

RESULT 100

US-11-045-024-9026
 / Sequence 9026, Application US/11045024
 / Publication No. US20050271676A1
 / GENERAL INFORMATION:
 / APPLICANT: Sette, Alessandro
 / APPLICANT: Sidney, John
 / APPLICANT: Southwood, Scott
 / APPLICANT: Livingston, Brian
 / APPLICANT: Chesnut, Robert
 / APPLICANT: Baker, Denise Marie
 / APPLICANT: Celis, Eateban
 / APPLICANT: Kubo, Ralph
 / APPLICANT: Grey, Howard M.
 / APPLICANT: Bpimmune Inc.
 / TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 / FILE REFERENCE: 2060.0040007
 / CURRENT APPLICATION NUMBER: US/11/045,024
 / CURRENT FILING DATE: 2005-01-28
 / PRIOR APPLICATION NUMBER: US 09/412,863
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: US 08/027,146
 / PRIOR FILING DATE: 1993-03-05
 / PRIOR APPLICATION NUMBER: US 08/073,205
 / PRIOR FILING DATE: 1993-06-04
 / PRIOR APPLICATION NUMBER: US 08/103,396
 / PRIOR FILING DATE: 1993-08-06
 / PRIOR APPLICATION NUMBER: US 08/159,184
 / PRIOR FILING DATE: 1993-11-29
 / PRIOR APPLICATION NUMBER: US 08/159,339
 / PRIOR FILING DATE: 1993-11-29
 / PRIOR APPLICATION NUMBER: US 08/205,713
 / PRIOR FILING DATE: 1994-03-04
 / PRIOR APPLICATION NUMBER: US 08/347,610
 / PRIOR FILING DATE: 1994-12-01
 / NUMBER OF SEQ ID NOS: 14528
 / SOFTWARE: PasterSeq for Windows Version 4.0
 / SEQ ID NO 9026
 / LENGTH: 11
 / TYPE: PRT
 / ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-9026

Query Match 21.0%; Score 22; DB 7; Length 11;
 Best Local Similarity 44.4%; Pred. No. 4.5e+02;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 PGRIVSEEG 17
 Db 1 PGLLETSEG 9

Search completed: January 20, 2006, 19:46:30
 Job time : 9.07692 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 ; Search time 11.3462 Seconds
(without alignments)
169.602 Million cell updates/sec

Title: US-09-662-293-4
Perfect score: 105
Sequence: 1 DPAKGMSPGFIVGSEGVLS 20

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : PIR 80: *
1: p1r1: *
2: p1r2: *
3: p1r3: *
4: p1r4: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	length	DB ID	Description
1	32	30.5	15	2	F57789
2	31	29.5	17	2	PH0082
3	28	26.7	10	2	S26506
4	28	26.7	15	2	S54712
5	28	26.7	20	2	B60801
6	27	25.7	16	2	C49048
7	27	25.7	16	2	PS0210
8	26	24.8	9	2	S65433
9	26	24.8	9	2	A43065
10	26	24.8	9	2	B60246
11	26	24.8	9	2	A26744
12	26	24.8	9	2	A61057
13	26	24.8	9	2	A60579
14	26	24.8	9	2	A61363
15	26	24.8	9	2	A61358
16	26	24.8	11	2	S13379
17	26	24.8	11	2	B26744
18	26	24.8	11	2	A61365
19	26	24.8	12	2	A61360
20	26	24.8	12	2	A61359
21	26	24.8	13	2	A61361
22	26	24.8	14	2	A61362
23	26	24.8	15	2	A36279
24	26	24.8	17	1	A61339
25	26	24.8	20	1	A61339
26	25	23.8	10	2	A36454
27	25	23.8	10	2	C60527
28	25	23.8	12	2	T46794
29	25	23.8	20	2	A33878

30	25	23.8	20	2	A61576
31	25	23.8	20	2	A46644
32	24	22.9	10	2	B60588
33	24	22.9	10	2	B60788
34	24	22.9	15	2	I65478
35	24	22.9	15	2	PT0097
36	24	22.9	17	2	S77834
37	24	22.9	18	2	S57518
38	24	22.9	19	2	C37072
39	24	22.9	19	2	S11611
40	24	22.9	20	2	PQ0688
41	24	22.9	20	2	PQ0687
42	23	21.9	9	2	S35538
43	23	21.9	10	2	C60588
44	23	21.9	10	2	B60527
45	23	21.9	10	2	I60588
46	23	21.9	12	2	C36201
47	23	21.9	13	2	A59387
48	23	21.9	18	2	S13974
49	23	21.9	19	2	S29766
50	23	21.9	19	2	B28457
51	23	21.9	20	2	B39108
52	23	21.9	20	2	A31516
53	23	21.9	20	2	S38288
54	23	21.9	20	2	S06150
55	22.5	21.4	15	2	PA0040
56	22	21.0	9	2	PA0033
57	22	21.0	10	2	D60527
58	22	21.0	12	2	PS0213
59	22	21.0	12	2	S65409
60	22	21.0	14	2	A35377
61	22	21.0	14	2	PS0255
62	22	21.0	15	2	PA0110
63	22	21.0	16	2	A59042
64	22	21.0	18	2	A36133
65	22	21.0	18	2	I59649
66	22	21.0	20	2	S19240
67	22	21.0	20	2	B33290
68	22	21.0	20	2	C56385
69	21	20.0	8	2	A35768
70	21	20.0	9	2	PD0027
71	21	20.0	10	2	F60527
72	21	20.0	10	2	S39030
73	21	20.0	11	2	A40693
74	21	20.0	12	2	S39762
75	21	20.0	12	2	B58502
76	21	20.0	14	2	B60683
77	21	20.0	15	2	B39109
78	21	20.0	15	2	S05700
79	21	20.0	15	2	PL0110
80	21	20.0	16	2	S55307
81	21	20.0	16	2	A31963
82	21	20.0	17	2	S01104
83	21	20.0	17	2	I55612
84	21	20.0	17	2	I51203
85	21	20.0	18	2	A39997
86	21	20.0	18	2	A35678
87	21	20.0	19	2	B29501
88	21	20.0	19	2	A48400
89	21	20.0	19	2	S23233
90	21	20.0	19	2	S02808
91	21	20.0	19	2	S22232
92	21	20.0	20	2	B48400
93	21	20.0	20	2	S65399
94	21	20.0	20	2	A61414
95	21	20.0	20	2	I53671
96	20.5	19.5	20	2	S05411
97	20.5	19.5	20	2	A39543
98	20	19.0	8	2	PT0559
99	20	19.0	8	2	PT0554
100	20	19.0	9	2	B41983

insulin-like growth temperature-labile sperm-activating p sperm-activating p c-Ki-ras - hamster glucathione peroxi DNA-directed RNA p T cell receptor be proteoglycan 65k c ribosomal protein photosystem I 14.0 photosystem I 14.1 ribosomal protein sperm-activating p sperm-activating p 1-aminocyclopropan VCAM-1 5'UTR bindi chlorophyll a/b-bi cytochrome c (BDH) proteoglycan II, b lipoprotein Acld p lectin, galactose/ 50k allergen - per photosystem I chai malate dehydrogena protein QA300033 - sperm-activating p 28k protein 4412 - histone H2B - huma GTP-binding protei 20k protein 5503 - translation elonga alpha-conotoxin Bp hypothetical protee human leukocyte an histone H2B (clone histone H2B - huma nitrophenol 3 - Rh T-cell receptor al pev-tachykinin - p sperm-activating p lysyl-bradykinin - transgelin - sheep cytochrome P450 UTP 43.2K bile stone p malate dehydrogena hypothetical 1.5K insulin-like growth complement factor glutathione transf pyruvate dehydroge hypothetical protee thyroid hormone re myosin heavy chain group III allergen hypothetical protee fibrinopeptide A - phosphocarrier pro vitronectin - ghee vitronectin - bovine vitronectin - goat phosphocarrier pro immunodeficiency v chemokine (KC 3 neurofilament heavy carboxylesterase (collagen alpha 1(I T-cell receptor be T-cell receptor be of downstream to b

ALIGNMENTS

RESULT 1

F57789
 gallbladder stone matrix protein 2, 41K - human (fragment)
 C1:Species: Homo sapiens (man)
 C1:Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 09-Jul-2004
 C1:Accession: F57789
 R1:Binette, J.P.; Binette, M.B.
 submitted to the Protein Sequence Database, February 1996
 A1:Description: The proteins of gallbladder stones.
 A1:Reference number: A57789
 A1:Accession: F57789
 A1:Status: preliminary
 A1:Molecule type: protein
 A1:Residues: 1-15 <BIN>
 A1:Cross-references: UNIPROT:Q7MAP9; UNIPARC:UPI000017C122
 A1:Note: 9-Phe was also found

Query Match 30.5%; Score 32; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 79;
 Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PGPFVGEHG 17
 | | | | |
 Db 5 PDGFEGSSG 14

RESULT 2

neuroglial protein, short form - fruit fly (Drosophila sp.) (fragment)
 PH0082
 C1:Species: Drosophila sp.
 C1:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C1:Accession: PH0082
 R1:Hortsch, M.; Bieber, A.J.; Patel, N.H.; Goodman, C.S.
 Neuron 4, 697-709, 1990
 A1>Title: Differential splicing generates a nervous system-specific form of Drosophila ne
 A1:Reference number: PH0082; MUID:90262720; PMID:1693086
 A1:Accession: PH0082
 A1:Status: preliminary
 A1:Molecule type: mRNA
 A1:Residues: 1-17 <HOR>
 A1:Cross-references: UNIPARC:UPI000017BEEF

Query Match 29.5%; Score 31; DB 2; Length 17;
 Best Local Similarity 40.0%; Pred. No. 1.3e+02;
 Matches 6; Conservative 3; Mismatches 6; Indels 0; Gaps 0;

QY 5 GMSPPGIVGEGVL 19
 | | | | |
 Db 1 GMMEDGSFIGTGRL 15

RESULT 3

S26506
 collagen alpha 1(VI) chain - bovine (fragment)
 C1:Species: Bos primigenius taurus (cattle)
 C1:Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
 C1:Accession: S26506
 R1:Jander, R.; Rautenberg, J.; Glanville, R.W.
 Eur. J. Biochem. 133, 39-46, 1983
 A1>Title: Further characterization of the three polypeptide chains of bovine and human sh
 A1:Reference number: S26506; MUID:83209648; PMID:6652033
 A1:Accession: S26506
 A1:Status: preliminary
 A1:Molecule type: protein
 A1:Residues: 1-10 <JAN>
 A1:Cross-references: UNIPROT:Q7M2N0; UNIPARC:UPI000017C4B3
 C1:Keywords: hydroxyproline
 F19/Modified site: hydroxyproline (Pro) #status experimental
 Query Match 26.7%; Score 28; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.1e+02;
 Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 PAKGMSPPG 10
 | | | | |
 Db 4 PARG--PPG 10

RESULT 4

SS4712
 zein Zp22/6 protein - maize
 C1:Species: Zea mays (maize)
 C1:Date: 23-Aug-1995 #sequence_revision 19-Oct-1995 #text_change 09-Jul-2004
 C1:Accession: SS4712
 R1:Chaudhuri, S.; Messing, J.
 Mol. Gen. Genet. 246, 707-715, 1995
 A1>Title: RFLP mapping of the maize dzr1 locus, which regulates methionine-rich 10 kDa ze
 A1:Reference number: SS4712; MUID:95206245; PMID:7898438
 A1:Accession: SS4712
 A1:Status: preliminary
 A1:Molecule type: protein
 A1:Residues: 1-15 <CHA>
 A1:Cross-references: UNIPROT:Q7M1F8; UNIPARC:UPI000017B16A

Query Match 26.7%; Score 28; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 3.4e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFI 12
 | | | | |
 Db 4 PQGSIAAPPALI 14

RESULT 5

B60801
 acrosome stabilizing factor small chain - rabbit (fragment)
 C1:Species: Oryctolagus cuniculus (domestic rabbit)
 C1:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C1:Accession: B60801
 R1:Wilson, W.L.; Oliphant, G.
 Biol. Reprod. 37, 159-169, 1987
 A1>Title: Isolation and biochemical characterization of the subunits of the rabbit sperm
 A1:Reference number: A60801; MUID:88000873; PMID:3651543
 A1:Accession: B60801
 A1:Molecule type: protein
 A1:Residues: 1-20 <WIL>
 A1:Cross-references: UNIPARC:UPI000017C5B4
 C1:Comment: spermatozoa must undergo capacitation and the acrosome reaction to become cap
 C1:Keywords: glycoprotein; semen

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPPG 10
 | | | | |
 Db 1 DTKKAAREPPG 10

RESULT 6

C49048
 T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
 C1:Species: Homo sapiens (man)
 C1:Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 30-May-1997
 C1:Accession: C49048
 R1:Sioud, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
 Eur. J. Immunol. 22, 2413-2418, 1992
 A1>Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
 A1:Reference number: A49048; MUID:92387250; PMID:1387614
 A1:Accession: C49048
 A1:Status: preliminary; not compared with conceptual translation
 A1:Molecule type: mRNA
 A1:Residues: 1-16 <SIO>

A/Cross-references: UNIPARC:UPI000017C3A9
 A/Experimental source: patient EV, IL-2R+ synovial T-cells
 A/Note: sequence extracted from NCBI backbone (NCBIP:113265)
 C/Keywords: T-cell receptor

Query Match 25.7%; Score 27; DB 2; Length 16;
 Best Local Similarity 57.1%; Pred. No. 5.2e+02;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 PGPG 14
 DB 10 PGPTFG 16

RESULT 7

PS0210
 28K protein 4209 - rice (strain Nihonbare) (fragment)

C/Species: Oryza sativa (rice)
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
 C/Accession: PS0210

R/Trautle, A.; Miyatake, N.
 Submitted to JIPID, April 1993

A/Reference number: PS0208
 A/Accession: PS0210

A/Molecule type: protein

A/Residues: 1-16 <TSA>

A/Cross-references: UNIPROT:Q7M281; UNIPARC:UPI000017B0F9

A/Experimental source: germ, brain, strain Nihonbare
 C/Comment: molecular weight 28K, pI 7.3.

Query Match 25.7%; Score 27; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 5.2e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVGS 15
 DB 1 PGLVIGD 7

RESULT 8

865433
 bradykinin - horn fly (fragment)

C/Species: Haematobia irritans (horn fly)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997

C/Accession: 865433
 R/MiJfield, G.; Fitzgerald, C.; Gough, J.; Riding, G.; Elvin, C.; Kemp, D.; Willadsen, F.

Bur. J. Biochem. 237, 414-423, 1996

A/Title: Cloning and characterisation of angiotensin-converting enzyme from the dipteran
 A/Reference number: 865431; PMID:96215437; PMID:8647080

A/Accession: 865433

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <MID>

A/Cross-references: UNIPARC:UPI000002CFA4

A/Note: the source is designated as Haematobia irritans exigua

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPG 11
 DB 2 PGPG 5

RESULT 9

A43065
 hydroxyproline-3-bradykinin - frog (Helleophryne purcellii)

C/Species: Helleophryne purcellii
 C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C/Accession: A43065

R/Nakajima, T.; Yasuhara, T.; Eppamer, G.F.; Vissler, J.
 Experientia 35, 1133, 1979

A/Title: Occurrence of HYP(3)-bradykinin in methanol extracts of the skin of the South
 A/Reference number: A43065; PMID:80024576; PMID:488255

A/Accession: A43065
 A/Molecule type: protein

A/Residues: 1-9 <NAK>

A/Cross-references: UNIPROT:Q7L217; UNIPARC:UPI000002CFA4

C/Keywords: bradykinin; hydroxyproline; skin

F/3/Modified site: hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPG 11
 DB 2 PGPG 5

RESULT 10

B60246
 ornitho-kinin - chicken

C/Species: Gallus gallus (chicken)
 C/Date: 11-Dec-1992 #sequence_revision 11-Dec-1992 #text_change 16-Aug-2004

C/Accession: B60246

R/Kimura, M.; Sueyoshi, T.; Morita, T.; Tanaka, K.; Iwanaga, S.

Adv. Exp. Med. Biol. 247A, 359-367, 1989

A/Title: Ornitho-kininogen and ornitho-kinin: isolation, characterization and chemical

A/Reference number: A60246; PMID:90102072; PMID:2603803

A/Accession: B60246

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <KIM>

A/Cross-references: UNIPROT:Q7L250; UNIPARC:UPI000017A4F8

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPG 11
 DB 2 PGPG 5

RESULT 11

A26744
 bradykinin-like peptide - garden dagger wasp

N/Alternate names: Thr-6-bradykinin
 C/Species: Megascolla flavifrons (garden dagger wasp)

C/Date: 08-Mar-1989 #sequence_revision 08-Mar-1989 #text_change 05-Oct-2004

C/Accession: A26744

R/Yasuhara, T.; Mantel, P.; Nakajima, T.; Plek, T.

Toxicol 25, 527-535, 1987

A/Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wa

A/Reference number: A94322; PMID:87293024; PMID:3617088

A/Accession: A26744

A/Molecule type: protein

A/Residues: 1-9 <YAS>

A/Cross-references: UNIPARC:UPI000012DF29

Query Match 24.8%; Score 26; DB 2; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPG 11
 DB 2 PGPG 5

RESULT 12

A61057
 Thr-6 bradykinin - scollid wasp (Colpa interrupta)

C/Species: Colpa interrupta
 C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 05-Oct-2004

C/Accession: A61057
R.Piek, T.; Hue, B.; Mantel, P.; Nakajima, T.; Pelhate, M.; Yasuhara, T.
Comp. Biochem. Physiol. C 96, 157-162, 1990
A/Title: Threonine(6)-bradykinin in the venom of the wasp Colpa interrupta (F.) presynap
A/Reference number: A61057; PMID:91130217; PMID:1980872
A/Accession: A61057
A/Molecule type: protein
A/Residues: 1-9 <PIR>
A/Cross-references: UNIPARC:UPI000012DP29
C/Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 2 PPGF 5

RESULT 13

A60579
bradykinin-like peptide - slider turtle
C/Species: Pseudemys scripta (slider)
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 05-Oct-2004
C/Accession: A60579
R.Conlon, J.M.; Hicks, J.W.; Smith, D.D.
Endocrinology 126, 985-991, 1990
A/Title: Isolation and biological activity of a novel kinin (Thr(6))bradykinin) from th
A/Reference number: A60579; PMID:9012625; PMID:2298179
A/Accession: A60579
A/Molecule type: protein
A/Residues: 1-9 <CON>
A/Cross-references: UNIPARC:UPI000012DP29
C/Comment: This peptide increases aortic blood flow but, unlike bradykinin in mammalian
C/Keywords: plasma

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 2 PPGF 5

RESULT 14

A61363
bradykinin - common frog
C/Species: Rana temporaria (common frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61363
R.Anaelst, A.; Brepamer, V.; Bertaccini, G.
Comp. Biochem. Physiol. A 14, 43-52, 1965
A/Title: Occurrence of bradykinin in the skin of Rana temporaria.
A/Reference number: A61363
A/Accession: A61363
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <ANA>
A/Cross-references: UNIPROT:Q7LZD8; UNIPARC:UPI000002CF4A
C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 2 PPGF 5

RESULT 15

A61358
bradykinin-like peptide I - Japanese pond frog
C/Species: Rana nigromaculata (Japanese pond frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61358
R.Nakajima, T.
Chem. Pharm. Bull. 16, 769-770, 1968
A/Title: Occurrence of a new active peptide on smooth muscle and bradykinin in the skin
A/Reference number: A61358; PMID:68412013; PMID:5677638
A/Accession: A61358
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9 <NAK>
A/Cross-references: UNIPROT:Q7LZ54; UNIPARC:UPI000017A4F0
C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 2 PPGF 5

RESULT 16

S13279
Ile-Ser-bradykinin - human (fragment)
N/Alternate names: T-kinin
C/Species: Homo sapiens (man)
C/Date: 02-Dec-1993 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004
C/Accession: S13279
R.Wunderer, G.; Walter, I.; Eschenbacher, B.; Lang, M.; Kellermann, J.; Kindermann, G.
Biol. Chem. Hoppe-Seyler 371, 977-981, 1990
A/Title: Ile-Ser-bradykinin is an aberrant permeability factor in various human malignan
A/Reference number: S13279; PMID:9116748; PMID:2076202
A/Accession: S13279
A/Molecule type: protein
A/Residues: 1-11 <WUN>
A/Cross-references: UNIPROT:Q7MAP1; UNIPARC:UPI0000148EBE
C/Keywords: bradykinin

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 4 PPGF 7

RESULT 17

B26744
megascollakinin - garden dagger wasp
N/Alternate names: 6-Thr-bradykinin-Lys-Ala
C/Species: Megascollia flavifrons (garden dagger wasp)
C/Date: 08-Mar-1999 #sequence_revision 08-Mar-1999 #text_change 05-Oct-2004
C/Accession: B26744; A28609
R.Yasuhara, T.; Mantel, P.; Nakajima, T.; Piek, T.
Toxicol 25, 527-535, 1987
A/Title: Two kinins isolated from an extract of the venom reservoirs of the solitary wa-
A/Reference number: A94322; PMID:87293024; PMID:5617088
A/Accession: B26744
A/Molecule type: protein
A/Residues: 1-11 <YAS>
A/Cross-references: UNIPROT:P12797; UNIPARC:UPI0000126AD6
R.Nakajima, T.; Piek, T.; Yasuhara, T.; Mantel, P.
Toxicol 26, 34, 1988
A/Title: Two kinins isolated from the venom of Megascollia flavifrons.
A/Reference number: A28609
A/Accession: A28609
A/Molecule type: protein
A/Residues: 1-11 <NAK>

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
|||
Db 4 PPGF 7

A/Cross-references: UNIPARC:UPI0000126AD6
C/Keywords: bradykinin; presynaptic neurotoxin; venom

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 2 PPGF 5

RESULT 18

A61365
phyllotoxin - Rohde's leaf frog
N/Alternate names: bradykinin-1-iso-leucyl-tyrosine O-sulfate
C/Species: Phyllomedusa rohdei (Rohde's leaf frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61365
R/Author: A.; Bertaccini, G.; Bregman, V.
Br. J. Pharmacol. 27, 479-485, 1966

A/Title: Pharmacological data on phyllotoxin (bradykinin-1-iso-leucyl-tyrosine O-sulfate)
A/Reference number: A61365; MUID:6719312; PMID:5970899
A/Accession: A61365
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <ANA>
A/Cross-references: UNIPROT:Q7LZ53; UNIPARC:UPI000017A4F2
C/Keywords: sulfoxide
P/11/Binding site: sulfate (Tyr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 2 PPGF 5

RESULT 19

A61360
vespakinin M - hornet (Vespa mandarinia)
C/Species: Vespa mandarinia
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61360
R/Kishimura, H.; Yasuhara, T.; Yoshida, H.; Nakajima, T.
Chem. Pharm. Bull. 24, 2896-2897, 1976
A/Title: Vespakinin-M, a novel bradykinin analogue containing hydroxyproline, in the ven
A/Reference number: A61360; MUID:7714342; PMID:1017116
A/Accession: A61360
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-12 <KRS>
A/Cross-references: UNIPROT:Q7M373; UNIPARC:UPI000017A4F3
P/4/Modified site: 4-hydroxyproline (Pro) #status experimental

Query Match 24.8%; Score 26; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 3 PPGF 6

RESULT 20

A61359
vespakinin X - hornet (Vespa xanthoptera)
C/Species: Vespa xanthoptera
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61359

R/Yasuhara, T.; Yoshida, H.; Nakajima, T.

Chem. Pharm. Bull. 25, 936-941, 1977

A/Title: Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The st

A/Reference number: A61359; MUID:87187853; PMID:264186

A/Accession: A61359

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-12 <YAS>

A/Cross-references: UNIPROT:Q7M372; UNIPARC:UPI000017A4F4

C/Keywords: venom

Query Match 24.8%; Score 26; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 5.4e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 3 PPGF 6

RESULT 21

A61361
bradykinin-like peptide - Bombina orientalis
C/Species: Bombina orientalis
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61361
R/Yasuhara, T.; Hira, M.; Nakajima, T.; Yanaihara, N.; Yanaihara, C.; Hashimoto, T.; Sa
Chem. Pharm. Bull. 21, 1388-1391, 1973
A/Title: Active peptides on smooth muscle in the skin of Bombina orientalis Boulenger a
A/Reference number: A61361; MUID:73256822; PMID:4732297
A/Accession: A61361
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-13 <YAS>
A/Cross-references: UNIPROT:P63060; UNIPARC:UPI000017A4F5
C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 13;
Best Local Similarity 100.0%; Pred. No. 6e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 2 PPGF 5

RESULT 22

A61362
bradykinin-like peptide III - Japanese pond frog
C/Species: Rana nigromaculata (Japanese pond frog)
C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 05-Oct-2004
C/Accession: A61362
R/Nakajima, T.
Chem. Pharm. Bull. 16, 2088-2089, 1968
A/Title: On the third active peptide on smooth muscle in the skin of Rana nigromaculata
A/Reference number: A61362; MUID:69117202; PMID:5751736
A/Accession: A61362
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <NAK>
A/Cross-references: UNIPROT:Q7LZ53; UNIPARC:UPI000017A4F1
C/Keywords: skin

Query Match 24.8%; Score 26; DB 2; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
Db 2 PPGF 5

RESULT 23

A36279
chemoattractant protein - earthworm (Lumbricus terrestris) (fragment)
C/Species: Lumbricus terrestris (Common earthworm)
C/Date: 18-Jan-1991 #sequence_rev18-Jan-1991 #text_change 09-Jul-2004
C/Accession: A36279
R/Jiang, X.C.; Inouchi, J.; Wang, D.; Halpern, M.
J. Biol. Chem. 265, 8736-8744, 1990
A/Title: Purification and characterization of a chemoattractant from electric shock-induced snakes.
A/Reference number: A36279; MUID:90256800; PMID:2160465
A/Accession: A36279
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-15 <JIA>
A/Cross-references: UNIPROT:O44335; UNIPARC:UPI000017BD77

Query Match 24.8%; Score 26; DB 2; Length 15;
Best Local Similarity 100.0%; Pred. No. 7e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
| | | | |
Db 5 PGPF 8

RESULT 24
A61339
vespulinin 1 - eastern yellowjacket
N/Contains: vespulinin 2
C/Species: Vespula maculifrons (eastern yellowjacket)
C/Date: 17-Jul-1994 #sequence_rev18-Oct-1994 #text_change 09-Jul-2004
C/Accession: A61339
R.Yoshida, H.; Geller, R.G.; Pisano, J.J.
Biochemistry 15, 61-64, 1976
A/Title: Vespulinins: new carbohydrate-containing bradykinin derivatives.
A/Reference number: A61339; MUID:76114777; PMID:1247511
A/Accession: A61339
A/Molecule type: protein
A/Residues: 1-17 <YOS>
A/Cross-references: UNIPROT:P57672; UNIPARC:UPI0000138459
C/Keywords: antihypertensive; bradykinin; glycoprotein; venom
F/1-17/Product: vespulinin 1 #status experimental <MARI>
F/3-17/Product: vespulinin 2 #status experimental <MARI>
F/9-17/Region: bradykinin-like
F/3,4/Binding site: carbohydrate (Thr) (covalent) #status experimental

Query Match 24.8%; Score 26; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGPF 11
| | | | |
Db 10 PGPF 13

RESULT 25
S39380
pectinesterase (EC 3.1.1.11) - papaya
N/Alternate names: pectin methylsterase
C/Species: Carica papaya (papaya)
C/Date: 19-Mar-1997 #sequence_rev18-Apr-1997 #text_change 17-Mar-1999
C/Accession: S39380
R/Lim, Y.M.; Chung, M.C.M.
Arch. Biochem. Biophys. 307, 15-20, 1993
A/Title: Isolation and characterization of pectin methylsterase from Papaya.
A/Reference number: S39380; MUID:94058247; PMID:8239653
A/Accession: S39380
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <LIM>
A/Cross-references: UNIPARC:UPI000017AF3D
C/Keywords: carboxylic ester hydrolase

Query Match 24.8%; Score 26; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 9.7e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGPFVGBGV 18
| : : : |
Db 5 PAAVAVDDGV 14

RESULT 26
A36454
trypsin-modulating oostatic factor - yellow fever mosquito
C/Species: Aedes aegypti (yellow fever mosquito)
C/Date: 12-Apr-1991 #sequence_rev12-Apr-1991 #text_change 09-Jul-2004
C/Accession: A36454; A61630
R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
FASEB J. 4, 3015-3020, 1990
A/Title: Mosquito oostatic factor: a novel decapeptide modulating trypsin-like enzyme bi
A/Reference number: A36454; MUID:90367888; PMID:2394318
A/Accession: A36454
A/Molecule type: protein
A/Residues: 1-10 <BOR>
A/Cross-references: UNIPROT:P19425; UNIPARC:UPI0000034259
R.Borovsky, D.; Carlson, D.A.; Griffin, P.R.; Shabanowitz, J.; Hunt, D.F.
Insect Biochem. Mol. Biol. 23, 703-712, 1993
A/Title: Mass spectrometry and characterization of Aedes aegypti trypsin modulating oost
A/Reference number: A61630; MUID:93357794; PMID:8335526
A/Accession: A61630
A/Molecule type: protein
A/Residues: 1-10 <BOR>
A/Cross-references: UNIPARC:UPI0000034259
A/Note: none of the amino acids is modified
C/Function: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ef
A/Description: inhibits synthesis of trypsin- and chymotrypsin-like enzymes by midgut ef
C/Keywords: hormone

Query Match 23.8%; Score 25; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 6.4e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEAKGMSPP 9
| | | | |
Db 2 DPAPEPPP 10

RESULT 27
C60527
sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAB-I) - sea urchin (Tripneustes gratilla)
N/Alternate names: speract homolog TG-4
C/Species: Tripneustes gratilla
C/Date: 17-Apr-1993 #sequence_rev17-Apr-1993 #text_change 16-Aug-2004
C/Accession: C60527; D39572
R.Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, M.; Si
Comp. Biochem. Physiol. B 94, 739-751, 1989
A/Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinometra mathaei and Heterocentrotus mammillatus.
A/Reference number: A60527
A/Accession: C60527
A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Cross-references: UNIPROT:O7M376; UNIPARC:UPI000017A4E5
A/Note: this peptide did not contain bromophenylalanine
R.Yoshino, K.; Takao, T.; Suhara, M.; Kitai, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Si
Biochemistry 30, 6203-6209, 1991
A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated
A/Reference number: A39572; MUID:91283461; PMID:2059627
A/Accession: D39572
A/Molecule type: protein
A/Residues: 1-10 <YOS>
A/Cross-references: UNIPARC:UPI000017A4E5
A/Note: this peptide contained bromophenylalanine
C/Keywords: bromine

F/2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 23.8%; Score 25; DB 2; Length 10;

Best Local Similarity 55.6%; Pred. No. 6.4e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPTVGEVGV 18

DB 1 GFSIGGGGV 9

RESULT 28

T46794

hypothetical protein [imported] - Haloarcula marismortui (fragment)

C/Species: Haloarcula marismortui

C/Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 09-Jul-2004

C/Accession: T46794

R/Arndt, E.

PEBB Lett. 267, 193-198, 1990

A/Title: Nucleotide sequence of four genes encoding ribosomal proteins from the 'S10 and

A/Reference number: S10731; MUID:90356772; PMID:2133141

A/Accession: T46794

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-12 <ARN>

A/Cross-references: UNIPROT:P10971, UNIPARC:UPI000016F7C4, EMBL:X55311, NID:943610; PIDD

Query Match 23.8%; Score 25; DB 2; Length 12;

Best Local Similarity 75.0%; Pred. No. 7.8e+02;

Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 IVGEGVL 19

DB 1 IQGEGDL 8

RESULT 29

A33878

myosin light chain kinase, smooth muscle - turkey (fragment)

C/Species: Meleagris gallopavo (common turkey)

C/Date: 27-Feb-1990 #sequence_revision 27-Feb-1990 #text_change 09-Jul-2004

C/Accession: A33878

R/Ikebe, M.; Maruta, S.; Reardon, S.

J. Biol. Chem. 264, 6967-6971, 1989

A/Title: Location of the inhibitory region of smooth muscle myosin light chain kinase.

A/Reference number: A33878; MUID:9214114; PMID:2708351

A/Accession: A33878

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <IKK>

A/Cross-references: UNIPROT:Q7LZH3, UNIPARC:UPI00001755EC

C/Superfamily: myosin-light-chain kinase, nonmuscle; fibronectin type III repeat homolog

C/Keywords: smooth muscle

Query Match 23.8%; Score 25; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGSP 9

DB 8 PPKATRP 15

RESULT 30

A61576

Insulin-like growth factor I - unidentified organism (fragment)

N/Alternate names: Microtetraspora glauca ribosomal protein L30 [misidentification]

C/Species: unidentified organism

C/Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 04-Feb-2000

C/Accession: A61576

R/Ochi, K.; Miyadoh, S.; Tamura, T.

Int. J. Syst. Bacteriol. 41, 234-239, 1991

A/Title: Polyacrylamide gel electrophoresis analysis of ribosomal protein AT-L30 as a nd

A/Reference number: A61576; MUID:91307971; PMID:1854638

A/Accession: A61576

A/Molecule type: protein

A/Residues: 1-20 <OCH>

A/Cross-references: UNIPARC:UPI0000176668

A/Note: the species was designated Microtetraspora glauca and the protein called ribosc

gets an error

C/Superfamily: Insulin

Query Match 23.8%; Score 25; DB 2; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.4e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 11 PTVGEG 17

DB 10 FVXGERG 16

RESULT 31

A46644

temperature-labile cholesterol ester hydrolase - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 28-Apr-1995

C/Accession: A46644

R/Wee, S.; Grogan, W.M.

J. Biol. Chem. 268, 8158-8163, 1993

A/Title: Testicular temperature-labile cholesterol ester hydrolase. Relationship to iso-

divalent cations.

A/Reference number: A46644; MUID:93216794; PMID:8463327

A/Accession: A46644

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <WEB>

A/Cross-references: UNIPARC:UPI000006581

A/Experimental source: testis

A/Note: sequence extracted from NCBI backbone (NCBIP:129155)

Query Match 23.8%; Score 25; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 1.4e+03;

Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPRPRVGB 15

DB 6 VSPPAVVA 15

RESULT 32

B60588

sperm-activating peptide (Ala-3, Gly-5 SAP-I) - sea urchin (Strongylocentrotus nudus)

N/Alternate names: speract homolog

C/Species: Strongylocentrotus nudus

C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004

C/Accession: B60588

R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamagut

Comp. Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related p-

otus nudus, Schinometra macleod and Heterocentrotus mamillatus.

A/Reference number: A60527

A/Accession: B60588

A/Molecule type: protein

A/Residues: 1-10 <YOS>

A/Cross-references: UNIPROT:Q7M4B6, UNIPARC:UPI000017A4DA

Query Match 22.9%; Score 24; DB 2; Length 10;

Best Local Similarity 55.6%; Pred. No. 9.2e+02;

Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPTVGEVGV 18

DB 1 GFALGGGGV 9

RESULT 33

E60788
 sperm-activating peptide (Ala-3, Gly-5 speract) - sea urchin (Pseudocentrotus depressus)
 C:Species: Pseudocentrotus depressus
 C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-2004
 C:Accession: E60788
 R: Suzuki, N.; Kajitani, H.; Nomura, K.; Garberez, D.L.; Yoshino, K.; Kurita, M.; Tanaka, H.
 Comp. Biochem. Physiol. B 89, 687-693, 1988
 A:Title: Some more speract derivatives associated with eggs of sea urchins, Pseudocentrotus depressus
 A:Reference number: A60787; PMID:88242184; PMID:3378407
 A:Accession: E60788
 A:Molecule type: protein
 A:Residues: 1-10 <SUZ>
 A:Cross-references: UNIPROT:Q7M4D4; UNIPARC:UPI000017A4DA
 A:Comment: This oligopeptide from egg jelly is one of several from this species, all of at shows some, but not absolute, species restriction.

Query Match 22.9%; Score 24; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 9.2e+02;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFIVGEGV 18
 ||| : |||
 Db 1 GFALGGGV 9

RESULT 34
 165478
 c-Ki-ras - hamster (fragment)
 C:Species: Cricetinae gen. sp. (hamster)
 C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 28-Feb-1997
 C:Accession: 165478
 R: Takahashi, T.; Meyer, M.P.; Cano, M.; Wang, Q.J.; Mountjoy, C.P.; Sanger, W.; Adrian, C.
 Carcinogenesis 16, 931-939, 1995
 A:Title: Differences in molecular biological, biological and growth characteristics between hamster and rat c-Ki-ras oncogenes
 A:Reference number: 152734; PMID:95246257; PMID:7728976
 A:Accession: 165478
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-15 <RNS>
 A:Cross-references: UNIPARC:UPI000017C607; GB:S77069; NID:g914177
 C:Genetics:
 A:Gene: c-Ki-ras

Query Match 22.9%; Score 24; DB 2; Length 15;
 Best Local Similarity 57.1%; Pred. No. 1.5e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 IVGEGV 18
 ||| : |||
 Db 8 VVGADGV 14

RESULT 35
 PT0097
 glutathione peroxidase, non-selenium containing - mouse (fragment)
 N:Alternate names: antioxidant protein 2
 C:Species: Mus musculus (house mouse)
 C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 24-Nov-1999
 C:Accession: PT0097
 R: Kawakami, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tangeita, A.
 submitted to JIPIID, July 1998
 A:Description: Proteome analysis of mouse brain.
 A:Reference number: PT0091
 A:Accession: PT0097
 A:Molecule type: protein
 A:Residues: 1-15 <KAW>
 A:Cross-references: UNIPARC:UPI000017C66B
 A:Experimental source: brain, striatum

Query Match 22.9%; Score 24; DB 2; Length 15;
 Best Local Similarity 44.4%; Pred. No. 1.5e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 8 PPGFVIGEE 16
 ||| : |||
 Db 1 PGGLLGKE 9

RESULT 36
 577834
 DNA-directed RNA polymerase (EC 2.7.7.6) beta' chain - Mycoplasma capricolum (fragment)
 N:Alternate names: hypothetical protein mc396
 C:Species: Mycoplasma capricolum
 C:Date: 09-Oct-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004
 C:Accession: 577834; S46904
 R: Borik, P.; Ouzounis, C.; Casari, G.; Schneider, R.; Sander, C.; Dolan, M.; Gilbert, W.; Mol. Microbiol. 16, 955-967, 1995
 A:Title: Exploring the Mycoplasma capricolum genome: a minimal cell reveals its physiologic
 A:Reference number: 577739; PMID:96059641; PMID:7476192
 A:Accession: 577834
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-17 <BOR>
 A:Cross-references: UNIPROT:Q49077; UNIPARC:UPI00000BAD53; EMBL:Z33297; NID:g516238; PIR:G49077
 A:Experimental source: ATCC 27343
 A:Note: the nucleotide sequence was submitted to the EMBL Data Library, July 1994
 C:Genetics:
 A:Genetic code: SGC3
 C:Keywords: nucleotidyltransferase; transcription

Query Match 22.9%; Score 24; DB 2; Length 17;
 Best Local Similarity 45.5%; Pred. No. 1.7e+03;
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 6 MSPPGFVIGEE 16
 ||| : |||
 Db 1 MGAPSIIVNNE 11

RESULT 37
 557518
 T cell receptor beta chain V region - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999
 C:Accession: 557518
 R: Burrows, S.R.; Silling, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.
 submitted to the EMBL Data Library, June 1995
 A:Description: T cell receptor repertoire for a viral epitope in humans is diversified
 A:Reference number: 557494
 A:Accession: 557518
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-18 <BUR>
 A:Cross-references: UNIPARC:UPI0000116735; EMBL:Z49920; NID:g887490; PIDN:CAA90166.1; PIR:G887490
 C:Keywords: T-cell receptor

Query Match 22.9%; Score 24; DB 2; Length 18;
 Best Local Similarity 38.5%; Pred. No. 1.8e+03;
 Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 3 AKGMSPPGFVIGEE 15
 ||| : |||
 Db 2 ASLSPPTGSTAGE 14

RESULT 38
 C37072
 proteoglycan 65k core peptide KS-C - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 15-Feb-1991 #sequence_revision 15-Feb-1991 #text_change 30-Sep-1993
 C:Accession: C37072
 R: Krueger Jr., R.C.; Fields, T.A.; Hildreth IV, J.; Schwartz, N.B.
 J. Biol. Chem. 265, 12075-12087, 1990
 A:Title: Chick cartilage chondroitin sulfate proteoglycan core protein. I. Generation and
 A:Reference number: A37072; PMID:90307743; PMID:2365711
 A:Accession: C37072

A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-19 <PRO>
A/Cross-references: UNIPARC:UPI000017C02E

Query Match 22.9%; Score 24; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 1.9e+03;
Matches 6; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 VGEGLVS 20
| | | | |
DB 5 VGEGLVS 12

RESULT 39

S11611
ribosomal protein S2 [validated] - Halobacterium salinarum (fragment)
N/Alternate names: ribosomal protein H85A
C/Species: Halobacterium salinarum

C/Date: 31-Dec-1990 #sequence_revision 31-Dec-1990 #text_change 09-Jul-2004
C/Accession: S11611

R/Yaguchi, M.; Visentin, L.P.; Zuker, M.; Matheson, A.T.; Roy, C.; Strom, A.R.
Zbl. Bakt. Hyg. I. Abt. Orig. C 3, 200-208, 1982

A/Title: Amino-terminal sequences of ribosomal proteins from the 30S subunit of archaea
A/Reference number: S11609

A/Accession: S11611
A/Molecule type: protein

A/Residues: 1-19 <YAG>
A/Cross-references: UNIPROT:Q7M546; UNIPARC:UPI000017CB39

A/Note: the protein is designated as ribosomal protein H85A
C/Keywords: protein biosynthesis; ribosome

Query Match 22.9%; Score 24; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.9e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPFG 10
| | | |
DB 15 SPFG 18

RESULT 40

P00688
photosystem I 14.0K B4 chain - common tobacco (fragment)
C/Species: Nicotiana tabacum (common tobacco)

C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C/Accession: P00688

R/Ookata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.
Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I, psal, psalB, psalF, psalH and psalI are
A/Reference number: P00667; PMID:94105345; PMID:8278548

A/Accession: P00688
A/Molecule type: protein

A/Residues: 1-20 <OBO>
A/Cross-references: UNIPARC:UPI000008D0B5

C/Keywords: chloroplast; photosynthesis; photosystem I

Query Match 22.9%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKGMSP 9
| | | | |
DB 13 AKGMSP 19

RESULT 41

P00687
photosystem I 14.1K B3 chain - common tobacco (fragment)
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C/Accession: P00687; P00675

R/Ookata, J.; Mikami, K.; Hayashida, N.; Nakamura, M.; Sugitara, M.

Plant Physiol. 102, 1259-1267, 1993

A/Title: Molecular heterogeneity of photosystem I, psal, psalB, psalF, psalH and psalI are
A/Reference number: P00667; PMID:94105345; PMID:8278548

A/Accession: P00687
A/Molecule type: protein

A/Residues: 1-20 <OBO>
A/Cross-references: UNIPARC:UPI00000972B7

A/Note: this peptide was designated photosystem I 14.1K B3 chain
A/Accession: P00675

A/Molecule type: protein
A/Residues: 2-11 <OB2>

A/Cross-references: UNIPARC:UPI000017B0AB
A/Note: this peptide was designated photosystem I 14.0K B4 chain
C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match 22.9%; Score 24; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKGMSP 9
| | | | |
DB 14 AKGMSP 20

RESULT 42

S35538
ribosomal protein S7 - Mycobacterium intracellulare (fragment)
C/Species: Mycobacterium intracellulare

C/Date: 09-Dec-1993 #sequence_revision 14-Nov-1997 #text_change 12-Jul-2004
C/Accession: S35538

R/Nair, J.; Rouse, D.; Morris, S.
Nucleic Acids Res. 21, 1039, 1993

A/Title: Nucleotide sequence analysis of the ribosomal S12 gene of Mycobacterium intrac
A/Reference number: S35537; PMID:93197130; PMID:8451173

A/Accession: S35538
A/Status: nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA
A/Residues: 1-9 <NAT>

A/Cross-references: UNIPROT:P33564; UNIPARC:UPI000016FA77; EMBL:L08171; NID:9149994; PI
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, February 1993
C/Keywords: protein biosynthesis; ribosome

Query Match 21.9%; Score 23; DB 2; Length 9;
Best Local Similarity 57.1%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8
| | | |
DB 2 PAKGMP 8

RESULT 43

C60588
sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Strongylocentrotus nudus)
N/Alternate names: speract homolog

C/Species: Strongylocentrotus nudus
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C/Accession: C60588

R/Toshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamag
Comp. Biochem. Physiol. B 94, 739-751, 1989

A/Title: A halogenated amino acid-containing sperm activating peptide and its related p
otus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.

A/Reference number: A60527
A/Accession: C60588

A/Molecule type: protein
A/Residues: 1-10 <YOS>

A/Cross-references: UNIPROT:Q7M4B4; UNIPARC:UPI000017A4F4

Query Match 21.9%; Score 23; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVGEV 18
||:|
Db 1 GFSLGCGGV 9

RESULT 44

E60527

sperm-activating peptide (Ser-3, Gly-5 SAP-I) - sea urchin (Tripneustes gratilla)

N.Alternate names: speract homolog TG-7

C.Species: Tripneustes gratilla

C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004

C.Accession: E60527, G39572

R.Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, M.

Biochemistry 30, 6203-6209, 1991

A.Title: A halogenated amino acid-containing sperm activating peptide and its related pe

otus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.

A.Reference number: A60527

A.Accession: E60527

A.Molecule type: protein

A.Residues: 1-10 <YOS>

A.Cross-references: UNIPROT:Q7M3T7; UNIPARC:UPI000017A4E4

A.Note: This peptide did not contain bromophenylalanine

R.Yoshino, K.; Takao, T.; Suhara, M.; Kikui, T.; Hori, H.; Nomura, K.; Yamaguchi, M.; Sh

Biochemistry 30, 6203-6209, 1991

A.Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated

A.Reference number: A39572; PMID:91283461; PMID:2059627

A.Accession: G39572

A.Molecule type: protein

A.Residues: 1-10 <Y02>

A.Cross-references: UNIPARC:UPI000017A4E4

A.Note: this peptide contained bromophenylalanine

C.Keywords: bromine

F.2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVGEV 18
||:|
Db 1 GFSLGCGGV 9

RESULT 45
160588
sperm-activating peptide (Glu-3, Met-4, Gly-5, Thr-7 SAP-I) - slate-pencil urchin (Hetero
C.Species: Heterocentrotus mammillatus
C.Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
C.Accession: 160588
R.Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimomishi, Y.; Kurita, M.; Yamaguchi, M.

A.Title: A halogenated amino acid-containing sperm activating peptide and its related pe
otus nudus, Echinosmetra mathaei and Heterocentrotus mammillatus.
A.Reference number: A60527
A.Accession: 160588
A.Molecule type: protein
A.Residues: 1-10 <YOS>
A.Cross-references: UNIPROT:Q7M4C0; UNIPARC:UPI000017A4E4

Query Match 21.9%; Score 23; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVGEV 18
||:|
Db 1 GFEMGGTGV 9

RESULT 46
C36201
1-aminocyclopropane-1-carboxylate synthase (EC 4.4.1.14) - apple tree (fragment)
C.Species: Malus domestica (apple tree)
C.Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 09-Jul-2004

C.Accession: C36201; C33103
R.Yip, W.K.; Dong, J.G.; Kenny, J.W.; Thompson, G.A.; Yang, S.F.
Proc. Natl. Acad. Sci. U.S.A. 87, 7930-7934, 1990
A.Title: Characterization and sequencing of the active site of 1-aminocyclopropane-1-car
A.Reference number: A36201; PMID:91045911; PMID:2122449
A.Accession: C36201

A.Molecule type: protein
A.Residues: 1-12 <YIP>

A.Cross-references: UNIPROT:Q9FUC3; UNIPROT:Q9SB01; UNIPROT:Q9SB94; UNIPROT:Q24062; UNIP

R.Experimental source: strain Golden delicious

C.Superfamily: 1-aminocyclopropane-1-carboxylate synthase

C.Keywords: carbon-sulfur lyase; ethylene biosynthesis; phosphoprotein; pyridoxal phosph

F.4/Binding site: pyridoxal phosphate (Lys) (covalent) #status experimental

Query Match 21.9%; Score 23; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.6e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 AKGMPGPF 11
||:|
Db 3 SKDLGLPGF 11

RESULT 47

A59387

VCAM-1 5'UTR binding protein - Rana pipiens (fragment)

C.Species: Rana pipiens

C.Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004

C.Accession: A59387

R.BANERJEE, H.

submitted to the Protein Sequence Database, February 2001

A.Description: Identification and characterization of a novel VCAM-1 5'UTR.

A.Reference number: A59387

A.Accession: A59387

A.Status: preliminary

A.Molecule type: protein

A.Residues: 1-13 <BAN>

A.Cross-references: UNIPROT:P82866; UNIPARC:UPI00000PDEZD

A.Experimental source: CCL-145

A.Note: VCAM-1 5' untranslated region binding protein with a probable translation inhibi

Query Match 21.9%; Score 23; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 1.8e+03;
Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DPAKMSPP 9
||:|
Db 4 DPVAGYKSP 12

RESULT 48

S13974

chlorophyll a/b-binding protein type I - garden pea (fragment)

C.Species: Pisum sativum (garden pea)

C.Date: 19-Mar-1997 #sequence_revision 24-Mar-1999 #text_change 24-Mar-1999

C.Accession: S13974

R.Jahns, P.; Junge, W.

Eur. J. Biochem. 193, 731-736, 1990

A.Title: Dicyclohexylcarbodiimide-binding proteins related to the short circuit of the F

A.Reference number: S13973; PMID:91065379; PMID:2174365

A.Accession: S13974

A.Molecule type: protein

A.Residues: 1-18 <TAH>

A.Cross-references: UNIPARC:UPI000017B061

C.Genetics:

C.Keywords: chlorophyll; chloroplast; light-harvesting complex; photosystem I; thylakoi

Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 2.6e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGFVGE 15

Db 1 LAVGILVPR 10

RESULT 49

S29766

Cytochrome c(EDH) - Pseudomonas aeruginosa

C/Species: Pseudomonas aeruginosa

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S29766

R/Schrover, J.M.; Frank, J.; van Melink, J.B.; Duine, J.A.

Biochem. J. 290, 123-127, 1993

A/Title: Quaternary structure of quinoprotein ethanol dehydrogenase from Pseudomonas aer

A/Reference number: S29766; PMID:93176105; PMID:8382472

A/Accession: S29766

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-19 <SCH>

A/Cross-references: UNIPROT:Q9R5C8; UNIPARC:UPI000008913D

Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 19;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPPG 10
Db 12 KGLEPLG 18

RESULT 50

B28457

proteoglycan II, bone - human (tentative sequence) (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-May-1989 #sequence_revision 19-May-1989 #text_change 09-Jul-2004

C/Accession: B28457

R/Fisher, L.W.; Hawkins, G.R.; Tuross, N.; Termini, J.D.

J. Biol. Chem. 262, 9702-9708, 1987

A/Title: Purification and partial characterization of small proteoglycans I and II, bone

A/Reference number: A92656; PMID:87250639; PMID:3597437

A/Accession: B28457

A/Molecule type: protein

A/Residues: 1-19 <PIS>

A/Cross-references: UNIPROT:P07585; UNIPARC:UPI000017C328

Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 19;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKMSPP 8
Db 1 DPAKGIAP 8

RESULT 51

B39108

lipoprotein Acfd precursor - Vibrio cholerae (fragment)

C/Species: Vibrio cholerae

C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 13-Sep-1996

C/Accession: B39108

R/Parrot, C.; Taxman, B.; Mekalanos, J.J.

Proc. Natl. Acad. Sci. U.S.A. 88, 1641-1645, 1991

A/Title: TokR regulates the production of lipoproteins and the expression of serum resist

A/Reference number: A39108; PMID:91156664; PMID:2003374

A/Accession: B39108

A/Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra

A/Molecule type: DNA

A/Residues: 1-20 <PAR>

A/Cross-references: UNIPARC:UPI000017AAD2

Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 20;

Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 10 GPVIG 14
Db 12 GFLIG 16

RESULT 52

A31516

lectin, galactose/N-acetylgalactosamine-specific - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993

C/Accession: A31516

R/Ii, M.; Kawasaki, T.; Yamashina, I.

Biochem. Biophys. Res. Commun. 155, 720-725, 1988

A/Title: Structural similarity between the macrophage lectin specific for galactose/N-a

A/Reference number: A31516; PMID:8833956; PMID:3421964

A/Accession: A31516

A/Molecule type: protein

A/Residues: 1-20 <ITX>

A/Cross-references: UNIPARC:UPI000017C946

Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 20;

Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11
Db 10 DEAGKAPPSF 20

RESULT 53

S38288

50K allergen - perennial ryegrass (fragment)

C/Species: Lolium perenne (perennial ryegrass)

C/Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: S38288

R/Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.

Biol. Chem. Hoppe-Seyler 374, 855-861, 1993

A/Title: Comparison of four grass pollen species concerning their allergens of grass gr

A/Reference number: S38288; PMID:94092339; PMID:7505588

A/Accession: S38288

A/Molecule type: protein

A/Residues: 1-20 <PERT>

A/Cross-references: UNIPROT:Q7M264; UNIPARC:UPI000017B086

Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 20;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKMSPP 8
Db 13 PAKGATP 19

RESULT 54

S06150

photoystem I chain III - maize (fragment)

C/Species: Zea mays (maize)

C/Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 09-Jul-2004

C/Accession: S06150

R/Randall, S.; Valentein, A.; Thorber, J.P.

FEBS Lett. 256, 150-154, 1989

A/Title: Correlation of some published amino acid sequences for photoystem I polypepti

A/Reference number: S06149; PMID:90033290; PMID:2680596

A/Accession: S06150

A/Molecule type: protein

A/Residues: 1-20 <ANA>

A/Cross-references: UNIPROT:P13193; UNIPARC:UPI0000132514

A/Note: the authors identified this protein as light-harvesting complex I 17K protein

C/Keywords: chloroplast; photosynthesis; photosystem I; thylakoid

Query Match

Best Local Similarity 21.9%; Score 23; DB 2; Length 20;

Matches 60.0%; Pred. No. 2.9e+03;

	Matches	3; Conservative	2; Mismatches	0; Indels	0; Gaps
QY	5	GMSRP 9			
		:			
Db	4	GLRPP 8			

RESULT 55
PA0040
malate dehydrogenase (EC 1.1.1.37) glyoxysomal - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 31-Dec-2004
C/Accession: PA0040
R/Kamo, M.; Kawakami, T.; Miyatake, N.; Teughta, A.
submitted to JIPID, July 1994
A/Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A/Reference number: PA0001
A/Accession: PA0040
A/Molecule type: protein
A/Residues: 1-15 <KAM>
A/Cross-references: UNIPROT:Q93ZA7; UNIPARC:UPI000017AFD0
A/Experimental source: stem
C/Superfamily: L-lactate dehydrogenase
C/Keywords: glyoxysome; NAD; oxidoreductase

Query Match	21.4%	Score 22.5	DB 2	Length 15
Best Local Similarity	63.6%	Pred. No. 2.5e+03		
Matches	7	Conservative	0	Mismatches 3
				Indels 1
				Gaps 1

QY 3 AKGMSPPGFIV 13
||| |||
Db 2 AKG-GNPGFKV 11

RESULT 56
PA00033
protein QA300033 - Arabidopsis thaliana (fragment)
C:/Species: Arabidopsis thaliana (mouse-ear cress)
C:/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997
C:/Accession: PA00033
R/Kmo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.
submitted to JIPIID, July 1994
A:/Description: Separation and characterization of Arabidopsis proteins by two-dimensional
A:/Reference number: PA00001
A:/Accession: PA00033
A:/Molecule type: protein
A:/Residues: 1-9 <KAM>
A:/Cross-references: UNIPARC:UPI0000017AF6
A:/Experimental source: leaf

Query Match	21.0%	Score 22	DB 2	Length 9
Best Local Similarity	62.5%	Pred. No. 2.8e+05		
Matches 5; Conservative		1; Mismatches 2;	Indels 0;	Gaps 0;

Qy	12	IVGBEGVL	1
		:	
Db	2	IVGBXXV	9

RESULT 57
D60527
sperm-activating peptide (gly-5 SAp-I) - sea urchin (*Triploneustes gratillia*)
N/Alternate names: speract homolog TG-6
C/Species: *Triploneustes gratillia*
C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
A/Accession: D60527; P39572
R/Yoshino, K.I.; Kajitara, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, T.
A/Title: A halogenated amino acid-containing sperm activating peptide and its related peptidic analogs, *Echinometra mathaei* and *Heterocentrotus mamillatus*.
A/Accession: D60527
A/Reference number: A60527
A/Molecule type: protein

A:Residues: 1-10 <YOS>
A:Cross-references: UNIPROT:07M378; UNIPARC:UPI00001744E3
A:Note: this peptide did not contain bromophenylalanine
R:Yoshino, K., Takao, T., Sunara, M., Kitai, T., Hori, H., Nomura, K., Yamaguchi, M., Shiohama, K., 6203-6209, 1991
A:Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated
A:Reference number: A39572; MUID:91283461; PMID:2059627
A:Accession: F39572
A:Molecule type: protein
A:Residues: 1-10 <Y02>
A:Cross-references: UNIPARC:UPI00001744E3
A:Note: this peptide contained bromophenylalanine
C:Keywords: bromine
F:2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match	21.0%	Score 22,	DB 2,	Length 10,
Best Local Similarity	55.6%	Pred. No. 1.9e+03,		
Matches 5,	Conservative 1,	Mismatches 3,	Indels 0,	Gaps 0,

QY 10 GFIVGEEGV 18
||:|
Db 1 GFDLGGGGV 9

```

RESULT 58
PS0213
28K protein 4412 - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 09-Jul-2004
C/Accession: PS0213
R/Taigita, A.; Kamo, M.
submitted to JIPID, April 1993
A/Reference number: PS0209
A/Accession: PS0213
A/Molecule type: protein
A/Residues: 1-12 <TSU>
A/Cross-references: UNIPROT:Q7M280; UNIPARC:UPI000017B0FA
A/Experimental source: callus
A/Comment: molecular weight 28K, pI 4.6.

```

Query Match	21.0%	Score 22	DB 2	Length 12
Best Local Similarity	50.0%	Pred. No.	2.3e+03	
Matches	5	Conservative	0	Mismatches 5
				Indels 0
				Gaps 0

QY	8	PPGGIVGEEG	17
Db	3	PPPFITGTTEG	12

```

RESULT 59
S65409
histone H2B - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C/Accession: S65409
R/Frohm, M.; Gunne, H.; Bergman, A.C.; Agerberth, T.; Boman, A.
Eur. J. Biochem. 237, 86-92, 1996
A/Title: Biochemical and antibacterial analysis of human wound and blister
A/Reference number: S65409; PMID:86203912; PMID:8620898
A/Accession: S65409
A/Molecule type: protein
A/Residues: 1-12 <PRO>
A/Cross-references: UNIPROT:Q96CF4; UNIPROT:O60814; UNIPARC:UPI00001771AE
Keywords: chromosomal protein; DNA binding; nucleosome core

```

Query Match	21.0%	Score 22	DB 2	Length 12
Best Local Similarity	44.4%	Pred. NO.	2.3e+03	
Matches 4	Conservative 1	Mismatches 4	Indels 0	Gaps 0

```
QY      1 DPAKGMSP 9
        :|||
Db      2 BPAKSAPAP 10
```



```
RESULT 60
A35377
GTP-binding protein G-alpha-11 chain - rat (fragment)
C/Species: Rattus norvegicus (Norway rat)
C/Date: 17-Aug-1990 #sequence_revision 17-Aug-1990 #text_change 31-Oct-1997
C/Accession: A35377
R/Linder, M.E.; Ewald, D.A.; Miller, R.J.; Gilman, A.G.
J. Biol. Chem. 265, 8243-8251, 1990
A/Title: Purification and characterization of G-alpha and three types of G-alpha after
A/Reference number: A35377; PMID:90243707; PMID:2159473
A/Accession: A35377
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <LTI>
A/Cross-references: UNIPARC:UPI0000177872
C/Superfamily: GTP-binding regulatory protein Gs alpha chain

Query Match          21.0%; Score 22; DB 2; Length 14;
Best Local Similarity 36.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY          5 GMSPPGPIVGE 15
           | | | | |
Db          2 GAABEGFMTAE 12

RESULT 61
PS0255
20K protein 5503 - rice (strain Nihonbare) (fragment)
C/Species: Oryza sativa (rice)
C/Date: 03-Feb-1994 #sequence_revision 03-Feb-1994 #text_change 23-Mar-1995
C/Accession: PS0255
R/Tsugita, A.
submitted to JIPID, April 1993
A/Reference number: PS0206
A/Accession: PS0255
A/Molecule type: protein
A/Residues: 1-14 <TSU>
A/Cross-references: UNIPARC:UPI000017B0F2
A/Experimental source: leaf, chlorophyll, strain Nihonbare
A/Note: molecular weight 20K, pI 4.3

Query Match          21.0%; Score 22; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 2.8e+03;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY          12 IVGEEGVLS 20
           | | | | |
Db          3 IAKKGVIT 11

RESULT 62
PA0110
translational elongation factor eEF-1 beta' chain - Arabidopsis thaliana (fragment)
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 07-Apr-1995 #sequence_revision 26-May-1995 #text_change 31-Dec-2004
C/Accession: PA0110
R/Kamo, M.; Kawakami, T.; Tsugita, A.
submitted to JIPID, March 1995
A/Reference number: PA0109
A/Accession: PA0110
A/Molecule type: protein
A/Residues: 1-15 <KAM>
A/Cross-references: UNIPROT:Q9SCX3; UNIPARC:UPI000017B0LC
C/Superfamily: translational elongation factor eEF-1 beta chain

Query Match          21.0%; Score 22; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 3e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY          15 EEGVLS 20
           | | | | |

RESULT 63
A59042
alpha-conotoxin EPI - cone shell (Conus episcopatus)
C/Species: Conus episcopatus (blehop's cone)
C/Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 09-Jul-2004
C/Accession: A59042
R/Loughnan, M.; Bond, T.; Atkins, A.; Cuevas, J.; Adams, D.J.; Broxton, N.M.; Livett, B
J. Biol. Chem. 273, 15667-15674, 1998
A/Title: Alpha-conotoxin EPI, a novel sulfated peptide from Conus episcopatus that sele
A/Reference number: A59042; PMID:98288307; PMID:9624161
A/Accession: A59042
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <LOU>
A/Cross-references: UNIPROT:P56638; UNIPARC:UPI00001287BF
C/Superfamily: alpha-conotoxin
C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
F/1-16/Product: alpha-conotoxin EPI #status experimental <MAT>
F/2-8-3-16/Disulfide bonds: #status experimental
F/15/Binding site: sulfate (Tyr) (covalent) #status experimental
F/16/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match          21.0%; Score 22; DB 2; Length 16;
Best Local Similarity 36.4%; Pred. No. 3.2e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY          1 DPAKGMSPPGF 11
           | | | | |
Db          5 DPKCMNNPDY 15

RESULT 64
A36133
hypothetical protein (bkd 5' region) - Pseudomonas putida (fragment)
C/Species: Pseudomonas putida
C/Date: 30-Nov-1990 #sequence_revision 30-Nov-1990 #text_change 09-Jul-2004
C/Accession: A36133
R/Madhusudan, K.T.; Huang, G.; Burns, G.; Sokatch, J.R.
J. Bacteriol. 172, 5655-5663, 1990
A/Title: Transcriptional analysis of the promoter region of the Pseudomonas putida bran
A/Reference number: A36133; PMID:91008935; PMID:2211503
A/Accession: A36133
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-18 <MAD>
A/Cross-references: UNIPROT:Q00360; UNIPARC:UPI000017A993; GB:M33715

Query Match          21.0%; Score 22; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 3.7e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY          6 MSBPPIVGE 14
           | | | | |
Db          1 MTABGFLFG 9

RESULT 65
I59649
human leukocyte antigen alpha chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I59649
R/Fogdell, A.; Olerup, O.
Tissue Antigens 44, 19-24, 1994
A/Title: The DQA1*0104 allele is carried by DRB1*1001- and DRB1*1401-positive haplotypes
A/Reference number: I59649; PMID:95064785; PMID:7974465
A/Accession: I59649
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-18 <RES>
```

A:Cross-references: UNIPROT:Q30216; UNIPARC:UPI000089A43F; GB:S75685; NID:9913771; PIDN:
 C:Gene: GDB:HLA-DOA1
 A:Cross-references: GDB:120638; OMIM:146880
 A:Map position: 6p21.3-6p21.3

Query Match 21.0%; Score 22; DB 2; Length 18;
 Best Local Similarity 42.9%; Pred. No. 3.7e+03;
 Matches 6; Conservative 2; Mismatches 2; Indels 4; Gaps 1;

QY 6 MSPPGTIVGEGVL 19
 :|||:
 :|||:
 Db 9 MSP----CGEGGIV 18

RESULT 66

S19240
 histone H2B (clone pCH1.0BR) - chicken (fragment)
 C:Species: Gallus gallus (chicken)
 C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 A:Accession: I50648; S19240
 R:Sturm, R.A.; Dalton, S.; Wells, J.R.
 Nucleic Acids Res. 16, 8571-8586, 1988
 A:Title: Conservation of histone H2B/H2B intergene regions: a role for the H2B specific
 A:Reference number: I50647; MUID:88335608; PMID:3267232
 A:Accession: I50648
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-20 <S12>
 A:Cross-references: UNIPROT:Q90859; UNIPARC:UPI00000FD2CA; EMBL:X07765; NID:G63429; PIDN:
 C:Superfamily: histone H2B
 C:Keywords: chromosomal protein; nucleosome core

Query Match 21.0%; Score 22; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 4.2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSP 9
 :|||:
 :|||:
 Db 3 EPAKSNAP 11

RESULT 67

B33290
 histone H2B - human (fragments)
 C:Species: Homo sapiens (man)
 C:Date: 20-Dec-1989 #sequence_revision 20-Dec-1989 #text_change 18-Jun-1993
 A:Accession: B33290
 R:Baxter, G.D.; Smith, P.J.; Lavin, M.F.
 Biochem. Biophys. Res. Commun. 162, 30-37, 1989
 A:Title: Molecular changes associated with induction of cell death in a human T-cell leu
 A:Reference number: A33290; MUID:89322258; PMID:2546549
 A:Accession: B33290
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <BAK>
 A:Cross-references: UNIPARC:UPI000017C15D

Query Match 21.0%; Score 22; DB 2; Length 20;
 Best Local Similarity 44.4%; Pred. No. 4.2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSP 9
 :|||:
 :|||:
 Db 2 EPAKSNAP 10

RESULT 68

C56385
 nitrophorin 3 - Rhodnius prolixus (fragment)
 N:Alternate names: nitric oxide-carry protein NP3
 C:Species: Rhodnius prolixus
 C:Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004

C:Accession: C56385
 R:Champagne, D.B.; Nussenzveig, R.H.; Ribelto, J.M.C.
 J. Biol. Chem. 270, 8691-8695, 1995

A:Title: Purification, partial characterization, and cloning of nitric oxide-carrying he
 A:Reference number: A56385; MUID:95238361; PMID:7721773

A:Accession: C56385
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-20 <CHA>
 A:Cross-references: UNIPROT:Q7000; UNIPROT:Q9TY55; UNIPARC:UPI000017BE29
 C:Keywords: heme; salivary gland; vasodilator

Query Match 21.0%; Score 22; DB 2; Length 20;
 Best Local Similarity 30.8%; Pred. No. 4.2e+03;
 Matches 4; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 PAKGMSPPGTVG 14
 :|||:
 :|||:
 Db 8 PKKGIDKAKYFSG 20

RESULT 69

A35768
 T-cell receptor alpha chain V-J region (348-281) - mouse (fragment)
 C:Species: Mus musculus (house mouse)
 C:Date: 05-Oct-1990 #sequence_revision 05-Oct-1990 #text_change 30-May-1997
 A:Accession: A35768
 R:Kosaki, H.; Imai, K.; Nakayama, F.; Sado, T.; Moriwaki, K.; Taniguchi, M.
 Proc. Natl. Acad. Sci. U.S.A. 87, 5248-5252, 1990
 A:Title: Homogeneous junctional sequence of the VJ4+ T-cell antigen receptor alpha chain
 A:Reference number: A35768; MUID:90319089; PMID:2371269
 A:Accession: A35768
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-8 <KOS>
 A:Cross-references: UNIPARC:UPI000017C78B
 A:Note: the sequence shown follows the authors' translation at position 1 of TGT
 C:Keywords: T-cell receptor

Query Match 20.0%; Score 21; DB 2; Length 8;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 12 IYBERG 17
 :|||:
 :|||:
 Db 2 VVGDRG 7

RESULT 70

PD0027
 pen-tachyklin - penaeid shrimp (Penaeus vannamei) (fragment)
 C:Species: Penaeus vannamei
 C:Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
 A:Accession: PD0027
 R:Nieto, J.; Veelaert, D.; Derna, R.; Waelkens, B.; Ceratleens, A.; Coast, G.; Devreese,
 Biochem. Biophys. Res. Commun. 248, 406-411, 1998
 A:Title: Identification of one tachyklin- and two kinin-related peptides in the brain c
 A:Reference number: PD0027; MUID:98342103; PMID:9675150
 A:Accession: PD0027
 A:Status: preliminary
 A:Molecule type: protein
 A:Residues: 1-9 <NIB>
 A:Cross-references: UNIPROT:Q7M3L3; UNIPARC:UPI000017CB0C
 C:Comment: This peptide belongs to myotropic neuropeptides.

Query Match 20.0%; Score 21; DB 2; Length 9;
 Best Local Similarity 50.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 SPGRF 12
 :|||:
 :|||:
 Db 1 AFSGPL 6

RESULT 71
 P60527
 sperm-activating peptide (Gly-3,5 SAp-I) - sea urchin (Tripneustes gratilla)
 N/Alternate names: spermact homolog TC-8
 C/Species: tripneustes gratilla
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 16-Aug-2004
 C/Accession: P60527; H35572
 R/Yoshino, K.I.; Kajitani, H.; Nomura, K.; Takao, T.; Shimonishi, Y.; Kurita, M.; Yamaguchi, K.I.
 Comp. Biochem. Physiol. B 94, 739-751, 1989
 A/Title: A haemogenated amino acid-containing sperm activating peptide and its related polypeptide, Schinometra mathaei and Heterocentrotus mammillatus.
 A/Reference number: A60527
 A/Accession: P60527
 A/Molecule type: protein
 A/Residues: 1-10 <YOS>
 A/Cross-references: UNIPROT:Q7M379; UNIPARC:UPI000017A4E2
 A/Note: this peptide did not contain bromophenylalanine
 R/Yoshino, K.I.; Takao, T.; Suhara, M.; Kitai, T.; Horii, H.; Nomura, K.; Yamaguchi, M.; Shimonishi, Y.
 Biochemistry 30, 6203-6209, 1991
 A/Title: Identification of a novel amino acid, o-bromo-L-phenylalanine, in egg-associated sperm-activating peptide
 A/Reference number: A39572; PMID:91283461; PMID:2059627
 A/Accession: H39572
 A/Molecule type: protein
 A/Residues: 1-10 <YOS>
 A/Cross-references: UNIPARC:UPI000017A4E2
 A/Note: this peptide contained bromophenylalanine
 C/Keyword: bromine
 F/2/Modified site: 2'-bromophenylalanine (Phe) (partial) #status experimental

Query Match
 Best Local Similarity 20.0%; Score 21; DB 2; Length 10;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVIGEGV 18
 DB 1 GFGLGGGGV 9

RESULT 72
 S39030
 lyeyl-bradykinin - rainbow trout
 C/Species: Oncorhynchus mykiss (rainbow trout)
 C/Date: 19-May-1994 #sequence_revision 19-Apr-1996 #text_change 16-Aug-2004
 C/Accession: S39030
 R/Conlon, J.M.; Olson, K.R.
 FEBS Lett. 334, 75-78, 1993
 A/Title: Purification of a vasoactive peptide related to lyeyl-bradykinin from trout plasma
 A/Reference number: S39030; PMID:94039817; PMID:8224232
 A/Accession: S39030
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10 <CON>
 A/Cross-references: UNIPROT:Q9PRZ1; UNIPARC:UPI0000126AD7

Query Match
 Best Local Similarity 20.0%; Score 21; DB 2; Length 10;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGGF 11
 DB 3 PGGM 6

RESULT 73
 A40693
 transgelin - sheep (fragment)
 C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
 C/Date: 03-May-1994 #sequence_revision 03-May-1994 #text_change 09-Jul-2004
 C/Accession: A40693
 R/Shapland, C.; Hansen, J.J.; Totcy, N.F.; Lawson, D.
 J. Cell Biol. 121, 1065-1073, 1993
 A/Title: Purification and properties of transgelin: a transformation and shape change associated protein
 A/Reference number: A40693; PMID:93273790; PMID:8501116

A/Accession: A40693
 A/Molecule type: protein
 A/Residues: 1-11 <SHA>
 A/Cross-references: UNIPROT:Q7M2V7; UNIPARC:UPI00001776A2
 A/Experimental source: aorta
 C/Comment: This protein gets actin and is down regulated by transformation or loss of cytoskeleton
 C/Suprafamily: smooth muscle protein SM22; calponin repeat homology; smooth muscle protein
 C/Keywords: actin binding; cytoskeleton

Query Match
 Best Local Similarity 20.0%; Score 21; DB 2; Length 11;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 PAKGMS 7
 DB 3 PSYGMS 8

RESULT 74
 S39762
 cytochrome P450 UT-7b - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 19-May-1994 #sequence_revision 10-Nov-1995 #text_change 10-Nov-1995
 C/Accession: S39762
 R/Ohishi, N.; Imake, S.; Suzuki, T.; Funae, Y.
 Biochim. Biophys. Acta 1158, 227-236, 1993
 A/Title: Characterization of two P-450 isozymes placed in the rat CYP2D subfamily.
 A/Reference number: S39761; PMID:94072607; PMID:8251521
 A/Accession: S39762
 A/Molecule type: protein
 A/Residues: 1-12 <OH1>
 A/Cross-references: UNIPARC:UPI000017C8F7

Query Match
 Best Local Similarity 20.0%; Score 21; DB 2; Length 12;
 Matches 2; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 10 GFVIGEE 16
 DB 1 GLTICDD 7

RESULT 75
 B58502
 43.2K bile stone protein - unidentified bacterium (fragment)
 C/Species: unidentified bacterium
 C/Date: 07-Feb-1997 #sequence_revision 07-Feb-1997 #text_change 09-Jul-2004
 C/Accession: B58502
 R/Binet, J.P.; Binette, M.B.
 Submitted to the Protein Sequence Database, October 1996
 A/Description: The proteins of kidney and gallbladder stones.
 A/Reference number: A58501
 A/Accession: B58502
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-12 <BIN>
 A/Cross-references: UNIPROT:Q7MLD0; UNIPARC:UPI000017A8D4
 A/Experimental source: human bile with stones
 A/Note: a secondary sequence DVKIGVAGS was also found

Query Match
 Best Local Similarity 20.0%; Score 21; DB 2; Length 12;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 GFVIGEGV 18
 DB 2 GFALNEQPV 10

RESULT 76
 B60683
 malate dehydrogenase (decarboxylating) (EC 1.1.1.39) - millet (fragment)
 C/Species: Panicum sp. (millet)

CjDate: 24-Feb-1994 #sequence_revision 24-Feb-1994 #text_change 09-Jul-2004

CjAccession: B60683

RjMurata, T.; Ikeda, J.; Takano, M.; Ohnagi, R.

Plant Cell Physiol. 30, 429-437, 1989

AjTitle: Comparative studies of NAD-malic enzyme from leaves of various C-4 plants.

AjReference number: A60683

AjAccession: B60683

AjMolecule type: protein

AjResidues: 1-14 <MUR>

AjCross-references: UNIPROT:Q7MT9; UNIPARC:UPI000017B12P

CjKeywords: oxidoreductase; photosynthesis

Query Match 20.0%; Score 21; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 SPPG 10

DB 4 APPG 7

RESULT 77

B39109

hypothetical 1.5K protein - hepatitis C virus

NjAlternate names: hypothetical protein 2

CjSpecies: hepatitis C virus

CjDate: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 07-May-1999

CjAccession: B39109; J01585

RjHan, J.H.; Shyamala, V.; Richman, K.H.; Brauer, M.J.; Irvine, B.; Urdea, M.S.; Tekamp-

Proc. Natl. Acad. Sci. U.S.A. 88, 1711-1715, 1991

AjTitle: Characterization of the terminal region of hepatitis C viral RNA: identification

AjReference number: A39109; MUID:91156678; PMID:1705704

AjAccession: B39109

AjStatus: not compared with conceptual translation

AjMolecule type: mRNA

AjResidues: 1-15 <HAN>

AjCross-references: UNIPARC:UPI000014E546; GB:M58406

RjKumar, U.; Cheng, D.; Thomas, H.; Monjardino, J.

J. Gen. Virol. 73, 1521-1525, 1992

AjTitle: Cloning and sequencing of the structural region and expression of putative core

AjReference number: J01584; MUID:92300349; PMID:1318944

AjAccession: J01585

AjMolecule type: genomic RNA

AjResidues: 1-15 <KUM>

AjCross-references: UNIPARC:UPI000014E546

AjExperimental source: strain U.K.

Query Match 20.0%; Score 21; DB 2; Length 15;

Best Local Similarity 60.0%; Pred. No. 4.3e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 MSPG 10

DB 4 VQPG 8

RESULT 78

S05700

Insulin-like growth factor-binding protein, adult - human (fragment)

CjSpecies: Homo sapiens (man)

CjDate: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993

CjAccession: S05700

RjRogland, M.; Hosenlopp, P.; LePage, P.; Ballard, A.; Binoux, M.

FEBS Lett. 255, 253-258, 1989

AjTitle: Isolation from human cerebrospinal fluid of a new insulin-like growth factor-bi

AjReference number: S05699; MUID:90005986; PMID:2551732

AjAccession: S05700

AjMolecule type: protein

AjResidues: 1-15 <ROG>

AjCross-references: UNIPARC:UPI000017C274

Query Match

Best Local Similarity 20.0%; Score 21; DB 2; Length 15;

Matches 30.8%; Pred. No. 4.3e+03;

Matches 4; Conservative 1; Mismatches 8; Indels 0; Gaps 0;

QY 2 PAKGMSPPGFIYG 14

DB 3 PEGGQGVQALLPG 15

RESULT 79

PI0110

complement factor B1-Bb and B2-Bb - guinea pig (fragment)

CjSpecies: Cavia porcellus (guinea pig)

CjDate: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 15-Nov-1996

CjAccession: PI0110

RjMatsumita, M.; Okada, H.

Mol. Immunol. 26, 669-676, 1989

AjTitle: Two forms of guinea pig factor B of the alternative complement pathway with dif

AjReference number: A91136; MUID:89384686; PMID:279589

AjAccession: PI0110

AjMolecule type: protein

AjResidues: 1-15 <MAT>

AjCross-references: UNIPARC:UPI000017CA2B

CjKeywords: complement alternate pathway; glycoprotein

Query Match

Best Local Similarity 20.0%; Score 21; DB 2; Length 15;

Matches 57.1%; Pred. No. 4.3e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DPAKGM 7

DB 5 DPAGSMN 11

RESULT 80

S55307

glutathione transferase 3-3 - rat (fragments)

CjSpecies: Rattus norvegicus (Norway rat)

CjDate: 27-Oct-1995 #sequence_revision 03-Nov-1995 #text_change 07-May-1999

CjAccession: S55307

RjCooke, R.J.; Bjornstedt, R.; Douglas, K.T.; McKie, J.H.; King, M.D.; Coles, B.; Kett

Biochem. J. 302, 383-390, 1994

AjTitle: Photolability labelling of the active site of the rat glutathione transferases

AjReference number: S55307; MUID:94379965; PMID:8092989

AjAccession: S55307

AjStatus: preliminary

AjMolecule type: protein

AjResidues: 1-16 <COO>

AjCross-references: UNIPARC:UPI000017C91E

Query Match 20.0%; Score 21; DB 2; Length 16;

Best Local Similarity 37.5%; Pred. No. 4.6e+03;

Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 5 GMSPPGFIYGBGVIS 20

DB 1 GLTHPSQIMREKYLIS 16

RESULT 81

A31963

pyruvate dehydrogenase (lipoamide) (EC 1.2.4.1) alpha chain type I - pig roundworm (frag

CjSpecies: Ascaris suum (pig roundworm)

CjDate: 29-Jun-1989 #sequence_revision 29-Jun-1989 #text_change 09-Jul-2004

CjAccession: A31963

RjThissen, J.; Komnick, R.

J. Biol. Chem. 263, 19092-19097, 1988

AjTitle: Phosphorylation and inactivation of the pyruvate dehydrogenase from the anaerob

AjReference number: A31963; MUID:89066711; PMID:3198613

AjAccession: A31963

AjStatus: preliminary

AjMolecule type: protein

AjResidues: 1-16 <THI>

AjCross-references: UNIPROT:P26267; UNIPARC:UPI000017B69C

CjKeywords: mitochondrion; oxidoreductase; phosphoprotein

Query Match 20.0%; Score 21; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 4.6e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 MSPPG 10
| | |
| | |
Db 7 MSDPG 11

RESULT 82

S01104

hypothetical protein 3 - fruit fly (Drosophila melanogaster)

C/Species: Drosophila melanogaster

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004

C/Accession: S01104

R/Evelech, D.D.; Marsh, J.L.

Mol. Gen. Genet. 209, 290-298, 1987

A/Title: Overlapping transcription units in Drosophila: sequence and structure of the C

A/Reference number: S01102; MUID:88038375; PMID:3478553

A/Accession: S01104

A/Molecule type: DNA

A/Residues: 1-16 <EVS>

A/Cross-references: UNIPROT:O18378; UNIPARC:UPI0000835F4; EMBL:X05991; NID:G7759; PIDN:

C/Genetic:

A/Genes: Cg

A/Cross-references: FlyBase:FBgn0002036

Query Match 20.0%; Score 21; DB 2; Length 16;
Best Local Similarity 30.0%; Pred. No. 4.6e+03;
Matches 3; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 3 AKGMSPPGR 12
| | | | |
| | | | |
Db 2 AAGLTSPALV 11

RESULT 83

I55612

thyroid hormone receptor beta - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 05-Nov-1999

C/Accession: I55612

R/Adams, M.; Matthews, C.; Collingwood, T.N.; Tone, Y.; Beck-Peccoz, P.; Chatterjee, K.K.

J. Clin. Invest. 94, 506-515, 1994

A/Title: Genetic analysis of 29 kindreds with generalized and pituitary resistance to th

A/Reference number: I55612; MUID:9434950; PMID:8040303

A/Accession: I55612

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-17 <RBS>

A/Cross-references: UNIPARC:UPI00011F7B5; GB:S72623; NID:G633779; PIDN:AAB31420.1; PID:

C/Genetic:

A/Genes: TRbeta

Query Match 20.0%; Score 21; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 5e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFVIG 14
| | | | |
| | | | |
Db 6 PPFVLG 11

RESULT 84

I51203

myosin heavy chain - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 04-Sep-1997 #sequence_revision 07-Nov-1997 #text_change 09-Jul-2004

C/Accession: I51203

J. Kelley, C.A.; Takahashi, M.; Yu, J.H.; Adelstein, R.S.

J. Biol. Chem. 268, 12848-12854, 1993

A/Title: An insert of seven amino acids confers functional differences between smooth mu

A/Reference number: I51203; MUID:93286132; PMID:8509418

A/Accession: I51203

A/Status: preliminary; translated from GB/EMBL/DBJ

A/Molecule type: mRNA

A/Residues: 1-17 <KRL>

A/Cross-references: UNIPROT:Q91352; UNIPARC:UPI00000FD367; GB:S62578; NID:G366220; PIDN:

Query Match 20.0%; Score 21; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 5e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 9 PGFVIG 15
| | | | |
| | | | |
Db 10 PPFVIG 16

RESULT 85

A39997

group III allergen - house-dust mite (Dermatophagoides pteronyssinus)

C/Species: Dermatophagoides pteronyssinus

C/Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 30-Sep-1993

C/Accession: A39997

R/Stewart, G.A.; Ward, L.D.; Simpson, R.J.; Thompson, P.J.

submitted to the Protein Sequence Database, September 1991

A/Reference number: A39997

A/Accession: A39997

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 <STR>

A/Cross-references: UNIPARC:UPI000017BE12

Query Match 20.0%; Score 21; DB 2; Length 18;
Best Local Similarity 55.6%; Pred. No. 5.3e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 12 IVGEGVLS 20
| | | | |
| | | | |
Db 1 IVGEXALA 9

RESULT 86

A35678

hypothetical protein (proenkephalin 5' region) - mouse

C/Species: Mus musculus (house mouse)

C/Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 09-Jul-2004

C/Accession: A35678

R/Kilpatrick, D.L.; Zinn, S.A.; Fitzgerald, M.; Higuchi, H.; Sabol, S.L.; Meyerhardt, J

Mol. Cell. Biol. 10, 3717-3726, 1990

A/Title: Transcription of the rat and mouse proenkephalin genes is initiated at distinct

A/Reference number: A35678; MUID:90287163; PMID:2355920

A/Accession: A35678

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-18 <KTL>

A/Cross-references: UNIPROT:Q62256; UNIPARC:UPI0000028BA1; GB:M55181; NID:G201032; PIDN:

Query Match 20.0%; Score 21; DB 2; Length 18;
Best Local Similarity 44.4%; Pred. No. 5.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 PAKMSPPG 10
| | | | |
| | | | |
Db 9 PWEEDRIPG 17

RESULT 87

B29501

fibronopeptide A - European moose

C/Species: Alces alces alces (European moose, elk)

C/Date: 21-Nov-1987 #sequence_revision 21-Nov-1987 #text_change 09-Jul-2004

C/Accession: B29501

R/Blomback, B.; Blomback, M.; Hann, C.

unpublished results, cited by Blomback, B., and Blomback, M., in Chemotaxonomy and Ser

A:Reference number: A29501

A:Accession: B29501

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <BIO>

A:Cross-references: UniProt:Q7M315; UNIPARC:UPI0000177781

C:Superfamily: fibrinogen beta chain; fibrinogen beta/gamma homology; fibrinogen disulfide

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 80.0%; Pred. No. 5.6e+03;

Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5

DB 5 DPAKG 9

RESULT 88

A48400

phosphocarrier protein 1, HPr-1 - Streptococcus salivarius (fragment)

C:Species: Streptococcus salivarius

C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C:Accession: A48400

R:Vadboncoeur, C.; Konishi, Y.; Dumas, F.; Gauthier, L.; Frenette, M.

Biochimie 73, 1427-1430, 1991

A:Title: HPr polymorphism in oral streptococci is caused by the partial removal of the N

A:Reference number: A48400; MUID:92190346; PMID:1799636

A:Accession: A48400

A:Status: preliminary

A:Molecule type: protein

A:Residues: 1-19 <VAD>

A:Cross-references: UniProt:P24366; UNIPARC:UPI0000177781

A:Note: sequence extracted from NCBI backbone (NCBIP:88293)

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotran

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IVGEGV 18

DB 7 IVAGTGI 13

RESULT 89

S22233

vitronectin - sheep (fragment)

C:Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)

C:Date: 22-Nov-1993 #sequence_revision 29-Aug-1997 #text_change 29-Aug-1997

C:Accession: S22233

R:Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatchgo, T.; Ogawa, H.; Uchibori, H.; Matsui

Biochim. Biophys. Acta 1120, 1-10, 1992

A:Title: Vitronectin diversity in evolution but uniformity in ligand binding and size of

A:Reference number: S21768; MUID:92207982; PMID:1372829

A:Accession: S22233

A:Molecule type: protein

A:Residues: 1-19 <NAX>

A:Cross-references: UNIPARC:UPI000017C5A9

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 36.4%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11

DB 3 ESXKGRXTEGF 13

RESULT 90

S02808

nucleolin - bovine (fragment)

C:Species: Bos primigenius taurus (cattle)

C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C:Accession: S02808

R:Sapp, M.; Richter, A.; Weisshart, K.; Calzergues-Ferrer, M.; Amalric, F.; Wallace, M.C.

Eur. J. Biochem. 179, 541-548, 1989

A:Title: Characterization of a 48-kDa nucleic-acid-binding fragment of nucleolin.

A:Reference number: S02808; MUID:89153087; PMID:2920725

A:Accession: S02808

A:Molecule type: protein

A:Residues: 1-19 <SAP>

A:Cross-references: UniProt:Q7M2L8; UNIPARC:UPI000017C54E

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 57.1%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 AKGMSPP 9

DB 4 AKQKAP 10

RESULT 91

S22232

vitronectin - goat (fragment)

C:Species: Capra aegagrus hircus (domestic goat)

C:Date: 22-Nov-1993 #sequence_revision 29-Aug-1997 #text_change 09-Jul-2004

C:Accession: S22232

R:Nakashima, N.; Miyazaki, K.; Ishikawa, M.; Yatchgo, T.; Ogawa, H.; Uchibori, H.; Matsui

Biochim. Biophys. Acta 1120, 1-10, 1992

A:Title: Vitronectin diversity in evolution but uniformity in ligand binding and size of

A:Reference number: S21768; MUID:92207982; PMID:1372829

A:Accession: S22232

A:Molecule type: protein

A:Residues: 1-19 <NAX>

A:Cross-references: UniProt:Q9TR55; UNIPARC:UPI000017C591

Query Match 20.0%; Score 21; DB 2; Length 19;

Best Local Similarity 36.4%; Pred. No. 5.6e+03;

Matches 4; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DPAKMSPPGF 11

DB 3 ESXKGRXTEGF 13

RESULT 92

B48400

phosphocarrier protein 2, HPr-2 - Streptococcus salivarius (fragment)

C:Species: Streptococcus salivarius

C:Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 23-May-1997

C:Accession: B48400

R:Nakashima, N.; Konishi, Y.; Dumas, F.; Gauthier, L.; Frenette, M.

Biochimie 73, 1427-1430, 1991

A:Title: HPr polymorphism in oral streptococci is caused by the partial removal of the N

A:Reference number: A48400; MUID:92190346; PMID:1799636

A:Accession: B48400

A:Molecule type: protein

A:Residues: 1-20 <VAD>

A:Cross-references: UNIPARC:UPI0000177781

A:Note: sequence extracted from NCBI backbone (NCBIP:88290)

C:Superfamily: phosphotransferase system phosphohistidine-containing protein; phosphotran

Query Match 20.0%; Score 21; DB 2; Length 20;

Best Local Similarity 57.1%; Pred. No. 6e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 12 IVGEGV 18

DB 8 IVAGTGI 14

RESULT 93

S65399

Immunodeficiency virus type 1, HIV-1 gp120 - human (fragments)
 C/Species: Homo sapiens (man)
 C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999
 C/Accession: S65399
 R/Niwa, Y.; Yano, M.; Futaki, S.; Okumura, Y.; Kido, H.
 Eur. J. Biochem. 237, 64-70, 1996
 A/Title: T-cell membrane-associated serine protease, tryptase TL(2), binds human immunodeficiency virus type 1 inhibits cleavage of gp120.
 A/Reference number: S65399; MUID:96203909; PMID:8620895
 A/Accession: S65399
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-10,11-20 <NT>
 A/Cross-references: UNIPROT:Q10000030087; UNIPARC:UP10000178619
 C/Superfamily: type B retrovirus env polyprotein

Query Match 20.0%; Score 21; DB 2; Length 20;
 Best Local Similarity 28.6%; Pred. No. 6e+03;
 Matches 4; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

QY 2 PAKMSPPRIVGE 15
 DB 3 PGRAPVTIGRID 16

RESULT 94
 A61414
 Chymotrypsin (EC 3.4.21.1) - snapping turtle (fragment)
 C/Species: Chelydra serpentina (snapping turtle)
 C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 09-Jul-2004
 C/Accession: A61414
 R/Bhargava, A.K.; Barnard, E.A.
 J. Mol. Evol. 2, 187-198, 1973
 A/Title: Evolution in the pancreatic chymotrypsinogen series: N-terminal sequence detection
 A/Reference number: A61414; MUID:76146602; PMID:4807189
 A/Accession: A61414
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20

 A/Cross-references: UNIPROT:Q7L234; UNIPARC:UP10000178FB5
 C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match 20.0%; Score 21; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 6e+03;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 12 IVGGE 16
 DB 16 IVGDE 20

RESULT 95
 I53671
 neurofilament heavy subunit - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I53671
 R/Figlewicz, D.A.; Rouleau, G.A.; Krizus, A.; Julien, J.P.
 Gene 132, 297-300, 1993
 A/Title: Polymorphism in the multi-phosphorylation domain of the human neurofilament heavy subunit
 A/Reference number: I53671; MUID:94040777; PMID:8224877
 A/Accession: I53671
 A/Status: preliminary; translated from GB/EMBL/DDAT
 A/Molecule type: mRNA
 A/Residues: 1-20 <RSS>
 A/Cross-references: UNIPROT:Q16070; UNIPARC:UP10000072AP9; GB:S66488; NID:G452861; PIND: C/Genetics:
 A/Genes: GDB:NEFH
 A/Cross-references: GDB:120225; OMIM:162230
 A/Map position: 22q12.1-22q13.1

Query Match 20.0%; Score 21; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 6e+03;

Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PAKMSP 8
 DB 2 PERAKSP 8

RESULT 96
 S05411
 carboxylesterase (EC 3.1.1.1) - Sulfolobus acidocaldarius (fragment)
 N/Alternate names: serine esterase
 C/Species: Sulfolobus acidocaldarius
 C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004
 C/Accession: S05411
 R/Soder, H.; Goerlich, H.
 Biochem. J. 261, 993-998, 1989
 A/Title: Further kinetic and molecular characterization of an extremely heat-stable carboxylesterase
 A/Reference number: S05411; MUID:90026296; PMID:2508625
 A/Accession: S05411
 A/Molecule type: protein
 A/Residues: 1-20 <SO>
 A/Cross-references: UNIPROT:Q7M529; UNIPARC:UP1000017AB3
 A/Note: 1-Ala and 1-Ser were also found
 C/Keywords: carboxylic ester hydrolase; tetramer

Query Match 19.5%; Score 20.5; DB 2; Length 20;
 Best Local Similarity 35.7%; Pred. No. 7.1e+03;
 Matches 5; Conservative 3; Mismatches 5; Indels 1; Gaps 1;

QY 1 DPA-KGMSPPGFIV 13
 DB 3 DPTIKCLBSGFVI 16

RESULT 97
 A39543
 collagen alpha 1(IX) chain - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 28-Feb-1992 #sequence_revision 28-Feb-1992 #text_change 09-Jul-2004
 C/Accession: A39543
 R/Wu, J.J.; Lark, M.W.; Chun, L.R.; Eyre, D.R.
 J. Biol. Chem. 266, 5625-5628, 1991
 A/Title: Sites of bromelain cleavage in collagen types II, IX, X, and XI of cartilage
 A/Reference number: A39543; MUID:91170231; PMID:2005102
 A/Accession: A39543
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <WU>
 A/Cross-references: UNIPROT:Q7M207; UNIPARC:UP1000017AL5C
 C/Keywords: coiled coil; extracellular matrix; glycoprotein; trimer

Query Match 19.5%; Score 20.5; DB 2; Length 20;
 Best Local Similarity 37.5%; Pred. No. 7.1e+03;
 Matches 6; Conservative 0; Mismatches 3; Indels 7; Gaps 1;

QY 2 PAKMS-----PG 10
 DB 4 PDGAGAGLPGRPGRPG 19

RESULT 98
 PT0559
 T-cell receptor beta chain V-D-J region (126-1BH) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PT0559
 R/Feeney, A.O.
 J. Exp. Med. 174, 115-124, 1991
 A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A/Reference number: PT0509; MUID:91277601; PMID:1711558
 A/Accession: PT0559
 A/Status: translation not shown
 A/Molecule type: mRNA

A/Residues: 1-8 <PBE>
 A/Cross-references: UNIPARC:UPI000017C80B
 A/Experimental source: day 18 fetal thymus, strain BALB/c
 C/Keywords: T-cell receptor

Query Match 19.0%; Score 20; DB 2; Length 8;
 Best Local Similarity 100.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 8 PPG 10
 ||||
 Db 4 PPG 6

RESULT 99

PT0554
 T-cell receptor beta chain V-D-J region (126-1G) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PT0554
 R/Peeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A/Reference number: PT0509; MUID:91277601; PMID:1711558
 A/Accession: PT0554
 A/Status: translation not shown
 A/Molecule type: mRNA
 A/Residues: 1-8 <PBE>
 A/Cross-references: UNIPARC:UPI000017C815
 A/Experimental source: day 18 fetal thymus, strain BALB/c
 C/Keywords: T-cell receptor

Query Match 19.0%; Score 20; DB 2; Length 8;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 QY 14 GEEGV 18
 ||||
 Db 3 GDEGL 7

RESULT 100

B41983
 orf downstream to bacterioferritin - Azotobacter vinelandii (fragment)
 C/Species: Azotobacter vinelandii
 C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
 C/Accession: B41983
 R/Grossman, M.J.; Hinton, S.M.; Minak-Bernero, V.; Slaughter, C.; Stiefel, E.I.
 Proc. Natl. Acad. Sci. U.S.A. 89, 2419-2423, 1992
 A/Title: Unification of the ferritin family of proteins.
 A/Reference number: A41983; MUID:92196129; PMID:1549605
 A/Accession: B41983
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: nucleic acid; protein
 A/Residues: 1-9 <GRO>
 A/Cross-references: UNIPROT:P25825; UNIPARC:UPI000013A327; GB:M83692; NID:g142297; PIDN:
 A/Note: sequence extracted from NCBI backbone (NCBIP:88442)

Query Match 19.0%; Score 20; DB 2; Length 9;
 Best Local Similarity 75.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 6 MSPP 9
 ||||
 Db 1 MAPP 4

Search completed: January 20, 2006, 19:12:12
 Job time : 12.3462 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 66.5385 Seconds

(without alignments)
212.066 Million cell updates/sec

Title: US-09-662-293-4

Perfect score: 105

Sequence: 1 DPAKGMSPGFIVGSEGVLS 20

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: uniprot_05.80:*
2: uniprot_sprot:*
3: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	32	30.5	15	2	Q7MA99 HUMAN
2	30	28.6	17	2	Q6N699 VITVY
3	30	28.6	18	2	Q8NFB4 HUMAN
4	28	26.7	10	2	Q7M2N0 BOVIN
5	28	26.7	15	2	Q7MLF8 MAIZE
6	28	26.7	16	2	Q7SM54 IDELA
7	28	26.7	20	2	Q71H55 LACDL
8	28	26.7	20	2	Q79CF0 RHILR
9	27	25.7	16	2	Q7M281 ORISA
10	27	25.7	16	2	Q972Q4 BRANA
11	27	25.7	19	2	Q9N195 BOVIN
12	26	24.8	9	1	BRK1 RANMI
13	26	24.8	9	1	KNL3 BOMVA
14	26	24.8	9	1	KNL3 CYPDO
15	26	24.8	9	2	P84497 TRASC
16	26	24.8	9	2	Q7LZ50 CHICK
17	26	24.8	9	2	Q7LZJ8 RANTR
18	26	24.8	9	2	Q7LZ17 GNEOB
19	26	24.8	11	1	BRKP PHYRO
20	26	24.8	11	1	BRK MEGFL
21	26	24.8	11	2	Q75B11 HUMAN
22	26	24.8	11	2	Q7M4P1 HUMAN
23	26	24.8	12	1	VESP VESXA
24	26	24.8	12	1	VESP VESXA
25	26	24.8	13	1	BRK PARID
26	26	24.8	13	1	SCW2 TITDI
27	26	24.8	14	1	BRK3 RANMI
28	26	24.8	15	2	Q9R5T1 9FIAO
29	26	24.8	17	1	VESP VESMC
30	26	24.8	17	1	VESP VESMC
31	26	24.8	18	2	Q16053 HUMAN

32	25.5	24.3	18	2	Q763U4 USEUD	Q763U4 naravelia 1
33	25.5	24.3	18	2	Q763U5 CLERYI	Q763U5 clematis vi
34	25.5	24.3	18	2	Q763W5 USEUD	Q763W5 clematis ja
35	25	23.8	10	1	TMOF ABDAB	P19425 aedes aegypt
36	25	23.8	10	2	Q7M3T6 TRIGR	Q7M3T6 trigenetes
37	25	23.8	12	2	Q4M620 GCALI	Q4M620 norovirus n
38	25	23.8	12	2	Q84268 9PAPI	Q84268 human papil
39	25	23.8	13	1	PABR AEGSU	P43173 aescalis euu
40	25	23.8	13	2	Q16007 HUMAN	Q16007 homo sapien
41	25	23.8	18	2	Q92190 MOUSE	Q92190 mus musculu
42	25	23.8	19	1	TRP3 LERMA	P81735 leucophaea
43	25	23.8	20	1	PYRX PSERFL	P56586 pseudomnas
44	25	23.8	20	2	Q90V83 9MTRI	Q90V83 ratus sp.
45	25	23.8	20	2	Q7LZK3 MECA	Q7LZK3 meleagris g
46	24	22.9	10	2	Q7M4B6 STRNU	Q7M4B6 strongyloce
47	24	22.9	10	2	Q7M4D4 PSBDP	Q7M4D4 pseudocent
48	24	22.9	11	2	P82436 TOBAC	P82436 nicotiana t
49	24	22.9	15	2	Q80X04 MESAU	Q80X04 mesocricetu
50	24	22.9	17	2	Q9HE01 PARBR	Q9HE01 paracoccidi
51	24	22.9	17	2	Q9HE02 AJDEB	Q9HE02 ajellomyces
52	24	22.9	17	2	Q9HE03 AJDEB	Q9HE03 ajellomyces
53	24	22.9	17	2	Q49077 MYCCA	Q49077 mycoplasma
54	24	22.9	19	2	Q7M546 HALSA	Q7M546 halobacteri
55	24	22.9	19	2	Q77S06 9CIRC	Q77S06 porcine circ
56	24	22.9	19	2	Q9YTT3 9CIRC	Q9YTT3 porcine circ
57	24	22.9	20	2	Q9T218 NICSY	Q9T218 nicotiana s
58	24	22.9	20	2	Q9T219 NICSY	Q9T219 nicotiana s
59	23.5	22.4	12	2	Q518Y4 9CALI	Q518Y4 norovirus t
60	23.5	22.4	12	2	Q518Y5 9CALI	Q518Y5 norovirus t
61	23.5	22.4	16	2	Q506K8 9CALI	Q506K8 norovirus h
62	23.5	22.4	19	2	Q88290 9CALI	Q88290 small round
63	23.5	22.4	19	2	Q51T04 9CALI	Q51T04 norovirus s
64	23	21.9	8	1	RS7 MYCIT	P33564 mycobacteri
65	23	21.9	9	2	Q8M4T7 9PRIM	Q8M4T7 eulemur ful
66	23	21.9	9	2	Q8M4T8 9PRIM	Q8M4T8 eulemur ful
67	23	21.9	10	2	Q7M3T7 TRIGR	Q7M3T7 trigenetes
68	23	21.9	10	2	Q7M4B4 STRNU	Q7M4B4 strongyloce
69	23	21.9	10	2	Q7M4CO HETMA	Q7M4CO heterocent
70	23	21.9	12	2	Q4M618 9CALI	Q4M618 norovirus n
71	23	21.9	13	2	Q60F86 9BRYO	Q60F86 sphagnum g
72	23	21.9	13	2	Q60F89 TAKLE	Q60F89 takakia lep
73	23	21.9	13	2	P82866 RANPI	P82866 rana pipien
74	23	21.9	15	1	UC19 MAIZE	P80525 zea mays (m
75	23	21.9	15	1	Q561Y4 9FLAV	Q561Y4 tick-borne
76	23	21.9	15	2	Q561Z6 9FLAV	Q561Z6 tick-borne
77	23	21.9	16	2	Q9UCG5 HUMAN	Q9UCG5 homo sapien
78	23	21.9	17	1	BIOP1 PHYXY	P84521 phyllomedus
79	23	21.9	17	2	Q9UCU9 HUMAN	Q9UCU9 homo sapien
80	23	21.9	17	2	Q9UBJ5 HUMAN	Q9UBJ5 homo sapien
81	23	21.9	17	2	Q9RSJ3 MYCCA	Q9RSJ3 mycoplasma
82	23	21.9	18	2	Q9TWH0 9TRYP	Q9TWH0 trypanosoma
83	23	21.9	18	2	Q5ERY3 9BRYO	Q5ERY3 polytrichum
84	23	21.9	18	2	Q5ERY6 9BRYO	Q5ERY6 andreaea ru
85	23	21.9	18	2	Q8SKY0 CUSRE	Q8SKY0 cucurbita rel
86	23	21.9	18	2	Q9QV98 9MTRI	Q9QV98 mus sp. . v
87	23	21.9	19	1	FIRA ANTAM	P14440 antilocapra
88	23	21.9	19	1	FIRA BISBO	P14441 bisson bonas
89	23	21.9	19	1	FIRA MONUM	P14457 mus musculu
90	23	21.9	19	2	Q9SRYS DROMB	Q9SRYS drosophila
91	23	21.9	19	2	Q9N613 TOXOC	Q9N613 toxoplasma
92	23	21.9	19	2	Q63058 LATCL	Q63058 latirraea cl
93	23	21.9	19	2	Q9RS08 PSERAE	Q9RS08 pseudomonas
94	23	21.9	19	2	Q9JK02 MOUSE	Q9JK02 mus musculu
95	23	21.9	20	2	PSAP MAIZE	P13193 zea mays (m
96	23	21.9	20	2	Q8NED5 HUMAN	Q8NED5 homo sapien
97	23	21.9	20	2	Q7M264 TOLPR	Q7M264 lolium pere
98	23	21.9	20	2	Q9S8U1 TRIKI	Q9S8U1 trichosanthe
99	23	21.9	20	2	Q9S8Y0 PHILPR	Q9S8Y0 phleum prat
100	23	21.9	20	2	Q9R519 9MYCO	Q9R519 mycobacteri

ALIGNMENTS

```

RESULT 1
Q7M4P9_HUMAN PRELIMINARY; PRT; 15 AA.
AC Q7M4P9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
DE Galbladder stone matrix protein 2, 41k (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B.;
RL Submitted (FEB-1996) to the PIR data bank.
DR PIR; F57789; F57789.
FT NON_TER 1 1
SQ SEQUENCE 15 AA; 1539 MW; D08774ED4B7A4786 CRC64;

Query Match
Best Local Similarity 30.5%; Score 32; DB 2; Length 15;
Matches 6; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 8 PPGFTVGBEG 17
DB 5 PDGFTGSSG 14

RESULT 2
Q6N69_VITVI PRELIMINARY; PRT; 17 AA.
AC Q6N69;
DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, last sequence update)
DE 25-OCT-2004 (TrEMBLrel. 28, last annotation update)
DE 20S proteasome beta subunit (Fragment).
OS Vitis vinifera (Grape).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC Vitaceae; Vitis.
OX NCBI_TaxId=29760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Leaf;
RA Carvalho M.B., Caeiro A.S., Price C.B., Teixeira A.R., Ferreira R.B.;
RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY684130; AAU04834.1; -; mRNA.
DR GO; GO:0005829; C:cytosol; IEA.
KW Proteasome.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1808 MW; C19F776A03A88D9F CRC64;

Query Match
Best Local Similarity 28.6%; Score 30; DB 2; Length 17;
Matches 7; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 2 PAKGSPPGFIVGB 15
DB 3 PAKGTTTAFIFKE 16

RESULT 3
Q8NFB4_HUMAN PRELIMINARY; PRT; 18 AA.
AC Q8NFB4;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, last annotation update)

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DE Mutant enamelIn (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OX NCBI_TaxId=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22294456; PubMed=12407086;
RA Kida M., Ariga T., Shizkawa T., Oguchi H., Sakiyama Y.;
RT "Autosomal-dominant hypoplastic form of amelogenesis imperfecta caused
by an enamelIn gene mutation at the exon-intron boundary.";
RT J. Dent. Res. 81:738-742(2002).
DR EMBL; AF530444; AAM97323.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 18 18
SQ SEQUENCE 18 AA; 1893 MW; 492D2B23BBB512 CRC64;

Query Match
Best Local Similarity 28.6%; Score 30; DB 2; Length 18;
Matches 7; Conservative 2; Mismatches 3; Indels 4; Gaps 1;

QY 6 MSPGPF---IVGEEG 17
DB 2 LPPGVCGRPPISNEEG 17

RESULT 4
Q7M2N0_BOVIN PRELIMINARY; PRT; 10 AA.
AC Q7M2N0;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Collagen alpha 1(VI) chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP PROTEIN SEQUENCE.
RX PubMed=6852033;
RA Jander R., Rautenberg U., Glanville R.W.;
RT "Further characterization of the three polypeptide chains of bovine
and human short-chain collagen (Intima collagen).";
RL Eur. J. Biochem. 133:39-46(1983).
DR PIR; S26506; S26506.
FT NON_TER 1 1
FT NON_TER 10 10
SQ SEQUENCE 10 AA; 965 MW; CAA96668640DC776 CRC64;

Query Match
Best Local Similarity 26.7%; Score 28; DB 2; Length 10;
Matches 6; Conservative 1; Mismatches 0; Indels 2; Gaps 1;

QY 2 PAKGSPPG 10
DB 4 PAKG--PPG 10

RESULT 5
Q7M1F8_MAIZE PRELIMINARY; PRT; 15 AA.
AC Q7M1F8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, last sequence update)
DE 01-MAR-2004 (TrEMBLrel. 26, last annotation update)
DE Zein Zp22/6 protein.
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.

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OX NCBI_TaxID=4577;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95206245; PubMed=7898438; DOI=10.1007/BF00290716;
 RA Chaudhuri S., Messing J.;
 RT "RFLP mapping of the maize drr1 locus, which regulates methionine-rich
 RL 10 kDa zein accumulation.";
 DR Mol. Gen. Genet. 246:707-715 (1995).
 PIR; 854712; 854712.
 SQ SEQUENCE 15 AA; 1605 MW; 5DFB414D8D001609 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 15;
 Best Local Similarity 36.4%; Pred. No. 3.5e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 2 PAKGSPPGRI 12
 DB 4 PQGSLAPPAII 14

RESULT 6

ID Q7BM54_9DELA PRELIMINARY; PRT; 16 AA.
 AC Q7BM54;
 DT 01-OCT-2003 (TrEMBLrel. 25, Created)
 DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
 DE Tax protein (Fragment).
 OS Human T-lymphotropic virus 1.
 OC Viruses; Retroviridae; Retroviridae; Deltaretrovirus.
 NCBI_TaxID=11908;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Gonzalez Perez M.F., Garcia Salz A.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF529962; AAB87693.1; -; Genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1782 MW; 9CDDDFPR4146BA2F CRC64;

Query Match 26.7%; Score 28; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 3.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPPG 10
 DB 2 GLBPPG 7

RESULT 7

ID Q71HR5_LACDL PRELIMINARY; PRT; 20 AA.
 AC Q71HR5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Hisidyl-tRNA synthetase (EC 6.1.1.21) (Fragment).
 OS Lactobacillus delbrueckii (subsp. lactis).
 OC Bacteria; Firmicutes; Lactobacillales; Lactobacillaceae;
 OC Lactobacillus.
 NCBI_TaxID=29397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN-ATCC 4797;
 RA Langenheim J.F., Ulrich R.L.;
 RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF496531; AA007223.1; -; Genomic DNA.
 DR GO; GO:0004821; F:hydrolase-ATPase activity; IEA.
 DR GO; GO:0016874; F:ligase activity; IEA.
 KM Aminoacyl-tRNA synthetase; ligase.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 20 AA; 2123 MW; 43ABC93211F8210C CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 4.7e+03;
 Matches 5; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 10 GPVIGEGVL 19
 DB 11 GFGIGERRLM 20

RESULT 8

ID Q79CF0_RHILE PRELIMINARY; PRT; 20 AA.
 AC Q79CF0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DE 4-hydroxybenzoate hydroxylase (EC 1.14.13.2) (Fragment).
 GN Name=poba;
 OS Rhizobium leguminosarum.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Rhizobiaceae; Rhizobium/Agrobacterium group; Rhizobium.
 NCBI_TaxID=384;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA STRAIN-B155;
 RA Wong C.M., Dilworth M.J., Glenn A.R.;
 RT "4-Hydroxybenzoate hydroxylase (poba) is positively regulated by poba
 RL in Rhizobium leguminosarum bv. viciae1.";
 RL FEMS Microbiol. Lett. 0:0-0(1995).
 DR EMBL; U40388; AAA83007.1; -; Genomic_DNA.
 DR HSSP; P20586; 1K01.
 DR GO; GO:0018659; F:4-hydroxybenzoate 3-monooxygenase activity; IEA.
 DR GO; GO:0016491; F:oxidoreductase activity; IEA.
 DR InterPro; IPR002938; MoxY_PAD binding.
 DR Pfam; PF01494; PAD_binding_3; 1.
 KM Oxidoreductase.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2011 MW; 378D1B9CB7605522 CRC64;

Query Match 26.7%; Score 28; DB 2; Length 20;
 Best Local Similarity 36.4%; Pred. No. 4.7e+03;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

OY 5 GMSPPG 15
 DB 9 GSGPGSLGQ 19

RESULT 9

ID Q7M281_ORYSA PRELIMINARY; PRT; 16 AA.
 AC Q7M281;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 28k protein 4209 (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Ehrhartoideae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Teugita A., Miyake N.;
 RL Submitted (APR-1993) to the PIR data bank.
 DR PIR; PS0210; PS0210.
 DR Gramene; Q7M281; -;
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 16 AA; 1579 MW; DAC3ABBA68B47CAC CRC64;

Query Match 25.7%; Score 27; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 5.3e+03;

OY 25.7%; Score 27; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 5.3e+03;

Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 9 PGFIVE 15
DB 1 PELVIGD 7

RESULT 10
Q9T2Q4_BRANA PRELIMINARY; PRT; 16 AA.

AC Q9T2Q4; 09T2Q4; 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Chaperonin-60 L33 fragment (Fragment).
OS Brassica napus (Rape).
OC Mitochondrion.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC euroside II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxId=3708;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=94302168; PubMed=7913238; DOI=10.1104/pp.105.1.233;
RA Cloney L.P., Bekkeou D.R., Feist G.L., Lane W.S., Hemmingsen S.M.;
RT "Brassica napus plastid and mitochondrial chaperonin-60 proteins
contain multiple distinct polypeptides."
RL Plant Physiol. 105:233-241(1994).
FT NON_TER 1 16
FT SEQUENCE 16 AA; 1901 MW; CFAE799B7C938063 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 5.3e+03;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 3 AKGMPGPFIVEE 16
DB 3 ARGYISPYITDEK 16

RESULT 11
Q9N195_BOVIN PRELIMINARY; PRT; 19 AA.

AC Q9N195; 01-OCT-2000 (TRENBLREL. 15, Created)
DT 01-OCT-2000 (TRENBLREL. 15, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE Parvalbumin (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxId=9913;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21599054; PubMed=11736808;
RA Ariza F., Harrison B., Drinkwater R.D.;
RT "The assignment by linkage mapping of four genes from human chromosome 22 to bovine chromosome 5 and 17."
RL Anim. Genet. 32:371-374(2001).
DR EMBL, AF217654; AAF26420.1; -; Genomic_DNA.
FT NON_TER 1 19
FT SEQUENCE 19 AA; 2151 MW; DSEA9D89C3BE951 CRC64;

Query Match 25.7%; Score 27; DB 2; Length 19;
Best Local Similarity 71.4%; Pred. No. 6.4e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 KGMSPG 10
DB 5 KGFSPDG 11

RESULT 12
BRK1_RANNI STANDARD; PRT; 9 AA.

AC Q7L254; 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Bradykinin-like peptide I.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana;
OC Pelophylax.
OX NCBI_TaxId=8409;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=68412013; PubMed=5677638;
RA Nakajima T.;
RT "Occurrence of a new active peptide on smooth muscle and bradykinin in the skin of Rana nigromaculata hallowell."
RL Chem. Pharm. Bull. 16:769-770(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC PIR; A61358; A61358.
DR Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
KW SEQUENCE 9 AA; 1017 MW; 3687D771A9C86777 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF 11
DB 2 PGF 5

RESULT 13
KNL3_BOMVA STANDARD; PRT; 9 AA.

AC P83058; 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE [Three]bradykinin.
OS Bombina variegata (Yellow-bellied toad).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxId=8348;

RN [1]
RP PROTEIN SEQUENCE, SUBCELLULAR LOCATION, AND TISSUE SPECIFICITY.
RX TISSUE-Skin secretion;
RX MEDLINE=22217713; PubMed=12230583;
RA Chen T., Orr D.F., Bjourson A.J., McLean S., O'Rourke M., Hirst D.G., Rao P., Shaw C.;
RT "Novel bradykinins and their precursor cDNAs from European yellow-bellied toad (Bombina variegata) skin."
RL Eur. J. Biochem. 269:4693-4700(2002).
CC -1- FUNCTION: Produces in vitro relaxation of rat arterial smooth muscle and constriction of intestinal smooth muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----

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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

KW Amphibian defense peptide; Bradykinin; Direct protein sequencing
KW Vasoactive; Vasodilator.
SQ SEQUENCE 9 AA; 1074 MW; 3393D771A9C86777 CRC64;

```

every Match      24.8%; Score 26; DB 1; Length 9;
1st Local Similarity 100.0%; Pred. No. 2.2e+06;
Catches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY	8	PPGP	11
Db	2	PPGP	5

RESULT 14	
KNL3_CYPDO	
ID_KNL3_CYPDO	STANDARD;
ID_KNL3_CYPDO	PRT;
ID_KNL3_CYPDO	.9 AA

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CC removed.

DR GO; GO:0005615, C:extracellular space, IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure, ISS.
DR GO; GO:0045877; P:positive regulation of smooth muscle contract. . .; ISS
KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 9 AA, 1074 MW, 3393D771A9C86777 CRC64;

every Match	24.8%	Score 26;	DB 1;	Length 9;
1st Local Similarity	100.0%	Pred. No. 2.2e+06;		
4; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	8	PPGF	1.1
Db	2	PPGF	5

RESULT 15
P84497 TRASC
ID P84497 TRASC PRELIMINARY;
PRT; 9 AA

Query Match	24.8%	Score 26;	DB 2;	Length 9;
Best Local Similarity	100.0%	Pred. No. 2.2e+05;		
Matches 4;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	8	PPGF	11
Db	2	PPGF	5

RESULT 16	
Q7L250 CHICK	
ID	Q7L250_CHICK PRELIMINARY;
AC	Q7L250; PRT; 9 AA.
DT	01-MAR-2004 (TrEMBLrel. 26, Created)
DT	01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT	01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE	Omnitho-kinin.
OS	Gallus gallus (Chicken).
OC	Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Archaeoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC	Gallus.
OX	NCBI_TaxID=9031;
RN	[1]
RP	PROTEIN SEQUENCE.
RX	MEDLINE=90102072; PubMed=2603803;
RA	Kimura M., Sueyoshi T., Morita T., Tanaka K., Iwanaga S.;
RT	Omnitho-kininogen and omnitho-kinin: isolation, characterization and
RT	chemical structure. "
PL	Adv. Exp. Med. Biol. 247A:355-367 (1989).
PR	PIR; B60246; B60246.
QO	SEQUENCE 9 AA; 1040 MW; 339D3771A9C86777 CRC64;

Query Match	24.8%	Score	26	DB 2:	Length	9
Best Local Similarity	100.0%	Pred. No.	2.2e+06			
Matches	4	Conservative	0	Mismatches	0	Indels
				Gaps	0	

QY	8	PPGF	1
Db	2	PPGF	5

RESULT 17	
Q7LZJ8 RANTE	
ID Q7LZJ8 RANTE PRELIMINARY;	PRT;
88888888	9 AA

DE Bradykinin.
OS Rana temporaria (European common frog).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Buteleostomi;

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OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Rana.
OX NCBI_TaxID=8407;
RN [1]
RN PROTEIN SEQUENCE.
RA Anaetael A., Erspamer V., Bertaccini G.,
RT "Occurrence of bradykinin in the skin of Rana temporaria.",
RL Comp. Biochem. Physiol. 14:43-52 (1965).
DR PIR; A61363; A61363.
SQ SEQUENCE 9 AA; 1060 MW; 3393D775B9C86777 CRC64;

Query Match          24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
   |||
   |||
DB 2 PPGF 5

RESULT 18
Q7L217_9NEOB
ID Q7L217_9NEOB PRELIMINARY; PRT; 9 AA.
AC Q7L217;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Hydroxyproline-3-bradykinin.
OS Helophryne purcelli (Cape ghost frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Helaophrynidae;
OC Helophryne.
OX NCBI_TaxID=31911;
RN [1]
RN PROTEIN SEQUENCE.
RA Nakajima T., Yasuhara T., Erspamer G.F., Viseer J.;
RT "Occurrence of HYP(3)-bradykinin in methanol extracts of the skin of
RT the South African leptodactylid frog Helophryne purcelli.";
RL Experimentia 35:1133-1133 (1979).
DR PIR; A43065; A43065.
SQ SEQUENCE 9 AA; 1060 MW; 3393D775B9C86777 CRC64;

Query Match          24.8%; Score 26; DB 2; Length 9;
Best Local Similarity 100.0%; Pred. No. 2.2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
   |||
   |||
DB 2 PPGF 5

RESULT 19
BRKP_PHYRO
ID BRKP_PHYRO STANDARD; PRT; 11 AA.
AC Q7L252;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Phyllokinin (Bradykinin1-Isolucyl-L-tyrosine O-sulfate).
OS Phyllomedusa rohdei (Rohde's leaf frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hyliidae;
OC Phyllomedusinae; Phyllomedusa.
OX NCBI_TaxID=8394;
RN [1]
RN PROTEIN SEQUENCE, AND SULFATION OF TYR-11.

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RX MEDLINE=67179312; PubMed=5970899;
RA Anaetael A., Bertaccini G., Erspamer V.;
RT "Pharmacological data on phyllokinin (bradykinin1-Isolucyl-L-tyrosine O-
RT sulphate) and bradykinin1-Isolucyl-L-tyrosine.";
RL Br. J. Pharmacol. 27:479-485 (1966).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
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CC removed.
CC -----
DR PIR; A61365; A61365.
KW Bradykinin; direct protein sequencing; Sulfation; Vasodilator;
FT MOD_RES 11
KW MOD_RES 11 Sulfotyrosine.
SQ SEQUENCE 11 AA; 1337 MW; 25051393D775B9C8 CRC64;

Query Match          24.8%; Score 26; DB 1; Length 11;
Best Local Similarity 100.0%; Pred. No. 5.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGF 11
   |||
   |||
DB 2 PPGF 5

RESULT 20
BRK_MEGFL
ID BRK_MEGFL STANDARD; PRT; 11 AA.
AC P12797;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Megascollactin ((Thr6)bradykinin-Lys-Ala) [Concalins: Bradykinin-like
DE peptide ((Thr6)bradykinin)].
OS Megascollia flavifrons (Garden dagger wasp) (Solitary wasp).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Scolidae; Megascollia.
OX NCBI_TaxID=7437;
RN [1]
RN PROTEIN SEQUENCE.
RP TISSUE=Venom;
RX MEDLINE=87293024; PubMed=3617088; DOI=10.1016/0041-0101(87)90288-1;
RA Yasuhara T., Mantel P., Nakajima T., Plek T.;
RT "Two kinsins isolated from an extract of the venom reservoirs of the
RT solitary wasp Megascollia flavifrons.",
RL Toxicon 25:527-535 (1987).
RN [2]
RN PROTEIN SEQUENCE.
RP TISSUE=Venom;
RA Nakajima T., Plek T., Yasuhara T., Mantel P.;
RT "Two kinsins isolated from the venom of Megascollia flavifrons.";
RL Toxicon 26:34-34 (1988).
CC -1- FUNCTION: Both proteins have bradykinin-like, although lower
CC activities (e.g. smooth muscle contraction).
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC -----
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CC -----
DR PIR; A26744; A26744.
DR PIR; B26744; B26744.
DR GO; GO:0005615; C:extracellular space; IDA.
DR GO; GO:0045776; P:negative regulation of blood pressure; ISS.
DR GO; GO:0045987; P:positive regulation of smooth muscle contra. . .; TAS.

```

KM Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
 FT PEPTIDE 1 11 Megascollakinin.
 PEPTIDE 1 9 Bradykinin-like peptide.
 SQ SEQUENCE 11 AA; 1274 MW; 33867333D771A5C8 CRC64.

Query Match 24.8%; Score 26; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAGE 11
 DB 2 PAGE 5

RESULT 21

075811 HUMAN
 ID 075811 HUMAN PRELIMINARY; PRT; 11 AA.

AC 075811
 DT 01-NOV-1998 (TEMBLrel. 08, Created)
 DT 01-NOV-1998 (TEMBLrel. 08, Last sequence update)
 DT 01-NOV-1998 (TEMBLrel. 08, Last annotation update)
 DE ErbB-3 R2 (Fragment).
 GN Name=c-erbB-3;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovarian carcinoma;
 RX MEDLINE=98345147; PubMed=9681822; DOI=10.1038/sj.onc.1201866;
 RA Lee H., Matile N.J.;
 RT "Isolation and characterization of four alternative c-erbB3 transcripts
 RT expressed in ovarian carcinoma-derived cell lines and normal human
 RT tissues";
 RL Oncogene 16:3243-3252(1998).
 DR EMBL; U88358; AAC39858.1; -; mRNA.
 FT NON_TER 1
 SQ SEQUENCE 11 AA; 1017 MW; 21B236366B72878 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 11;
 Best Local Similarity 40.0%; Pred. No. 5.1e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSPG 10
 DB 1 BPCGGLCPKG 10

RESULT 22
 07M4P1 HUMAN
 ID 07M4P1 HUMAN PRELIMINARY; PRT; 11 AA.

AC 07M4P1
 DT 01-MAR-2004 (TEMBLrel. 26, Created)
 DT 01-MAR-2004 (TEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, Last annotation update)
 DE 11e-8er-bradykinin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=9116748; PubMed=2076202;
 RA Wunderer G., Walter I., Eschenbacher B., Lang M., Kellermann J.,
 RA Kindermann G.;
 RT "11e-8er-bradykinin is an aberrant permeability factor in various
 RT human malignant effusions";
 RL Biol. Chem. Hoppe-Seyler 371:977-981(1990).
 DR PIR; S13279; S13279. 1
 FT NON_TER 1

FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1260 MW; 33D55258B9C86777 CRC64;

Query Match 24.8%; Score 26; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 5.1e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAGE 11
 DB 4 PAGE 7

RESULT 23

VESP_VESMA
 ID VESP_VESMA STANDARD; PRT; 12 AA.

AC 07M3T3;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Vespakinin M.
 OS Vespa mandarinia (Hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7446;
 RN [1]
 RP PROTEIN SEQUENCE, AND HYDROXYLATION.
 RC TISSUE=Venom;
 RX MEDLINE=77114342; PubMed=1017116;
 RA Kishimura H., Yasuhara T., Yoshida H., Nakajima T.;
 RT "Vespakinin-M, a novel bradykinin analogue containing hydroxyproline,
 RT in the venom of Vespa mandarinia Smth.";
 RL Chem. Pharm. Bull. 24:2896-2897(1976).
 CC -1- FUNCTION: Bradykinin are a potent but short-lived agent of
 CC arteriolar dilation and increased capillary permeability (By
 CC similarity).
 CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoir.
 CC -1- SIMILARITY: Belongs to the bradykinin family.

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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC DR PIR; A61360; A61360.
 KM Bradykinin; Direct protein sequencing; Hydroxylation; Vasoactive;
 KW Vasodilator.
 FT MOD_RES 4
 SQ SEQUENCE 12 AA; 1346 MW; 34F513C44C75B9C8 CRC64;

Query Match 24.8%; Score 26; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PAGE 11
 DB 3 PAGE 6

RESULT 24
 VESP_VESXA
 ID VESP_VESXA STANDARD; PRT; 12 AA.

AC 07M3T2;
 DT 05-JUL-2004 (Rel. 44, Created)
 DT 05-JUL-2004 (Rel. 44, Last sequence update)
 DT 10-MAY-2005 (Rel. 47, Last annotation update)
 DE Vespakinin X.
 OS Vespa xanthoptera (Japanese hornet).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
 OC Vespidae; Vespinae; Vespa.
 OX NCBI_TaxID=7446;

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RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=87187853; PubMed=264186;
RA Yasuhara T., Yoshida H., Nakajima T.;
RT "Chemical investigation of the hornet (Vespa xanthoptera Cameron) venom. The structure of a new bradykinin analogue vespakinin-X.";
RL Chem. Bull. 25:936-941(1977).
CC -1- FUNCTION: Bradykinin are a potent but short-lived agent of arteriolar dilation and increased capillary permeability (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
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CC PIR: A61359; A61359.
KM Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 12 AA; 1344 MW; 2C9513C3D275B9C8 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF 11
DB 3 PGF 6

RESULT 25
BRK PARID STANDARD; PRT; 13 AA.
AC P42717;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Waspkinin.
OS Parapolybia indica.
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea; OC Vespidae; Polistinae; Parapolybia.
OX NCBI_Taxid=31921;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RA Toki T., Yasuhara T., Nakajima T.;
RT "Isolation and sequential analysis of peptides on the venom sac of Parapolybia indica.";
RL Eisai Debuteu 39:105-111(1988).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not removed.
CC KM Bradykinin; Direct protein sequencing; Pyrrolidone carboxylic acid; Vasoactive; Vasodilator.
FT MOD_RES 1 Pyrrolidone carboxylic acid.
SQ SEQUENCE 13 AA; 1573 MW; 2673CB3D83ECC867 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PGF 11

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DB 5 PGF 8

RESULT 26
SCX2 TTIDI STANDARD; PRT; 13 AA.
AC P60261;
DT 29-MAR-2004 (Rel. 43, Created)
DT 29-MAR-2004 (Rel. 43, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Toxin Td11-2 (Fragment).
OS Tityus discrepans (Venezuelan scorpion).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Scorpiones; OC Butlida; Butlidae; Tityus.
OX NCBI_Taxid=57059;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX PubMed=8783453; DOI=10.1016/0041-0101(95)00156-5;
RA D'Suze G., Corona F., Posani L.D., Sevcik C.;
RT "High performance liquid chromatography purification and amino acid sequence of toxins from the muscarinic fraction of Tityus discrepans scorpion venom.";
RL Toxicon 34:591-598(1996).
CC -1- FUNCTION: Binds voltage-independently to sodium channels and shift the voltage of activation toward more negative potentials (By similarity). This toxin is active against mammals and crustaceans.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the venom gland.
CC -1- SIMILARITY: Belongs to the alpha/beta-scorpion toxin family. Beta-toxin subfamily.
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CC KM Direct protein sequencing; Ionic channel inhibitor; Neurotoxin; KW Sodium channel inhibitor; Toxin.
FT NON_TER 13
SQ SEQUENCE 13 AA; 1444 MW; 256147777B34867 CRC64;

Query Match
Best Local Similarity 24.8%; Score 26; DB 1; Length 13;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 10 PGF 17
DB 3 GYLPGNEG 10

RESULT 27
BRK3 RANNI STANDARD; PRT; 14 AA.
AC 07LZ53;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Bradykinin-like peptide III.
OS Rana nigromaculata (Japanese pond frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana; OC Pelophylax.
OX NCBI_Taxid=8409;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Skin;
RX MEDLINE=69117202; PubMed=5751736;
RA Nakajima T.;
RT "On the third active peptide on smooth muscle in the skin of Rana nigromaculata hallowell.";

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RL Chem. Pharm. Bull. 16:2088-2089(1968).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the bradykinin family.
-----
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-----
CC
CC PIR; A61362; A61362.
KW Bradykinin; Direct protein sequencing; Vasoactive; Vasodilator.
SQ SEQUENCE 14 AA; 1486 MW; 33344EB3978393D7 CRC64;

Query Match      24.8%; Score 26; DB 1; Length 14;
Best Local Similarity 100.0%; Pred. No. 6.6e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 PPGP 11
DB 2 PPGP 5

RESULT 28
O9R5T1_9FLAO PRELIMINARY; PRT; 15 AA.
AC O9R5T1;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DB 3-HYDROXYPHENYLACETATE 6-hydroxylase, PAD-dependent monooxygenase
DE (Fragment).
OS Flavobacterium.
OC Bacteria; Bacteroidetes; Flavobacteria; Flavobacteriales;
OC Flavobacteriaceae.
OX NCBI_TaxID=237;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=92037613; PubMed=1935954;
RA Van Berkel W.J., Van Den Tweel W.J.;
RT "Purification and characterization of 3-hydroxyphenylacetate 6-
RT hydroxylase: a novel PAD-dependent monooxygenase from a Flavobacterium
RT species.";
RL Eur. J. Biochem. 201:585-592(1991).
FT NON_TER 1
FT NON_TER 15
SQ SEQUENCE 15 AA; 1416 MW; D673378E0221F9D9 CRC64;

Query Match      24.8%; Score 26; DB 2; Length 15;
Best Local Similarity 55.6%; Pred. No. 7.1e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DPAKGMSP 9
DB 7 DAASGAVPP 15

RESULT 29
TL09_SPIOL STANDARD; PRT; 17 AA.
AC P82671;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Thylakoid lumenal 9 kDa protein (P9) (Fragment).
OS Spinacia oleracea (Spinach).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC Caryophyllales; Amaranthaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP PROTEIN SEQUENCE.

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RA Kieselbach T., Pettersson U., Byström M., Schroeder W.P.;
RL Submitted (MAY-2000) to Swiss-Prot.
CC -1- SUBCELLULAR LOCATION: Chloroplast; within the thylakoid lumen.
-----
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-----
CC
CC Chloroplast; Direct protein sequencing; Thylakoid.
KW Bradykinin;
FT NON_TER 17
SQ SEQUENCE 17 AA; 1684 MW; A8B04C2AEBDBDC1 CRC64;

Query Match      24.8%; Score 26; DB 1; Length 17;
Best Local Similarity 44.4%; Pred. No. 8.1e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPVGEKV 18
DB 1 GFLSGSTGI 9

RESULT 30
VESP_VESMC STANDARD; PRT; 17 AA.
AC P57672;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DB Vesputakitin 1 [Contains: Vesputakitin 2]
DE Vesputa maculifrons (Baetern yellow jacket) (Waap).
OS Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Hymenoptera; Apocrita; Aculeata; Vespoidea;
OC Vespiidae; Vespiinae; Vesputa.
OX NCBI_TaxID=7453;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Venom;
RX MEDLINE=76114777; PubMed=1247511;
RA Yoshida H., Geller R.G., Pileano J.J.;
RT "Vesputakitins: new carbohydrate-containing bradykinin derivatives.";
RL Biochemistry 15:61-64(1976).
RN [2]
RP SYNTHESIS.
RX MEDLINE=88057857; PubMed=3679673;
RA Rocchi R., Biondi L., Filippa F., Scolaro B.;
RT "Synthesis, conformation, and biological activity of the carbohydrate-
RT free vesputakitin 1.";
RL Int. J. Pept. Protein Res. 30:240-256(1987).
CC -1- FUNCTION: Induces smooth muscle contraction.
CC -1- SUBCELLULAR LOCATION: Secreted; venom reservoirs.
CC -1- SIMILARITY: Belongs to the bradykinin family.
-----
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-----
CC
CC PIR; A61339; A61339.
KW Bradykinin; Direct protein sequencing; Glycoprotein; Vasoactive;
KW Vasodilator.
FT PEPTIDE 1 17 Vesputakitin 1.
FT PEPTIDE 3 17 Vesputakitin 2.
FT CARBOHYD 3 3 O-linked (GalNAc . . .)
FT CARBOHYD 4 4 O-linked (GalNAc . . .)
SQ SEQUENCE 17 AA; 1960 MW; 58B2CBAB6412323 CRC64;

Query Match      24.8%; Score 26; DB 1; Length 17;
Best Local Similarity 100.0%; Pred. No. 8.1e+03;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 8 PGPF 11
 ||||
 Db 10 PGPF 13

RESULT 31

Q16053 HUMAN
 ID Q16053_HUMAN PRELIMINARY; PRT; 18 AA.
 AC Q16053
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Type I procollagen alpha 1 chain (Fragment).
 GN Name=COL1A1;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominoidea;
 OC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93339042; PubMed=8339541;
 RA Wirtz M.K., Rao V.H., Glanville R.W., Labhard M.E., Pretorius P.J.,
 RA de Vries W.N., de Wet W., Hollister D.W.,
 RT "A cysteine for glycine substitution at position 175 in an alpha 1 (I)
 RT chain of type I collagen produces a clinically heterogeneous form of
 RT osteogenesis imperfecta.";
 RL Connect. Tissue Res. 29:1-11(1993).
 DR EMBL; S64717; AAB27677.1; -; mRNA.
 DR PIR; I60114; CGHUS.
 KM Collagen.
 FT NON TER
 SQ SEQUENCE 18 AA; 1640 MW; E66475B62F05583A CRC64;

Query Match 24.8%; Score 26; DB 2; Length 18;
 Best Local Similarity 100.0%; Pred. No. 8.7e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 32

Q763U4 USRUD
 ID Q763U4_USRUD PRELIMINARY; PRT; 18 AA.
 AC Q763U4;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RNA polymerase beta subunit (Fragment).
 GN Name=rpob;
 OS Naravetia laurifolia.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Naravetia.
 OC NCBI_TaxID=231673;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Mileda O., Kita K., Handa T., Yukawa T.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB116905; BAC82230.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER
 SQ SEQUENCE 18 AA; 1953 MW; 20325A4785C6AF52 CRC64;

Query Match 24.3%; Score 25.5; DB 2; Length 18;
 Best Local Similarity 58.3%; Pred. No. 1e+04;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 DPAKGMSP-PGF 11

Db 4 DNEGSMSTIPGF 15

RESULT 33

Q763U5 CLEVI
 ID Q763U5_CLEVI PRELIMINARY; PRT; 18 AA.
 AC Q763U5
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RNA polymerase beta subunit (Fragment).
 GN Name=rpob;
 OS Clematis vitalba (Evergreen clematis) (Traveller's joy).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Clematis.
 OC NCBI_TaxID=37490;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Mileda O., Kita K., Handa T., Yukawa T.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB116904; BAC82229.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER
 SQ SEQUENCE 18 AA; 1953 MW; 20325A4785C6AF52 CRC64;

Query Match 24.3%; Score 25.5; DB 2; Length 18;
 Best Local Similarity 58.3%; Pred. No. 1e+04;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 DPAKGMSP-PGF 11
 ||||
 Db 4 DNEGSMSTIPGF 15

RESULT 34

Q763W5 USRUD
 ID Q763W5_USRUD PRELIMINARY; PRT; 20 AA.
 AC Q763W5;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE RNA polymerase beta subunit (Fragment).
 GN Name=rpob;
 OS Clematis japonica.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; Ranunculales;
 OC Ranunculaceae; Clematis.
 OC NCBI_TaxID=231650;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Mileda O., Kita K., Handa T., Yukawa T.;
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB116884; BAC82209.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KM Chloroplast.
 FT NON TER
 SQ SEQUENCE 20 AA; 2229 MW; 8E32F0325A4785C6 CRC64;

Query Match 24.3%; Score 25.5; DB 2; Length 20;
 Best Local Similarity 58.3%; Pred. No. 1.2e+04;
 Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY 1 DPAKGMSP-PGF 11
 ||||
 Db 4 DNEGSMSTIPGF 15

RESULT 35

TMOF_AEDAB
ID TMOF_AEDAB STANDARD; PRT; 10 AA.
AC p19425;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Trypsin-modulating oostatic factor (TMOF) (OOSH).
OC Aedes aegypti (Yellowfever mosquito).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Culicidae;
OC Culinidae; Culicini; Aedes; Stegomyia.
OX NCBI_TaxID=7159;
RN (1)
RP PROTEIN SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
[2]
RP PROTEIN SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=90367888; PubMed=2394318;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mosquito oostatic factor: a novel decapeptide modulating trypsin-like
enzyme biosynthesis in the midgut.";
RL FASEB J. 4:3015-3020(1990).
[2]
RP PROTEIN SEQUENCE.
RC STRAIN=Vero beach; TISSUE=Ovary;
RX MEDLINE=93357794; PubMed=8353526; DOI=10.1016/0965-1748(93)90044-S;
RA Borovsky D., Carlson D.A., Griffin P.R., Shabanowitz J., Hunt D.F.;
RT "Mass spectrometry and characterization of Aedes aegypti trypsin
modulating oostatic factor (TMOF) and its analogs.";
RL Insect Biochem. Mol. Biol. 23:703-712(1993).
CC -1- FUNCTION: Has an oostatic activity. Inhibits trypsin biosynthesis
in the midgut which indirectly reduces the vitellogenin
concentration in the hemolymph resulting in inhibition of oocyte
development.
CC -1- DEVELOPMENTAL STAGE: Synthesized and released from follicular
epithelium 18-24 hours after a blood meal. Synthesis peaks at 36
hours and stops at 56 hours.
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use as long as its content is in no way modified and this statement is not
removed.
CC PIR; A36454; A36454.
KW Direct protein sequencing; Hormone.
FT COMPIAS 3 10 Poly-Pro.
FT VARIANT 1 2 YD -> DY (in TMOF(B)).
SQ SEQUENCE 10 AA; 1047 MW; 236D0A7777776DC7 CRC64;
Query Match 23.8%; Score 25; DB 1; Length 10;
Best Local Similarity 55.6%; Pred. No. 6.6e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY 1 DPAKMGSP 9
|||
DB 2 DPAPPPPP 10
RESULT 36
QTM3T6 TRIGR PRELIMINARY; PRT; 10 AA.
ID QTM3T6
AC QTM3T6
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Sperm-activating peptide (Ser-3, Ile-4, Gly-5 SAP-I).
OS Tripteneutes gracillia (Hawaiian sea urchin).
OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinzoza;
OC Echinoidea; Euechinozoa; Echinacea; Temnopileuroidea; Toxopneustidae;
OC Tripteneutes;
OX NCBI_TaxID=7673;
RN (1)
RP PROTEIN SEQUENCE.
RA Yoshino K.I., Kajlura H., Nomura K., Takao T., Shimomishi Y.,

RA Kurita M., Yamaguchi M., Suzuki N.;
RT "A halogenated amino acid-containing sperm activating peptide and its
related peptides isolated from the egg jelly of sea urchins,
Tripteneutes gracillia, Pseudobolita maculata, Strongylocentrotus
nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
RL Comp. Biochem. Physiol. 94:739-751(1989).
RN [2]
RP PROTEIN SEQUENCE.
RX MEDLINE=91283461; PubMed=2059627;
RA Yoshino K., Takao T., Sunara M., Kitai T., Hori H., Nomura K.,
Yamaguchi M., Shimomishi Y., Suzuki N.;
RT "Identification of a novel amino acid, o-bromo-L-phenylalanine, in
egg-associated peptides that activate spermatozoa.";
RL Biochemistry 30:6203-6209(1991).
DR PIR; C60527; C60527.
SQ SEQUENCE 10 AA; 807 MW; 91EB537878787045 CRC64;
Query Match 23.8%; Score 25; DB 2; Length 10;
Best Local Similarity 55.6%; Pred. No. 6.6e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 10 GFIVGEGV 18
|||
DB 1 GFIVGEGV 9
RESULT 37
Q4W620 9CALI PRELIMINARY; PRT; 12 AA.
ID Q4W620
AC Q4W620
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE RNA dependent RNA polymerase (Fragment).
GN Name=ORF1;
OS Norovirus NV/Yu1/1/95/Jp.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
OC Norovirus.
OX NCBI_TaxID=329818;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Yu1;
RX MEDLINE=98351364; PubMed=9688078;
RA Saito H., Saito S., Kamada K., Harata S., Sato H., Morita M.,
Miyajima Y.;
RT "Application of RT-PCR designed from the sequence of the local SRSV
strain to the screening in viral gastroenteritis outbreaks.";
RL Microbiol. Immunol. 42:439-446(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Yu1;
RA Saito H.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB214364; BAD98806.1; -; Genomic_RNA.
FT NON_TER 1 1
SQ SEQUENCE 12 AA; 1228 MW; 25568821D71452C8 CRC64;
Query Match 23.8%; Score 25; DB 2; Length 12;
Best Local Similarity 46.2%; Pred. No. 8e+03;
Matches 6; Conservative 3; Mismatches 2; Indels 2; Gaps 1;
QY 6 MSPPGFVGEGV 18
::|::|
DB 1 LAPEG--VVEDGV 11
RESULT 38
Q84268 9PAPI PRELIMINARY; PRT; 12 AA.
ID Q84268
AC Q84268
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

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DE B1 ORF (Fragment).
OS Human papillomavirus.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC unclassified Papillomaviridae.
NC NCB1_TaxID=10566;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=89095007; PubMed=2536104;
RA Choo K.-B., Cheung W.-F., Liew L.-N., Lee H.-H., Han S.-H.;
RT "Presence of Genated Human Papillomavirus Type 16 Episomes in a
   Cervical Carcinoma Cell Line.";
RL J. VIROL. 63:782-789(1989).
DR EMBL; M24215; AAA46945.1; -; Genomic_DNA.
FT NON TER
SQ SEQUENCE 12 AA; 1178 MW; 993F1P424D51A861 CRC64;

Query Match 23.8%; Score 25; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8e+03;
Matches 6; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 6 MSPPGVGEEG 17
Db 1 MADPTGNGEEG 12

RESULT 39
FARB_ASCSU STANDARD; PRT; 13 AA.
ID P43173;
AC 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE FMRFamide-like neuropeptide Af11.
OS Ascaris suum (Pig roundworm) (Ascaris lumbricoides)
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Ascaridida; Ascaridoidea;
OC Ascarididae; Ascaris.
NC NCB1_TaxID=6253;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=95580362; PubMed=7651904; DOI=10.1016/0196-9781(94)00211-N;
RA Cowden C., Stretton A.O.W.;
RT "Eight novel FMRFamide-like neuropeptides isolated from the nematode
   Ascaris suum.";
RL Peptides 16:491-500(1995).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the FARB (FMRFamide related peptide)
   family.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amlatation; Direct protein sequencing; Neuroptide.
KW MOD RES 13 Phenylalanine amide.
FT MOD RES 13
SQ SEQUENCE 13 AA; 1495 MW; 9CABG50D686B05 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 13;
Best Local Similarity 50.0%; Pred. No. 8.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 GMSPPGFI 12
Db 4 GISBPNFL 11

RESULT 40
O16007 HUMAN PRELIMINARY; PRT; 13 AA.
ID O16007;
AC O16007;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)

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DT 01-NOV-1996 (TREMBLrel. 08, Last annotation update)
DE Lysosomal acid beta-galactosidase (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
NC NCB1_TaxID=9606;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=91369478; PubMed=1909871;
RA Morreau H., Bonten B., Zhou X.Y., D'Azzo A.;
RT "Organization of the gene encoding human lysosomal beta-
   galactosidase.";
RL DNA Cell Biol. 10:495-504(1991).
DR EMBL; S59584; AAB19814.1; -; Genomic_DNA.
FT NON TER
SQ SEQUENCE 13 AA; 1482 MW; D70DAE928194412 CRC64;

Query Match 23.8%; Score 25; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 8.7e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 9 PGFTV 13
Db 2 PGFTV 6

RESULT 41
O92190 MOUSE PRELIMINARY; PRT; 18 AA.
ID O92190;
AC O92190;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Mus musculus Ptn-P.
GN Name=Ptnp;
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
NC NCB1_TaxID=10090;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=99009213; PubMed=9790898; DOI=10.1006/hbrc.1998.9405;
RA Schroeder B., Groschup M., Hunsmann G., Bodemer W.;
RT "A differentially expressed prion gene mRNA is found in prion-infected
   mouse brains and in NZA cells but not in uninfected mice.";
RL Biochem. Biophys. Res. Commun. 251:6-6(1998).
DR EMBL; Y17510; CAA76774.1; -; Genomic_DNA.
DR MGI; MGI:97769; Ptnp.
DR GO; GO:0005783; C:cytoplasmic reticulum; IDA.
DR GO; GO:0005794; C:Golgi apparatus; IDA.
DR GO; GO:0045121; C:lipid raft; IDA.
DR GO; GO:0005507; F:copper ion binding; IDA.
DR GO; GO:0006878; F:copper ion homeostasis; TAS.
DR GO; GO:0006139; P:nucleus; nucleoside, nucleotide and nucl. . .; TAS.
DR GO; GO:0006979; P:response to oxidative stress; IDA.
SQ SEQUENCE 18 AA; 1973 MW; F35D48870B0E6B3 CRC64;

Query Match 23.8%; Score 25; DB 2; Length 18;
Best Local Similarity 58.3%; Pred. No. 1.2e+04;
Matches 7; Conservative 2; Mismatches 1; Indels 2; Gaps 1;

Qy 11 FIVGE-BGVLS 20
Db 3 FIVAEBOGVLT 14

RESULT 42
TRP3_LEUMA STANDARD; PRT; 19 AA.
ID TRP3_LEUMA;
AC P81735;

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DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DB Tachykinin-related peptide 3 (Lentrop 3).
OS Leucophaea maderae (Maderia cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberoidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Midgut; PubMed=8897641;
RX MEDLINE=97053012; PubMed=8897641;
RA Muren J.B., Naessel D.R.;
RT Isolation of five tachykinin-related peptides from the midgut of the
RT cockroach Leucophaea maderae: existence of N-terminally extended
RT isoforms.";
RL Regul. Pept. 65:185-196(1996).
CC -1- FUNCTION: Myoactive peptide. Increases the amplitude and frequency
CC of spontaneous contractions and tonus of hindgut muscle.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Midgut.
CC -----
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CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Amidation; Direct protein sequencing; Neuropeptide; Tachykinin.
FT MOD RES 19 19 Arginineamide.
SQ SEQUENCE 19 AA; 1930 MW; 99B5471A011625B5 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 19;
Best Local Similarity 36.4%; Pred. No. 1.3e+04;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 2 PAKMSPPGPI 12
Db 6 PGSKAPSGFL 16

RESULT 43
PYRX PSRFL STANDARD; PRT; 20 AA.
AC P56586;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Dihydroorotase-like protein (Aspartate carboxyltransferase 45 kDa
DE Non-catalytic chain) (Fragment).
GN Name=pyrC';
OS Pseudomonas fluorescens.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxID=294;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=ATCC 13525;
RX MEDLINE=94052183; PubMed=8234318;
RA Bergh S.T., Evans D.R.;
RT Subunit structure of a class A aspartate transcarboxylase from
RT Pseudomonas fluorescens.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:9818-9822(1993).
CC -1- FUNCTION: Non-functional DHOase.
CC -1- SUBUNIT: Heterododecamer of 6 active pyrB subunits and 6 non-
CC catalytic pyrC' subunits.
CC -1- SIMILARITY: Belongs to the DHOase family. PyrC' subfamily.
CC -----
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CC removed.
CC -----
DR HAMAP; MF_00220; acylcyl; 1.
KW Direct protein sequencing; Pyrimidine biosynthesis.
FT NON TER 20
SQ SEQUENCE 20 AA; 2063 MW; 735D157A430778B1 CRC64;

Query Match 23.8%; Score 25; DB 1; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.4e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKM 6
Db 12 DPASGL 17

RESULT 44
Q9QV83 9MURI PRELIMINARY; PRT; 20 AA.
ID Q9QV83_9MURI PRELIMINARY;
AC Q9QV83;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE Temperature-labile cholesterol ester hydrolase (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93216794; PubMed=8463327;
RA Wee S., Grogan W.M.;
RT Testicular temperature-labile cholesterol ester hydrolase.
RT Relationship to isoenzymes from other tissues, correlation with
RT spermatogenesis, and inhibition by physiological concentrations of
RT divalent cations.";
RL J. Biol. Chem. 268:8158-8163(1993).
SQ SEQUENCE 20 AA; 2080 MW; BR9D076DB6DBAFC CRC64;

Query Match 23.8%; Score 25; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 MSPPGFVGE 15
Db 6 VSPPAVVL 15

RESULT 45
Q7LZH3 MELGA PRELIMINARY; PRT; 20 AA.
ID Q7LZH3_MELGA PRELIMINARY;
AC Q7LZH3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Myosin light chain kinase, smooth muscle (Fragment).
OS Meleagris gallopavo (Common turkey).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Meleagris.
OX NCBI_TaxID=9103;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89214114; PubMed=2708351;
RA Ikebe M., Marita S., Reardon S.;
RT Location of the inhibitory region of smooth muscle myosin light chain
RT kinase.";
RL J. Biol. Chem. 264:6967-6971(1989).
DR PIR; A33878; A33878.
FT NON TER 1 1
SQ SEQUENCE 20 AA; 2147 MW; B1EFD5269872B93 CRC64;

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Query Match 23.8%; Score 25; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PAKGMSPP 9
 ||:|
 DB 8 PPKAATPP 15

RESULT 46

Q7M4B6_STRNU
 ID Q7M4B6_STRNU PRELIMINARY; PRT; 10 AA.

AC Q7M4B6;
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sperm-activating peptide (A1a-3, Gly-5 SAP-1).
 OS Strongylocentrotus nudus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Strongylocentrotidae;
 OC Strongylocentrotus.
 NCBI_TaxID=7666;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Yoshino K.I., Kajitara H., Nomura K., Takao T., Shimonishi Y.,
 RA Kurita M., Yamaguchi M., Suzuki N.;
 RT "A halogenated amino acid-containing sperm activating peptide and its
 RT related peptides isolated from the egg jelly of sea urchins,
 RT tripneustes gratilla, pseudoboleia maculata, strongylocentrotus
 RT nudus, echinometra mathaei and heterocentrotus mammillatus.";
 RL Comp. Biochem. Physiol. 94:739-751(1989).
 DR PIR; B60588; B60588.
 SQ SEQUENCE 10 AA; 791 MW; CBBB537878772D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 9.4e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GRVGESEV 18
 ||:|
 DB 1 GFLAGGGV 9

RESULT 47
 Q7M4D4_PSEDP PRELIMINARY; PRT; 10 AA.

AC Q7M4D4;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE Sperm-activating peptide (A1a-3, Gly-5 speract).
 OS Pseudocentrotus depressus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoida; Echinidae;
 OC Pseudocentrotus.
 NCBI_TaxID=7678;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Suzuki N., Kajitara H., Nomura K., Garbers D.L., Yoshino K., Kurita M.,
 RA Tanaka H., Yamaguchi M.;
 RT "Some more speract derivatives associated with eggs of sea urchins,
 RT pseudocentrotus depressus, strongylocentrotus purpuratus,
 RT hemicentrotus pulcherrimus and Anthocidaris crassispina";
 RL Comp. Biochem. Physiol. 89:687-693(1988).
 RN [2]

PROTEIN SEQUENCE.
 RP Pubmed=3378407;
 RA Suzuki N., Kajitara H., Nomura K., Garbers D.L., Yoshino K., Kurita M.,
 RA Tanaka H., Yamaguchi M.;
 RT "Some more speract derivatives associated with eggs of sea urchins,
 RT pseudocentrotus depressus, strongylocentrotus purpuratus,
 RT hemicentrotus pulcherrimus and Anthocidaris crassispina";
 RL Comp. Biochem. Physiol. B, Comp. Biochem. 89:687-693(1988).

DR PIR; E60788; E60788.
 SQ SEQUENCE 10 AA; 791 MW; CBBB537878772D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 9.4e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GRVGESEV 18
 ||:|
 DB 1 GFLAGGGV 9

RESULT 48

P82436_TOBAC
 ID P82436_TOBAC PRELIMINARY; PRT; 11 AA.

AC P82436;
 DT 01-JUN-2000 (TREMBLrel. 14, Created)
 DT 01-JUN-2000 (TREMBLrel. 14, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE 65 kDa cell wall protein (Fragment).
 OS Nicotiana tabacum (Common tobacco).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 NCBI_TaxID=4097;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC STRAIN=cv. PETIT HAVANA;
 RA Blee K.A., Bonham V.A., Mitchell G.P., Robertson D., Slabas A.R.,
 RA Woljaszek P., Bolwell G.P.;
 RT "Proteomic study of secondary cell wall proteins from transformed
 RT tobacco culture.";
 RL Planta 200:0(2000).
 CC -1- SUBCELLULAR LOCATION: CELL WALL.
 CC -1- TISSUE SPECIFICITY: XYLEM.
 DR GO; GO:0005618; C:cell wall; IEA.
 KW Cell wall.
 FT NON TER 11 11
 SQ SEQUENCE 11 AA; 1068 MW; 34FD25CCB325B67 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 11;
 Best Local Similarity 80.0%; Pred. No. 1e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 6 MSPPG 10
 ||||
 DB 1 MPPPG 5

RESULT 49
 O80X04_MESAU PRELIMINARY; PRT; 15 AA.

AC O80X04;
 DT 01-JUN-2003 (TREMBLrel. 24, Created)
 DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE C-Ki-ras (Fragment).
 OS Name=C-Ki-ras;
 OS Mesocricetus auratus (Golden hamster).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Cricetinae; Mesocricetus.
 NCBI_TaxID=10036;
 RN [1]

NUCLEOTIDE SEQUENCE.
 RP MEDLINE=95246257; Pubmed=7728976;
 RA Takehashi T., Moyer M.P., Cano M., Wang Q.D., Mountjoy C.P.,
 RA Sanger W., Adrian T.B., Sugitara H., Katoh H., Pour P.M.;
 RT "Differences in molecular biological, biological and growth
 RT characteristics between the immortal and malignant hamster pancreatic
 RT cells.";
 RL Carcinogenesis 16:931-939(1995).
 DR EMBL; S77069; AAP31994.1; -; Genomic_DNA.

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FT  NON TER      15      15
SQ  SEQUENCE     15 AA; 1538 MW;  C4B2EC93858939EB CRC64;
Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 15;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY  12 IVGEGV 18
    |||
Db  8 VVGADGV 14

RESULT 50
Q9HEQ1_PARB_R PRELIMINARY; PRT; 17 AA.
ID  Q9HEQ1_PARB_R PRELIMINARY; PRT; 17 AA.
AC  Q9HEQ1;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Alpha-tubulin (Fragment).
GN  Name=TUB1;
OS  Paracoccidiodae brasiliensis.
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC  Onygenales; microsporitic Onygenales; Paracoccidiodae.
OX  NCBI_TaxID=121759;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=PB18;
RA  Kasuga T., White T.J., Taylor J.W.;
RT  "The molecular clock in fungi in the class Plecomycetes.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  GO; GO:000874; C:microtubule; IEA.
DR  GO; GO:0005198; P:structural molecule activity; IEA.
DR  GO; GO:0007018; P:microtubule-based movement; IEA.
DR  InterPro; IPR002452; Alpha_tubulin.
DR  PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT  NON TER      17      17
SQ  SEQUENCE     17 AA; 2039 MW;  B8E787547655F90A CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 17;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  5 GMSPPGFI 12
    |||
Db  10 GIQPDGYL 17

RESULT 51
Q9HEQ2_AJED_R PRELIMINARY; PRT; 17 AA.
ID  Q9HEQ2_AJED_R PRELIMINARY; PRT; 17 AA.
AC  Q9HEQ2;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Alpha-tubulin (Fragment).
GN  Name=TUB1;
OS  Ajellomyces dermatitidis (Blastomyces dermatitidis).
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC  Onygenales; Ajellomycetaceae; Ajellomyces.
OX  NCBI_TaxID=5039;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC60915;
RA  Kasuga T., White T.J., Taylor J.W.;
RT  "The molecular clock in fungi in the class Plecomycetes.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY013113; MAG40954.1; -; Genomic_DNA.
DR  GO; GO:000874; C:microtubule; IEA.
DR  GO; GO:0005198; P:structural molecule activity; IEA.
DR  GO; GO:0007018; P:microtubule-based movement; IEA.

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DR  InterPro; IPR002452; Alpha_tubulin.
DR  PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT  NON TER      17      17
SQ  SEQUENCE     17 AA; 2039 MW;  B8E787547655F90A CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 17;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  5 GMSPPGFI 12
    |||
Db  10 GIQPDGYL 17

RESULT 52
Q9HEQ3_AJEC_A PRELIMINARY; PRT; 17 AA.
ID  Q9HEQ3_AJEC_A PRELIMINARY; PRT; 17 AA.
AC  Q9HEQ3;
DT  01-MAR-2001 (TrEMBLrel. 16, Created)
DT  01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT  01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE  Alpha-tubulin (Fragment).
GN  Name=TUB1;
OS  Ajellomyces capsulata (Histoplasma capsulatum).
OC  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC  Onygenales; Ajellomycetaceae; Ajellomyces.
OX  NCBI_TaxID=5037;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC26032;
RA  Kasuga T., White T.J., Taylor J.W.;
RT  "The molecular clock in fungi in the class Plecomycetes.";
RL  Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY013112; MAG40953.1; -; Genomic_DNA.
DR  GO; GO:000874; C:microtubule; IEA.
DR  GO; GO:0005198; P:structural molecule activity; IEA.
DR  GO; GO:0007018; P:microtubule-based movement; IEA.
DR  InterPro; IPR002452; Alpha_tubulin.
DR  PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT  NON TER      17      17
SQ  SEQUENCE     17 AA; 2039 MW;  B8E787547655F90A CRC64;

Query Match
Best Local Similarity 22.9%; Score 24; DB 2; Length 17;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY  5 GMSPPGFI 12
    |||
Db  10 GIQPDGYL 17

RESULT 53
Q49077_MYCC_A PRELIMINARY; PRT; 17 AA.
ID  Q49077_MYCC_A PRELIMINARY; PRT; 17 AA.
AC  Q49077;
DT  01-NOV-1996 (TrEMBLrel. 01, Created)
DT  01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT  01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE  DNA-directed RNA polymerase (beta) (Fragment).
OS  Mycoplasma capricolum.
OC  Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX  NCBI_TaxID=2095;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RC  STRAIN=ATCC 27343;
RA  Bork P., Ouzounis C., Casati G., Schneider R., Sander C., Dolan M.,
RT  Gilbert W., Gillelev P.M.;
RT  "Exploring the Mycoplasma capricolum genome: a minimal cell reveals
its physiology";
RL  Mol. Microbiol. 16:955-967 (1995).

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DR EMBL; Z33297; CAA63830.1; -; Genomic_DNA.
 DR PIR; S77834; S77834.
 DR GO; GO:0003899; F:DNA-directed RNA polymerase activity; IEA.
 KW DNA-directed RNA polymerase.
 FT NON_TER
 SQ SEQUENCE 17 AA; 1930 MW; B353351EF997B46 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 17;
 Best Local Similarity 45.5%; Pred. No. 1.7e+04;
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 6 MSPGFVGE 16
 Db 1 MGAPSIIVNE 11

RESULT 54
 Q7M546 HALSA PRELIMINARY; PRT; 19 AA.
 AC Q7M546;
 DT 01-MAR-2004 (TREMBLrel. 26, Created)
 DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
 DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)
 DE Ribosomal protein S2 (Fragment).
 OS Halobacterium salinarum (Halobacterium halobium).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobacterium.
 OK NCBI_TaxID=2242;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Yaguchi M., Visentin L.P., Zuker M., Matheson A.T., Roy C.,
 RA Strom A.R.;
 RT "Amino-terminal sequences of ribosomal proteins from the 30S subunit
 of archaeobacterium Halobacterium cutriburum.";
 RL Submitted (DEC-1990) to the PIR data bank.
 DR PIR; S1611; S1611.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 19 AA; 2062 MW; 3F35304BB4E4B0D CRC64;

Query Match 22.9%; Score 24; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 SPPG 10
 Db 15 SPPG 18

RESULT 55
 Q7S06_9CIRC PRELIMINARY; PRT; 19 AA.
 ID Q7S06_9CIRC PRELIMINARY; PRT; 19 AA.
 AC Q7S06;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE ORF-7.
 OS Porcine circovirus type 2-C.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OK NCBI_TaxID=85543;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL; AF109398; AAD03067.1; -; Genomic DNA.
 SQ SEQUENCE 19 AA; 1893 MW; 384FB58B920BC23 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 19;
 Best Local Similarity 37.5%; Pred. No. 1.9e+04;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
 Db 7 PSSAVTPP 14

RESULT 56
 Q9Y713_9CIRC PRELIMINARY; PRT; 19 AA.
 ID Q9Y713_9CIRC PRELIMINARY; PRT; 19 AA.
 AC Q9Y713;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ORF-7.
 OS Bovine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OK NCBI_TaxID=85542;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hamel A.L., Nayar G.P.S.;
 RL Submitted (FEB-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF109397; AAD11934.1; -; Genomic DNA.
 SQ SEQUENCE 19 AA; 1893 MW; 384FB58B920BC23 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 19;
 Best Local Similarity 37.5%; Pred. No. 1.9e+04;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 2 PAKGMSPP 9
 Db 7 PSSAVTPP 14

RESULT 57
 Q9T218_NICSY PRELIMINARY; PRT; 20 AA.
 ID Q9T218_NICSY PRELIMINARY; PRT; 20 AA.
 AC Q9T218;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 14.1 kDa photosystem I PSAB protein (Fragment).
 OS Nicotiana glauca (Wood tobacco).
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC lamids; Solanales; Solanaceae; Nicotiana.
 OK NCBI_TaxID=4096;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94105345; PubMed=8278548; DOI=10.1104/pp.102.4.1259;
 RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugitara M.;
 RT "Molecular heterogeneity of photosystem I. psab, psab, psab, psab, and
 psal are all present in isoforms in Nicotiana spp.";
 RL Plant Physiol. 102:1259-1267(1993).
 RL Plant Physiol. 102:1259-1267(1993).
 SQ SEQUENCE 20 AA; 1822 MW; E458944B2F5E5D94 CRC64;

Query Match 22.9%; Score 24; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 AKGMSPP 9
 Db 14 AEGGAP 20

RESULT 58
 Q9T219_NICSY PRELIMINARY; PRT; 20 AA.
 ID Q9T219_NICSY PRELIMINARY; PRT; 20 AA.
 AC Q9T219;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE 14 kDa photosystem I PSAB protein (Fragment).
 OS Nicotiana glauca (Wood tobacco).

OG Chloroplast.
 OC Burkholderia; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
 OC Lamiales; Solanales; Solanaceae; Nicotiana.
 RN NCBI_TaxID=4096;
 RN (1)
 RP PROTEIN SEQUENCE.
 RX MEDLINE=94105345; PubMed=8278548; DOI=10.1104/pp.102.4.1259;
 RA Obokata J., Mikami K., Hayashida N., Nakamura M., Sugitara M.,
 RT "Molecular heterogeneity of photosystem I. psad, psab, psaf, psah, and
 psal are all present in isoforms in Nicotiana spp.";
 RL Plant Physiol. 102:1259-1267(1993).
 SQ SEQUENCE 20 AA; 1832 MW; A8945894392825D CRC64;

Query Match 22.4%; Score 24; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 AKGMSPP 9
 DB 13 ABGEAPP 19

RESULT 59
 Q51S4_9CALI PRELIMINARY; PRT; 12 AA.
 ID Q51S4_9CALI PRELIMINARY;
 AC Q51S4_9CALI PRELIMINARY;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE RNA polymerase (Fragment).
 OS Norovirus Tak-69/Thailand.
 OC Viruses; ssRNA positive-strand viruses; no DNA stage; Caliciviridae;
 OC Norovirus.
 RN NCBI_TaxID=300739;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Tak-69/Thailand;
 RX PubMed=15623956;
 RA Gunatpong R., Hanman G.S., Oka T., Ogawa S., Kageyama T.,
 RA Pongsuwanana Y., Katayama K.,
 RT "Norovirus and sapovirus infections in Thailand.";
 RL Jpn. J. Infect. Dis. 57:276-278(2004).
 DR EMBL, AY646878; AAV69611.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1276 MW; C3988821D71452C9 CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.4e+04;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 PGFVGESEV 18
 DB 3 PSF-VNEDGV 11

RESULT 60
 Q51S5_9CALI PRELIMINARY; PRT; 12 AA.
 ID Q51S5_9CALI PRELIMINARY;
 AC Q51S5_9CALI PRELIMINARY;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE RNA polymerase (Fragment).
 OS Norovirus Tak-62/Thailand.
 OC Viruses; ssRNA positive-strand viruses; no DNA stage; Caliciviridae;
 OC Norovirus.
 RN NCBI_TaxID=300738;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Tak-62/Thailand;
 RX PubMed=15623956;
 RA Gunatpong R., Hanman G.S., Oka T., Ogawa S., Kageyama T.,

RA Pongsuwanana Y., Katayama K.,
 RT "Norovirus and sapovirus infections in Thailand.";
 RL Jpn. J. Infect. Dis. 57:276-278(2004).
 DR EMBL, AY646877; AAV69609.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 12 AA; 1276 MW; C3988821D71452C9 CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 12;
 Best Local Similarity 60.0%; Pred. No. 1.4e+04;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 PGFVGESEV 18
 DB 3 PSF-VNEDGV 11

RESULT 61
 Q506K8_9CALI PRELIMINARY; PRT; 16 AA.
 ID Q506K8_9CALI PRELIMINARY;
 AC Q506K8_9CALI PRELIMINARY;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE RNA-dependent RNA polymerase (Fragment).
 OS Norovirus Hu/Berlin/11/03/Germany.
 OC Viruses; ssRNA positive-strand viruses; no DNA stage; Caliciviridae;
 OC Norovirus.
 RN NCBI_TaxID=324082;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Hu/Berlin/11/03/Germany;
 RA Petznick S., Hoehne M., Schreier E.,
 RT "Characterization of a recombinant norovirus in Germany.";
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY994531; AAY25352.1; -; Genomic_RNA.
 KM RNA-directed RNA polymerase.
 FT NON_TER 1
 SQ SEQUENCE 16 AA; 1719 MW; 0FC888218BA59CCA CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 16;
 Best Local Similarity 60.0%; Pred. No. 1.9e+04;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 PGFVGESEV 18
 DB 7 PSF-VNEDGV 15

RESULT 62
 Q88290_9CALI PRELIMINARY; PRT; 18 AA.
 ID Q88290_9CALI PRELIMINARY;
 AC Q88290_9CALI PRELIMINARY;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE RNA polymerase (Fragment).
 OS Small round structured virus.
 OC Viruses; ssRNA positive-strand viruses; no DNA stage; Caliciviridae;
 OC Norovirus.
 RN NCBI_TaxID=37141;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Auckland;
 RA Regal W.J., Green D.H., Lewis G.D.,
 RL Submitted (JAN-1996) to the EMBL/GenBank/DBJ databases.
 DR EMBL, U46039; AAB00436.1; -; Genomic_RNA.
 FT NON_TER 1
 SQ SEQUENCE 18 AA; 2034 MW; 7FCC53718BA59CCA CRC64;

Query Match 22.4%; Score 23.5; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 2.1e+04;
 Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

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QY 9 PGFIVEEGV 18
   |||||
Db 9 PSF-VNEDGV 17

RESULT 63
Q5IT04_9CALI PRELIMINARY; PRT; 19 AA.
ID Q5IT04_9CALI
AC Q5IT04;
DT 10-MAY-2005 (TREMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TREMBLrel. 30, Last annotation update)
DR RNA polymerase (Fragment).
OS Norovirus Sakaao-14/Thailand.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Calicitviridae;
OC Norovirus.
NCBI_TaxID=300729;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sakaao-14/Thailand;
RX PubMed=15623956;
RA Gunatpong R., Hansman G.S., Oka T., Ogawa S., Kageyama T.,
  Pongsuwanana Y., Katsayama K.,
  "Norovirus and sapovirus infections in Thailand.";
  Jpn. J. Infect. Dis. 57:276-278(2004).
  EMBL; AF646868; AAV69591.1; -; Genomic_DNA.
  FT NON_TER 1
SQ SEQUENCE 19 AA; 2121 MW; 7FCC3A771BA59CCA CRC64;

Query Match
Best Local Similarity 22.4%; Score 23.5; DB 2; Length 19;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 9 PGFIVEEGV 18
   |||||
Db 10 PSF-VNEDGV 18

RESULT 64
RS7_MYCIT
ID RS7_MYCIT STANDARD; PRT; 8 AA.
AC P33564;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE 30S ribosomal protein S7 (Fragment).
GN Name=rspeg;
OS Mycobacterium intracellulare.
OC Bacteria; Actinobacteriae; Actinomycetales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium avium complex (MAC).
NCBI_TaxID=1767;
RN (1)
RP NUCLEOTIDE SEQUENCE (GENOMIC DNA).
RX MEDLINE=93197130; PubMed=8451173;
  Nair J., Rouse D.A., Morris S.L.;
  "Nucleotide sequence analysis of the ribosomal S12 gene of
  Mycobacterium intracellulare.";
  Nucleic Acids Res. 21:1039-1039(1993).
RT FUNCTION: One of the primary rRNA binding proteins, it binds
  directly to 16S rRNA where it nucleates assembly of the head
  domain of the 30S subunit. It is located at the subunit interface
  close to the decoding center, probably blocks exit of the E-site
  tRNA (by similarity).
CC -1- SUBUNIT: Part of the 30S ribosomal subunit. Contacts proteins S9
  and S11 (by similarity).
CC -1- SIMILARITY: Belongs to the ribosomal protein S7P family.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
  between the Swiss Institute of Bioinformatics and the EMBL outstation -
  the European Bioinformatics Institute. There are no restrictions on its
  use as long as its content is in no way modified and this statement is not
  removed.

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CC -----
DR EMBL; I08171; AAA5376.1; -; Genomic_DNA.
DR PIR; S35538; S35538.
DR HAMAP; MF_00480; -; 1.
DR InterPro; IPR000235; Ribosomal_S7.
DR PROSITE; PS00052; RIBOSOMAL_S7; PARTIAL.
KW Ribonucleoprotein; Ribosomal protein; RNA-binding; rRNA-binding;
  tRNA-binding.
FT INIT MET 0 0 By similarity.
FT NON_TER 8 8
SQ SEQUENCE 8 AA; 850 MW; 63276DC768732417 CRC64;

Query Match
Best Local Similarity 21.9%; Score 23; DB 1; Length 8;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGNSP 8
   |||||
Db 1 PRKGPAP 7

RESULT 65
Q8MJT7_9PRIM
ID Q8MJT7_9PRIM PRELIMINARY; PRT; 9 AA.
AC Q8MJT7;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus (Brown lemur).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnuriidae; Eulemur.
NCBI_TaxID=13515;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Wyner Y.M., Johnson S.B., Stumpf R., Desalle R.;
  Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
  DR EMBL; AF258049; AAM43870.1; -; Genomic_DNA.
  FT NON_TER 1
  FT NON_TER 1
  FT NON_TER 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

Query Match
Best Local Similarity 21.9%; Score 23; DB 2; Length 9;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 BEGVL 19
   |||||
Db 2 BEGIL 6

RESULT 66
Q8MJT8_9PRIM
ID Q8MJT8_9PRIM PRELIMINARY; PRT; 9 AA.
AC Q8MJT8;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TREMBLrel. 22, Last annotation update)
DE Hemopexin (Fragment).
OS Eulemur fulvus albocollaris.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Strepsirrhini;
OC Lemnuriidae; Eulemur.
NCBI_TaxID=122224;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Wyner Y.M., Johnson S.B., Stumpf R., Desalle R.;
  Submitted (APR-2000) to the EMBL/Genbank/DBJ databases.
  DR EMBL; AF258028; AAM43849.1; -; Genomic_DNA.
  FT NON_TER 1
  FT NON_TER 1
  FT NON_TER 9
SQ SEQUENCE 9 AA; 1110 MW; 738CC9C720587B1B CRC64;

```

Query Match 21.9%; Score 23; DB 2; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2.2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 15 EBGVL 19
 |||:
 2 EBGIL 6

RESULT 67
 ID Q7M3T7 TRIGR PRELIMINARY; PRT; 10 AA.

AC Q7M3T7;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Sperm-activating peptide (Ser-3, Gly-5 SAP-I).
 OS Tripteneutes gracillia (Hawaiian sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Temnopneuroidea; Toxopneustidae;
 OC Tripteneutes.
 OC NCBI_TaxID=7673;
 RX MEDLINE-91283461; PubMed-2059627;
 RA Yoshino K., Takao T., Suhara M., Kitai T., Hori H., Nomura K.,
 RA Kurita M., Yamaguchi M., Suzuki N.;
 RT "A halogenated amino acid-containing sperm activating peptide and its
 RT related peptides isolated from the egg jelly of sea urchins,
 RT Tripteneutes gracillia, Pseudobolitta maculata, Strongylocentrotus
 RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
 RL Comp. Biochem. Physiol. 94:739-751(1989).
 SO SEQUENCE 10 AA; 807 MW; 91EB5378787735 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPVIGEGV 18
 ||:|
 1 GFSLGGGV 9

RESULT 68
 ID Q7M4B4 STRNU PRELIMINARY; PRT; 10 AA.
 AC Q7M4B4;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Sperm-activating peptide (Ser-3, Gly-5 SAP-I).
 OS Strongylocentrotus nudus (Sea urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Strongylocentrotidae;
 OC Strongylocentrotus.
 OC NCBI_TaxID=7666;
 RX PROTEIN SEQUENCE.
 RA Yoshino K.I., Kajiyura H., Nomura K., Takao T., Shimoniishi Y.,
 RA Kurita M., Yamaguchi M., Suzuki N.;
 RT "A halogenated amino acid-containing sperm activating peptide and its
 RT related peptides isolated from the egg jelly of sea urchins,
 RT Tripteneutes gracillia, Pseudobolitta maculata, Strongylocentrotus
 RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";

RL Comp. Biochem. Physiol. 94:739-751(1989).
 DR PIR; C60588; C60588. 807 MW; 91EB5378787735 CRC64;
 SO SEQUENCE 10 AA; 807 MW; 91EB5378787735 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPVIGEGV 18
 ||:|
 1 GFSLGGGV 9

RESULT 69
 ID Q7M4C0 HETMA PRELIMINARY; PRT; 10 AA.

AC Q7M4C0;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DE Sperm-activating peptide (Glu-3, Met-4, Gly-5, Thr-7 SAP-I).
 OS Heterocentrotus mammillatus (Slate-pencil urchin).
 OC Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
 OC Echinoidea; Euechinoidea; Echinacea; Echinoidea; Echinometridae;
 OC Heterocentrotus.
 OC NCBI_TaxID=31180;
 RX PROTEIN SEQUENCE.
 RA Yoshino K.I., Kajiyura H., Nomura K., Takao T., Shimoniishi Y.,
 RA Kurita M., Yamaguchi M., Suzuki N.;
 RT "A halogenated amino acid-containing sperm activating peptide and its
 RT related peptides isolated from the egg jelly of sea urchins,
 RT Tripteneutes gracillia, Pseudobolitta maculata, Strongylocentrotus
 RT nudus, Echinometra mathaei and Heterocentrotus mammillatus.";
 RL Comp. Biochem. Physiol. 94:739-751(1989).
 DR PIR; I60588; I60588.
 SO SEQUENCE 10 AA; 911 MW; 7FEB5361A878769B CRC64;

Query Match 21.9%; Score 23; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1.3e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 GPVIGEGV 18
 ||:|
 1 GFEMGGTV 9

RESULT 70
 ID Q4W618 9CALI PRELIMINARY; PRT; 12 AA.
 AC Q4W618;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DE RNA dependent RNA polymerase (Fragment).
 GN Name=ORF1;
 OS Norovirus NV/Futatsui/1/05/JP.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;
 OC Norovirus.
 OC NCBI_TaxID=329819;
 RX NUCLEOTIDE SEQUENCE.
 RA Saito H.;
 RA Saito H.;
 RT "Outbreak of norovirus with water supply service line in the small
 RT village.";
 RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB214365; BAD98808.1; -; Genomic_RNA.
 PT NON TER 1
 SO SEQUENCE 12 AA; 1242 MW; 41988821D71452C7 CRC64;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 12 IYGESEV 18
 : ||:
 Db 5 LVNEDSV 11

RESULT 71
 Q60F86_9BRYO PRELIMINARY; PRT; 13 AA.
 ID Q60F86_9BRYO PRELIMINARY; PRT; 13 AA.
 AC Q60F86_9BRYO PRELIMINARY; PRT; 13 AA.
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DE 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 GN Ribosomal protein S11 (Fragment).
 OS Name=rp11;
 OS Sphagnum glaucophyllum.
 OG Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
 OC Sphagnopsida; Sphagnales; Sphagnaceae; Sphagnum.
 OX NCBI_TaxID=128204;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.;
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis
 RT of mosses.";
 RL Hikobia 0:0-0(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.;
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis
 RT of mosses.";
 RL Hikobia 0:0-0(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.;
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis
 RT of mosses.";
 RL Hikobia 14:171-175(2004).
 DR EMBL; AB193122; BAD60946.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro; IPR001971; Ribosomal_S11.
 DR Pfam; PF00411; Ribosomal_S11; 1.
 KW Chloroplast; Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1545 MW; 7A0CD3AB1E377774 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 9
 : ||:
 Db 1 PHNGCRPP 8

RT "Molecular evidence of an rpoA gene in the basal moss chloroplast
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis
 RT of mosses.";
 RL Hikobia 0:0-0(2004).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Sugita M., Sugita C., Arikawa T., Higuchi M.;
 RT "Molecular evidence of an rpoA gene in the basal moss chloroplast
 RT genomes: rpoA is a useful molecular marker for phylogenetic analysis
 RT of mosses.";
 RL Hikobia 14:171-175(2004).
 DR EMBL; AB193121; BAD60943.1; -; Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0005622; C:intracellular; IEA.
 DR GO; GO:0005840; C:ribosome; IEA.
 DR GO; GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO; GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro; IPR001971; Ribosomal_S11.
 DR Pfam; PF00411; Ribosomal_S11; 1.
 KW Chloroplast; Ribosomal protein.
 FT NON TER 1
 SQ SEQUENCE 13 AA; 1545 MW; 7A0CD3AB1E377774 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.8e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 9
 : ||:
 Db 1 PHNGCRPP 8

RESULT 73
 P82866_RANPI PRELIMINARY; PRT; 13 AA.
 ID P82866_RANPI PRELIMINARY; PRT; 13 AA.
 AC P82866;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
 DE RNA-binding protein (Fragment).
 OS Rana pipiens (Northern leopard frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 OX NCBI_TaxID=8404;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISSUE=embryonic epithelium;
 RA Banerjee H.N., Blackmon R.H., Moses A., Harmon G.L., Peterson B.L.,
 RA Khan A.;
 RT "Isolation, identification and characterization of a novel 5'UTR
 RT binding protein for VCAW-1.";
 RL Submitted (NOV-2000) to Swiss-Prot.
 CC -1- FUNCTION: Binds to the VCAW-1 5'UTR region.
 CC -1- SIMILARITY: Belongs to the fetuin family.
 DR PIR; A59387; A59387.
 DR GO; GO:0003723; F:RNA binding; IEA.
 DR InterPro; IPR001363; Prot inh. fetuin.
 DR PROSITE; PS01254; FETUIN_1; PARTIAL.
 DR PROSITE; PS01255; FETUIN_2; PARTIAL.
 KW RNA-binding.
 FT NON TER 13
 SQ SEQUENCE 13 AA; 1370 MW; C683612A61757DC2 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 1.8e+04;
 Matches 4; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
 QY 1 DPAKMSPP 9
 : ||:
 Db 4 DPVAGYKEP 12

RESULT 74

UC19_MA1ZB
ID UC19_MA1ZB STANDARD; PRT; 15 AA.
AC P80625;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 406) (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD Clade; Panicoidae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RC TISUB=COLEOPTILE;
RA Pourzel P., Riccardi F., Morin C., Damerval C., Huet J.-C., Pournollet J.-C., Zivy M., de Vienne D.;
RT "The maize two dimensional gel protein database: towards an integrated genome analysis program."
RL Theor. Appl. Genet. 93:997-1005(1996).
CC -; MISCELLANEOUS: On the 2D-gel the determined pI of this unknown protein is: 5.6, its MW is: 18.4 kDa.
CC -----
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CC -----
CC DR Maize-2DPAGE; P80625; COLEOPTILE.
DR DR MaizeDB; 123951; -.
KW Direct protein sequencing.
FT NON_TER 1 1
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1672 MW; 1CF69DAD6A737F9D CRC64;

Query Match 21.9%; Score 23; DB 1; Length 15;
Best Local Similarity 80.0%; Pred. No. 2.1e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 5 GMSPP 9
DB 9 GCSPP 13

RESULT 75
0561Y4_9FLAV PRELIMINARY; PRT; 15 AA.
ID 0561Y4_9FLAV PRELIMINARY; PRT; 15 AA.
AC 0561Y4;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE C protein (Fragment).
OS Tick-borne encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; OC Flavivirus; tick-borne encephalitis virus group.
OX NCBI_TaxID=11084;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BR85;
RA Casati S., Gern L., Piffaretti J.-C.;
RT "Diversity of the tick-borne Encephalitis Virus population infecting RT ixodes ricinus ticks in a risk region of central Switzerland (Canton Bern)."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY45366; AAX57481.1; -; Genomic_RNA.
FT NON_TER 15 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1523 MW; 735110858796B95D CRC64;

Query Match 21.9%; Score 23; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 KGMSP 9
DB 10 KGGAP 15

RESULT 76
0561Z6_9FLAV PRELIMINARY; PRT; 15 AA.
ID 0561Z6_9FLAV PRELIMINARY; PRT; 15 AA.
AC 0561Z6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE C protein (Fragment).
OS Tick-borne encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae; OC Flavivirus; tick-borne encephalitis virus group.
OX NCBI_TaxID=11084;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=BR241;
RA Casati S., Gern L., Piffaretti J.-C.;
RT "Diversity of the tick-borne Encephalitis Virus population infecting RT ixodes ricinus ticks in a risk region of central Switzerland (Canton Bern)."
RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY45350; AAX57469.1; -; Genomic_RNA.
FT NON_TER 15 15
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1523 MW; 735110858796B95D CRC64;

Query Match 21.9%; Score 23; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.1e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 4 KGMSP 9
DB 10 KGGAP 15

RESULT 77
09UCG5_HUMAN PRELIMINARY; PRT; 16 AA.
ID 09UCG5_HUMAN PRELIMINARY; PRT; 16 AA.
AC 09UCG5;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE T-suppressor LYMPHOKINE.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae; OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP PROTEIN SEQUENCE.
RC MEDLINE=9321626; PubMed=7682534;
RA Quan C.P., Watanabe S., Vuillier F., Pires R., Matsuo T., Stanislowski M., Pillot J., Bouvet J.P.;
RT "Purification and partial amino acid sequence of suppressive RT lymphokine from a CD8+ CD57+ human T hybridoma."
RL Immunology 78:205-209(1993).
SQ SEQUENCE 16 AA; 1587 MW; 4565578EBB6F9C29 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 13 VGBEG 17
DB 5 VGDEG 9

RESULT 78

BIOP1_PHYHY STANDARD; PRT; 17 AA.
 ID BIOP1_PHYHY
 AC P84521;
 DT 10-MAY-2005 (Rel. 47, Created)
 DT 10-MAY-2005 (Rel. 47, Last sequence update)
 DE Bioactive peptide 1.
 OS Phyllomedusa hypochondrialis (Orange-legged leaf frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hylidae; Hylidae;
 OC Phyllomedusinae; Phyllomedusa.
 NCBI_TaxID=317381;
 RN [1]
 RP PROTEIN SEQUENCE, MASS SPECTROMETRY, AND PYRROLIDONE CARBOXYLIC ACID.
 RC TISSUE=Venom;
 RA Thompson A.H.;
 RT "Bioactive peptides derived from the venom of the South American tree
 frog, Phyllomedusa hypochondrialis.";
 RL Submitted (APR-2005) to Swiss-Prot.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Venom.
 CC -1- MASS SPECTROMETRY: MW=1732.86; MW_ERR=0.1; METHOD=Electrospray;
 CC RANGES=1-17; NOTE=Ref.1.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Direct protein sequencing; Pyrrolidone carboxylic acid.
 KW MOD_RES 1 1
 FT UNSURE 11 11 L or I.
 FT UNSURE 14 14 L or I.
 SQ SEQUENCE 17 AA; 1750 MW; 23AC9C40FB8BF1F7 CRC64;
 Query Match 21.9%; Score 23; DB 1; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PAKGMSPPG 11
 DB 7 PYGGLSPLRP 16
 RESULT 79
 Q9UCU9_HUMAN PRELIMINARY; PRT; 17 AA.
 ID Q9UCU9;
 AC Q9UCU9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Proteoglycan 80 kDa polypeptide (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93054750; PubMed=1429726;
 RA Perdes G., Rahemulla F., Lane W.S., Asher R.A., Bignami A.;
 RT "Isolation of a large aggregating proteoglycan from human brain.";
 RL J. Biol. Chem. 267:23885-23887(1992).
 SQ SEQUENCE 17 AA; 1771 MW; 1BDA8561B2F71614 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 2.4e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 5 GMSPP 9
 DB 1
 RESULT 80
 Q9UCU9_HUMAN PRELIMINARY; PRT; 17 AA.
 ID Q9UCU9;
 AC Q9UCU9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PLAU protein (Fragment).
 GN Name=PLAU;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86050639; PubMed=3933505;
 RA Nagamine Y., Pearson D., Gratian M.;
 RT "Exon-intron boundary sliding in the generation of two mRNAs coding
 RT for porcine urokinase-like plasminogen activator.";
 RL Biochem. Biophys. Res. Commun. 132:563-569(1985).
 DR EMBL; K03027; AAA61257.1; -; Genomic_DNA.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1801 MW; 9989927E849E253 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 17;
 Best Local Similarity 55.6%; Pred. No. 2.4e+04;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DPAKMSPP 9
 DB 9 DKKPSPSP 17
 RESULT 81
 Q9RSJ3_MYCGA PRELIMINARY; PRT; 17 AA.
 ID Q9RSJ3;
 AC Q9RSJ3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Major hemagglutinin (Fragment).
 OS Mycoplasma gallisepticum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92563591; PubMed=1379991;
 RA Marham P.F., Glew M.D., Brandon M.R., Walker I.D., Whitehead K.G.;
 RT "Characterization of a major hemagglutinin protein from Mycoplasma
 RT gallisepticum.";
 RL Infect. Immun. 60:3885-3891(1992).
 SQ SEQUENCE 17 AA; 1692 MW; 466461BD34163413 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 9
 DB 8 PAPNPSP 15
 RESULT 82
 Q9TWH0_9TRYP PRELIMINARY; PRT; 18 AA.
 ID Q9TWH0;
 AC Q9TWH0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

Db 7 GKSP 11
 RESULT 80
 Q9UCU9_HUMAN PRELIMINARY; PRT; 17 AA.
 ID Q9UCU9;
 AC Q9UCU9;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE PLAU protein (Fragment).
 GN Name=PLAU;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86050639; PubMed=3933505;
 RA Nagamine Y., Pearson D., Gratian M.;
 RT "Exon-intron boundary sliding in the generation of two mRNAs coding
 RT for porcine urokinase-like plasminogen activator.";
 RL Biochem. Biophys. Res. Commun. 132:563-569(1985).
 DR EMBL; K03027; AAA61257.1; -; Genomic_DNA.
 FT NON_TER 1 1
 FT NON_TER 17 17
 SQ SEQUENCE 17 AA; 1801 MW; 9989927E849E253 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 17;
 Best Local Similarity 55.6%; Pred. No. 2.4e+04;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 1 DPAKMSPP 9
 DB 9 DKKPSPSP 17
 RESULT 81
 Q9RSJ3_MYCGA PRELIMINARY; PRT; 17 AA.
 ID Q9RSJ3;
 AC Q9RSJ3;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Major hemagglutinin (Fragment).
 OS Mycoplasma gallisepticum.
 OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
 OX NCBI_TaxID=2096;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92563591; PubMed=1379991;
 RA Marham P.F., Glew M.D., Brandon M.R., Walker I.D., Whitehead K.G.;
 RT "Characterization of a major hemagglutinin protein from Mycoplasma
 RT gallisepticum.";
 RL Infect. Immun. 60:3885-3891(1992).
 SQ SEQUENCE 17 AA; 1692 MW; 466461BD34163413 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 2.4e+04;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 9
 DB 8 PAPNPSP 15
 RESULT 82
 Q9TWH0_9TRYP PRELIMINARY; PRT; 18 AA.
 ID Q9TWH0;
 AC Q9TWH0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Histone 1.3 (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
ON NCBI_TaxID=5691;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=9537566; Pubmed=7647705; DOI=10.1016/0248-4900(96)89928-X;
RA Buril M., Schlimme W., Betschart B., Lindner H., Kampfer U.,
RT "Partial amino acid sequence and functional aspects of histone H1
proteins in Trypanosoma brucei brucei".
RL Biol. Cell 83:23-31(1995).
SQ SEQUENCE 18 AA; 1635 MW; B45007F85B67B4D CRC64;
FT NON_TER 1
FT SEQUENCE 18 AA; 2030 MW; 130F2PFE1E680B24 CRC64;
Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 2.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
Qy 3 AKGMSP 9
Db 12 AKSAPP 18
RESULT 83
QSEFY3_9BRYO PRELIMINARY; PRT; 18 AA.
ID QSEFY3;
AC QSEFY3;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN Name=rp11;
OS Polytichum pallidisetum.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Polytichopsida; Polytichales; Polytichaceae; Polytichum.
ON NCBI_TaxID=46548;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
RT "Phylogenetic significance of the rpoa loss in the chloroplast genome
of mosses".
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY886747; AM81784.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR InterPro; IPR001971; Ribosomal S11.
DR Prodom; PD001010; Ribosomal S11; 1.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
FT SEQUENCE 18 AA; 2030 MW; 130F2PFE1E680B24 CRC64;
Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 PAKGMSP 9
Db 6 PHNGCRP 13
RESULT 84
QSEFY6_9BRYO PRELIMINARY; PRT; 18 AA.
ID QSEFY6;
AC QSEFY6;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN Name=rp11;
OS Andrena rupestris.
OC Chloroplast.

OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Bryophyta;
OC Andreaeopsida; Andreales; Andreaeaceae; Andreaea.
ON NCBI_TaxID=13797;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Goffinet B., Wickett N.J., Shaw J.A., Cox C.J.;
RT "Phylogenetic significance of the rpoa loss in the chloroplast genome
of mosses".
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY886745; AM81779.1; -; Genomic_DNA.
DR GO; GO:0009507; C:chloroplast; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR InterPro; IPR001971; Ribosomal S11.
DR Prodom; PD001010; Ribosomal S11; 1.
KW Chloroplast; Ribosomal protein.
FT NON_TER 1
FT SEQUENCE 18 AA; 2088 MW; 130D426E1E680B24 CRC64;
Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 PAKGMSP 9
Db 6 PHNGCRP 13
RESULT 85
Q8SKY0_CUSRB
ID Q8SKY0_CUSRB PRELIMINARY; PRT; 18 AA.
AC Q8SKY0;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Ribosomal protein S11 (Fragment).
GN Name=rp11;
OS Cuscuta reflexa (southern Asian dodder).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC asterids; lamiales; Solanales; Convolvulaceae; Cuscutaeae; Cuscuta.
ON NCBI_TaxID=4129;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Berg S.;
RT "Sequence analysis and coding potential of the holoparasitic flowering
plant genus Cuscuta".
RL Thesis (2002), Department of Institute of Botany,
RL Christian-Albrechts-University, Kiel, Germany.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Krause K., Berg S., Krupinska K.;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the EMBL/GenBank protein S11P family.
DR EMBL; AJ433611; C628796.1; -; Genomic_DNA.
DR GO; GO:0005840; C:ribosome; IEA.
DR GO; GO:0003735; P:structural constituent of ribosome; IEA.
DR GO; GO:0006412; P:protein biosynthesis; IEA.
DR InterPro; IPR001971; Ribosomal S11.
DR Pfam; PF00411; Ribosomal S11; 1.
DR Prodom; PD001010; Ribosomal S11; 1.
KW Ribonucleoprotein; Ribosomal protein.
FT NON_TER 1
FT SEQUENCE 18 AA; 2088 MW; 130D427BF680B24 CRC64;
Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 50.0%; Pred. No. 2.5e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
Qy 2 PAKGMSP 9
Db 6 PHNGCRP 13

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RESULT 86
O9OV98_9MURI PRELIMINARY; PRT; 18 AA.
ID O9OV98_9MURI
AC O9OV98;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-MAY-2000 (TREMBLrel. 13, Last annotation update)
DE Vitronectin (Fragment).
OS Mus sp..
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10095;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=93155525; PubMed=7679136; DOI=10.1111/1523-1747.ep12462792;
RA Dahlback K., Wolf H.C., Dahlback B.;
RT "Vitronectin in mouse skin: immunohistochemical demonstration of its
RT association with cutaneous amyloid."
RL J. Invest. Dermatol. 100:166-170 (1993).
SQ SEQUENCE 18 AA, 1961 MW, 99ECB76571B6EC94 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 18;
Best Local Similarity 26.7%; Pred. No. 2.5e+04;
Matches 4; Conservative 3; Mismatches 8; Indels 0; Gaps 0;

OY 1 DPAKMSPPGFIYGE 15
: ||| :
Db 4 ESKKGRXQGFPMASK 18

RESULT 87
FIBA_ANTAM
ID FIBA_ANTAM STANDARD; PRT; 19 AA.
AC P14440;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
OS Name=FGA;
GN Antilocapra americana (Pronhorn).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Antilocapridae; Antilocapra.
OX NCBI_TaxID=9891;
RN [1]
RP PROTEIN SEQUENCE.
RA Mross G.A., Doolittle R.F.;
RT "Amino acid sequence studies on aridodacty fibrinopeptides."
RL Arch. Biochem. Biophys. 122:674-684 (1967).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC are in head to head conformation with the N-termini in a small
CC central domain (by similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central module to the C-terminal domains
CC (distal nodules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

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CC -----
CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
KW PEPTIDE 1 19 Fibrinopeptide A.
FT NON_TER 19
SQ SEQUENCE 19 AA, 1758 MW, 8BBA0873C861F375 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 55.6%; Pred. No. 2.7e+04;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 1 DPAKMSPP 9
: ||| :
Db 5 DPVGGSHP 13

RESULT 88
FIBA_BISBO
ID FIBA_BISBO STANDARD; PRT; 19 AA.
AC P14441;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
OS Name=FGA;
GN Bison bonasus (European bison).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bison.
OX NCBI_TaxID=9902;
RN [1]
RP PROTEIN SEQUENCE.
RA Blomback B., Grondahl N.J.;
RT "Studies on fibrinopeptides from mamale."
RL Acta Chem. Scand. 19:1789-1791 (1965).
CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC polymerize into fibrin and acting as a cofactor in platelet
CC aggregation.
CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC are in head to head conformation with the N-termini in a small
CC central domain (by similarity).
CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC chains connects the central module to the C-terminal domains
CC (distal nodules). The long C-terminal ends of the alpha chains
CC fold back, contributing a fourth strand to the coiled coil
CC structure.
CC -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC which cleaves fibrinopeptides A and B from alpha and beta chains,
CC and thus exposes the N-terminal polymerization sites responsible
CC for the formation of the soft clot.
-----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

CC Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
KW PEPTIDE 1 19 Fibrinopeptide A.
FT NON_TER 19
SQ SEQUENCE 19 AA, 1836 MW, 9BA55A0F47B59C5 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

OY 1 DPAKG 5
: ||| :
Db 5 DPAKG 9

RESULT 89
FIBA_MUNMU

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ID  FTBA_MUNMU  STANDARD;  PRT;  19 AA.
AC  P1457;
DT  01-JAN-1990 (Rel. 13, Created)
DT  01-JAN-1990 (Rel. 13, Last sequence update)
DE  01-FEB-2005 (Rel. 46, Last annotation update)
DE  Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
GN  Name=FGA;
OS  Muntiacus muntjak (Muntjak).
OC  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC  Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC  Pecora; Cervidae; Muntiacinae; Muntiacus.
OX  NCBI_TaxID=9888;
RN  [1]
RP  PROTEIN SEQUENCE.
RA  Mross G.A., Doolittle R.F.;
RT  "Amino acid sequence studies on arctiodactyl fibrinopeptides.";
RL  Arch. Biochem. Biophys. 122:674-684(1967).
CC  -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
CC  polymerize into fibrin and acting as a cofactor in platelet
CC  aggregation.
CC  -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
CC  nonidentical chains (alpha, beta and gamma). The 2 heterotrimers
CC  are in head to head conformation with the N-termini in a small
CC  central domain (By similarity).
CC  -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
CC  chains connects the central node to the C-terminal domains
CC  (distal nodes). The long C-terminal ends of the alpha chains
CC  fold back, contributing a fourth strand to the coiled coil
CC  structure.
CC  -1- PTM: Conversion of fibrinogen to fibrin is triggered by thrombin,
CC  which cleaves fibrinopeptides A and B from alpha and beta chains,
CC  and thus exposes the N-terminal polymerization sites responsible
CC  for the formation of the soft clot.
CC  -----
CC  This Swiss-Prot entry is copyright. It is produced through a collaboration
CC  between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use as long as its content is in no way modified and this statement is not
CC  removed.
CC  -----
KW  Blood coagulation; Coiled coil; Direct protein sequencing; Plasma.
FT  PEPTIDE 1 19 Fibrinopeptide A.
FT  NON_TER 19 19
SQ  SEQUENCE 19 AA; 1822 MW; 9BA1662873B45B5 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 19;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DPAKG 5
DB 5 DPASG 9

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RA  Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
RA  Munco J., Pacleb J., Paragas V., Park S., Phouanavong S., Wan K.,
RA  Yu C., Lewis S.B., Rubin G.M., Ceiniker S.;
RA  Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR  EMBL; AY061040; AL28588.1; -; mRNA.
DR  FLYbase; FBgn0050011; CG30011.
DR  FLYbase; FBgn0050011; Gen.
SQ  SEQUENCE 19 AA; 2105 MW; 07A74ED38EA1A7F3 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 GMSPPGRT 12
DB 6 GFSKPRPV 13

RESULT 91
ID  Q9N613_TOXGO  PRELIMINARY;  PRT;  19 AA.
AC  Q9N613;
DT  01-OCT-2000 (TEMBLrel. 15, Created)
DT  01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT  01-FEB-2005 (TEMBLrel. 29, Last annotation update)
DE  Beta-tubulin (Fragment).
GN  Name=TUB2;
OS  Toxoplasma gondii.
OC  Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC  Toxoplasma.
OX  NCBI_TaxID=5811;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RX  MEDLINE=21011398; PubMed=11128519;
RA  Lehmann T., Blackston C.R., Parmley S.F., Remington J.S., Dubey J.P.;
RT  "Strain typing of Toxoplasma gondii: comparison of antigen-coding and
RT  housekeeping genes.";
RL  J. Parasitol. 86:960-971(2000).
DR  EMBL; AF249703; AAF79161.1; -; Genomic DNA.
DR  EMBL; AF249702; AAF79160.1; -; Genomic DNA.
DR  EMBL; AF249701; AAF79159.1; -; Genomic DNA.
FT  NON_TER 1 1
FT  NON_TER 19 19
SQ  SEQUENCE 19 AA; 1995 MW; 5BDD964EDB7CED73 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 19;
Best Local Similarity 36.4%; Pred. No. 2.7e+04;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 GMSPPGRTVGB 15
DB 8 GIDPTGYCGD 18

RESULT 92
ID  O63058_LATCL  PRELIMINARY;  PRT;  19 AA.
AC  O63058;
DT  01-AUG-1998 (TEMBLrel. 07, Created)
DT  01-AUG-1998 (TEMBLrel. 07, Last sequence update)
DT  01-JUN-2003 (TEMBLrel. 24, Last annotation update)
DE  Ribosomal protein S11 (Fragment).
GN  Name=rpS11;
OS  Lathraea clandestina (Purple toothwort).
OC  Chloroplast.
OC  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC  asterids; Lamiales; Lamiaceae; Orobanchaceae;
OC  Orobanchaceae incertae sedis; Lathraea.
OX  NCBI_TaxID=41911;
RN  [1]
RP  NUCLEOTIDE SEQUENCE.
RA  Lusson N., Delavault P., Thalonarn P.;

```

RT "The rbcL gene from *Lathraea* (holoparasitic) is not transcribed by a
 RT plasmid-encoded RNA polymerase."
 RT Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: Belongs to the ribosomal protein S11P family.
 DR EMBL: AF039983; AAC16521.1; -, Genomic_DNA.
 DR GO: GO:0005907; C:chloroplast; IEA.
 DR GO: GO:0005840; C:ribosome; IEA.
 DR GO: GO:0003735; F:structural constituent of ribosome; IEA.
 DR GO: GO:0006412; F:protein biosynthesis; IEA.
 DR InterPro: IPR01971; Ribosomal_S11.
 DR Pfam: PF00411; Ribosomal_S11; I.
 DR ProDom: PD001010; Ribosomal_S11; 1.
 KW Chloroplast; Ribonucleoprotein; Ribosomal protein.
 FT NON_TER 1 1
 SQ SEQUENCE 19 AA; 2245 MW; 130D2AB3FE680B24 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 2.7e+04;
 Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 9
 Db 7 PANCGCRP 14
 RESULT 93
 Q9R5C8_PSEAE PRELIMINARY; PRT; 19 AA.
 AC Q9R5C8;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE Quinoprotein ethanol dehydrogenase (Fragment).
 OS Pseudomonas aeruginosa.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Pseudomonadaceae; Pseudomonas.
 OX NCBI_TaxID=287;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93176105; PubMed=8382472;
 RA Schover J.M., Frank J., van Wierink J.E., Dune J.A.;
 RT "Quaternary structure of quinoprotein ethanol dehydrogenase from
 RT Pseudomonas aeruginosa and its reoxidation with a novel cytochrome c
 RT from this organism."
 RL Biochem. J. 290:123-127(1993).
 DR PIR: S29766; S29766
 SQ SEQUENCE 19 AA; 1896 MW; F58A0AB5EA077835 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 57.1%; Pred. No. 2.7e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 KGMSPPG 10
 Db 12 KGLEPLG 18
 RESULT 94
 Q9AK02_MOUSE PRELIMINARY; PRT; 19 AA.
 AC Q9AK02;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2003 (TREMBLrel. 25, Last annotation update)
 DE Fructose-1,6-bisphosphatase (EC 3.1.3.11) (Fragment).
 GN Name=FBP2; Synonym=FBPase 2;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Skeletal muscle;
 RX MEDLINE=20237676; PubMed=10773464; DOI=10.1016/S0378-1119(00)00079-2;
 RA Tilmann H., Stein S., Liehr T., Beschrich K.;
 RT "Structure and chromosomal localization of the human and mouse muscle
 RT fructose-1,6-bisphosphatase genes."
 RL Gene 247:241-253(2000).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Skeletal muscle;
 RA Stein S.;
 RT "Mouse liver fructose-1,6-bisphosphatase: Gene structure,
 RT transcriptional start point, chromosomal localization, cDNA cloning,
 RT characterization of the recombinant protein, and analysis of tissue-
 RT specific expression."
 RL Arch. Biochem. Biophys. 0:0-0(0).
 DR EMBL: AJ243027; CAB90674.1; -, Genomic_DNA.
 DR HSBP; P06366; INTY.
 DR MGI; MGI:95491; FBP2.
 DR GO: GO:0042132; F:fructose-bisphosphatase activity; IEA.
 DR GO: GO:0016787; F:hydrolase activity; IEA.
 DR GO: GO:0042578; F:phosphoric ester hydrolase activity; IEA.
 DR GO: GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro: IPR00146; In_FB_phphtase.
 DR Pfam: PF00316; FBpase; I.
 DR ProDom: PD001491; In_FB_phphtase; 1.
 KW Carbohydrate metabolism; Hydrolase.
 FT NON_TER 1 1
 SQ SEQUENCE 19 AA; 2084 MW; AD2C153F5A375C18 CRC64;
 Query Match 21.9%; Score 23; DB 2; Length 19;
 Best Local Similarity 55.6%; Pred. No. 2.7e+04;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 2 PAKGMSPP 10
 Db 10 PANCKSPNG 18
 RESULT 95
 PSAF_MAIZE STANDARD; PRT; 20 AA.
 AC P13193;
 DT 01-JAN-1990 (Rel. 13, Created)
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE Photosystem I reaction centre subunit III (Light-harvesting complex I
 DE 17 kDa protein) (PSI-F) (Fragment).
 GN Name=PSAF;
 OS Zea mays (Maize).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
 OX NCBI_TaxID=4577;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC STRAIN=cv. N273;
 RX MEDLINE=90033290; PubMed=2680596; DOI=10.1016/0014-5793(89)81737-5;
 RA Anandan S., Vainstein A., Thorner J.P.;
 RT "Correlation of some published amino acid sequences for photosystem I
 RT polypeptides to a 17 kDa LHCI pigment-protein and to subunits III and
 RT IV of the core complex."
 RL FEBS Lett. 256:150-154(1989).
 CC -1- FUNCTION: Probably participates in efficiency of electron transfer
 CC from plastocyanin to P700 (or cytochrome 653 in algae and
 CC cyanobacteria). This plastocyanin-docking protein contributes to
 CC the specific association of plastocyanin to PSI.
 CC -1- SUBCELLULAR LOCATION: Associated with luminal side of the
 CC thylakoid membrane.
 CC -1- SIMILARITY: Belongs to the psaf family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -

CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR PIR, S06150, S06150.
 DR Gramene, P13193, -.
 DR MaltzDB, 69542, -.
 KW Chloplast, Direct protein sequencing; Membrane; Photosynthesis;
 KW Photosystem I; Thylakoid.
 FT NON_TER 20
 SO SEQUENCE 20 AA; 2112 MW; P0499F98F6188997 CRC64;

Query Match 21.9%; Score 23; DB 1; Length 20;
 Best Local Similarity 60.0%; Pred. No. 2.8e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 GMSPP 9
 DB 4 GLRTP 8

RESULT 96

ID Q8NBD5_HUMAN PRELIMINARY; PRT; 20 AA.
 AC Q8NBD5;
 DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 OC Homo.
 NCBI_TaxID=9606;
 RN (1)
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Testis;
 RA Strausberg R.;
 RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC031977; AAH31977.1; -, mRNA.
 KW Hypothetical protein.
 FT NON_TER 1
 SO SEQUENCE 20 AA; 2235 MW; D4992395BE26BC CRC64;

Query Match 21.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.8e+04;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 GIVGSE 16
 DB 14 GWALGE 20

RESULT 97

ID Q7M264_LOLPR PRELIMINARY; PRT; 20 AA.
 AC Q7M264;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE 50K allergen (Fragment).
 OS Lolium perenne (Perennial ryegrass).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Poaceae; Lolium.
 NCBI_TaxID=4522;
 RN (1)
 RP PROTEIN SEQUENCE.
 RA MEDLINE=94092339; PubMed=7505588;
 RA Petersen A., Schramm G., Becker W.M., Schlaak M.;
 RT "Comparison of four grass pollen species concerning their allergens of
 RT grass group V by 2D immunoblotting and microsequencing.";
 RL Biol. Chem. Hoppe-Seyler 374:855-861(1993).

DR PIR, S38288, S38288.
 FT NON_TER 1
 FT NON_TER 20
 SO SEQUENCE 20 AA; 1742 MW; 15C8174B4B49D8C CRC64;

Query Match 21.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.8e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8
 DB 13 PAAGATP 19

RESULT 98

ID Q9S8J1_TRIKI PRELIMINARY; PRT; 20 AA.
 AC Q9S8J1;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Intracellular basic DEFENSE-related protein class III chitinase
 DE homolog (Fragment).
 OS Trichosanthes kirilowii (Mongolian snake-gourd).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC Eusoids I; Cucurbitales; Cucurbitaceae; Trichosanthes.
 NCBI_TaxID=3677;
 RN (1)
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95125116; PubMed=7824645; DOI=10.1104/pp.106.3.1195;
 RA Savary B.J., Flores H.E.;
 RT "Biosynthesis of defense-related proteins in transformed root cultures
 RT of Trichosanthes kirilowii Maxim. var japonicum (Kittam.).";
 RL Plant Physiol. 106:1195-1204(1994).
 SO SEQUENCE 20 AA; 2025 MW; 3B45284BBA44BB62 CRC64;

Query Match 21.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 71.4%; Pred. No. 2.8e+04;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 14 GREGVLS 20
 DB 12 GNEGSL 18

RESULT 99

ID Q9S8Y0_PHLPR PRELIMINARY; PRT; 20 AA.
 AC Q9S8Y0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE Allergen PHL p V (Fragment).
 OS Phleum pratense (Common timothy).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Aveneae; Phleum.
 NCBI_TaxID=15957;
 RN (1)
 RP PROTEIN SEQUENCE.
 RX MEDLINE=92353723; PubMed=1643437;
 RA Petersen A., Becker W.M., Schlaak M.;
 RT "Characterization of isoforms of the major allergen Phl p V by two-
 RT dimensional immunoblotting and microsequencing.";
 RL Int. Arch. Allergy Immunol. 98:105-109(1992).

Query Match 21.9%; Score 23; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 2.8e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 PAKGMP 8

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OW protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 45.3462 Seconds
(without alignments)
116.273 Million cell updates/sec

Title: US-09-662-293-5

Perfect score: 67

Sequence: 1 DEKNSPECTLGP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 244163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Listing first 100 summaries

Database :

1: A_Genseq_21:*
2: geneseqdp1980s:*
3: geneseqdp1990s:*
4: geneseqdp2000s:*
5: geneseqdp2001s:*
6: geneseqdp2002s:*
7: geneseqdp2003as:*
8: geneseqdp2004s:*
9: geneseqdp2005s:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	67	100.0	12	3	AAV52514 House dms
2	67	100.0	12	5	AAU96318 Der HMW-m
3	54	50.7	20	2	AAV26547 Erythro
4	33	49.3	13	5	ABG66059 IGE Fcpep
5	32	47.8	13	7	ADCA2730 Peptide w
6	32	47.8	13	9	ADZ37865 Human kin
7	32	47.8	13	2	AAV26489 Erythro
8	31	46.3	20	6	ABP83269 G protein
9	30	44.8	18	5	ABV15265 IGF relat
10	30	44.8	19	2	AAV01776 Active fr
11	30	44.8	19	7	ADD29130 MTN-13/I
12	30	44.8	19	7	ADK40569 KDR & VEG
13	30	44.8	19	8	ADR40787 Cyclic KD
14	30	44.8	20	2	AAV26357 Erythro
15	30	44.8	20	2	AAV13684 Erythro
16	30	44.8	20	4	AAW26998 Monomer s
17	30	44.8	20	4	AAU05347 R1 and R2
18	29	43.3	10	4	AAAG88114 Saccharom
19	29	43.3	10	4	AAAG88115 Saccharom
20	29	43.3	10	8	ADT40845 NSARS vit
21	29	43.3	10	8	ADSB0262 SARS vitu
22	29	43.3	10	8	ADT38375 hSARS vit
23	29	43.3	15	5	ABH77729 N-termina
24	29	43.3	17	9	ADU91959 EPO-R ago

25	29	43.3	17	9	ADU91965 EPO-R ago
26	29	43.3	17	9	ADU92009 EPO-R ago
27	29	43.3	19	2	AAV26490 Erythro
28	29	43.3	19	8	ADBS3404 CMET-HGF
29	29	43.3	20	2	AAV13694 Erythro
30	29	43.3	20	2	AAV13720 Erythro
31	29	43.3	20	2	AAV13685 Erythro
32	29	43.3	20	2	AAV26375 Erythro
33	29	43.3	20	2	AAV26374 Erythro
34	29	43.3	20	2	AAW27034 Monomer s
35	29	43.3	20	2	AAW27008 Monomer s
36	29	43.3	20	4	AAW26999 Monomer s
37	29	43.3	20	4	AAU05356 R1 and R2
38	29	43.3	20	4	AAU05348 R1 and R2
39	29	43.3	20	4	AAU05381 R1 and R2
40	28	41.8	9	5	ABH83243 Human ETV
41	28	41.8	9	5	ABH83232 Wild-type
42	28	41.8	9	7	ADC59364 GST bindi
43	28	41.8	9	8	ADG20335 Antigenic
44	28	41.8	9	9	ADK08674 HLA class
45	28	41.8	10	2	AAW98996 I domain
46	28	41.8	13	6	ABR91275 P. papata
47	28	41.8	14	5	ABJ00601 B lymphoc
48	28	41.8	14	5	ABG33462 B lymphoc
49	28	41.8	14	7	ADB48057 Novel hum
50	28	41.8	14	8	ADJ55612 Novel hum
51	28	41.8	15	2	AAH59893 638 Inter
52	28	41.8	15	2	AAH63075 B. t. PS63
53	28	41.8	15	2	AAW13880 N-termina
54	28	41.8	15	2	AAW73115 B. t. toxi
55	28	41.8	15	3	AAH13902 Internal
56	28	41.8	15	5	AAU10365 Bacillus
57	28	41.8	15	6	ABR30097 Human can
58	28	41.8	15	6	ABR30031 Human can
59	28	41.8	15	6	ABR30127 Human can
60	28	41.8	15	6	ABR30078 Human can
61	28	41.8	15	6	ABR329975 Human can
62	28	41.8	15	6	ABR30106 Human can
63	28	41.8	15	6	ABR30059 Human can
64	28	41.8	15	6	ABR91283 P. papata
65	28	41.8	15	6	ABR91282 P. papata
66	28	41.8	15	9	ADK08687 HLA class
67	28	41.8	16	2	AAW81961 Rat ENDO-
68	28	41.8	16	6	ABR91286 P. papata
69	28	41.8	17	6	ABR91288 P. papata
70	28	41.8	17	9	ADU92006 EPO-R ago
71	28	41.8	18	2	AAV26517 Erythro
72	28	41.8	18	2	AAW67525 IGF-1/IGF
73	28	41.8	18	2	AAW67523 IGF-1/IGF
74	28	41.8	18	4	ABH38888 Peptide #
75	28	41.8	18	4	AAW23369 Peptide #
76	28	41.8	18	4	AAW2107 Human bon
77	28	41.8	18	4	AAW59539 Human bra
78	28	41.8	18	4	ABG51793 Human liv
79	28	41.8	18	4	AAAG3760 Synthetic
80	28	41.8	18	4	AAAG3762 Synthetic
81	28	41.8	18	5	ABH57684 Human pep
82	28	41.8	18	5	ABH57681 IGFBD-3 b
83	28	41.8	18	5	ABH57684 IGFBD-3 b
84	28	41.8	18	6	ADA03290 Angiotens
85	28	41.8	18	6	ABH56660 Angiotens
86	28	41.8	18	6	ADH84843 Synthetic
87	28	41.8	18	7	ADH84845 Synthetic
88	28	41.8	18	7	ADH48156 IGFBD-3 b
89	28	41.8	18	7	ADH48158 IGFBD-3 b
90	28	41.8	18	8	ADH47647 Insulin-1
91	28	41.8	18	8	ADH47649 Insulin-1
92	28	41.8	18	8	ADG39595 IGFBD-3 b
93	28	41.8	18	8	ADG39593 IGFBD-3 b
94	28	41.8	18	8	ADL62076 IGFBD-3 b
95	28	41.8	18	8	ADL62078 IGFBD-3 b
96	28	41.8	18	8	ADL57587 Inhibitor
97	28	41.8	18	8	ADL57589 Inhibitor

98	28	41.8	18	8	AD157480	Inhibitor
99	28	41.8	18	8	AD157482	Inhibitor
100	28	41.8	18	8	ADJ56638	Inhibitor

ALIGNMENTS

RESULT 1

AAV52514 standard; peptide; 12 AA.

AAV52514;

22-PEB-2000 (first entry)

House dust mite allergen protein (map) A/B fragment map(4).

Mite allergen protein; map; high molecular weight; HMW-map; allergy;

house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

canine; veterinary; antibody; vaccine; immunisation.

Dermatophagoides farinae.

WO954349-A2.

28-OCT-1999.

16-APR-1999; 99WO-US008524.

17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098509P.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER;

WPI; 2000-052700/04.

Novel high molecular weight Dermatophagoides nucleic acid polypeptides

used to modify an animals' hypersensitivity to mite allergens.

Claim 3; Page 69; 154pp; English.

Sequences AAV52510-Y52522 represent proteolytic fragments of

Dermatophagoides farinae high molecular weight mite allergen protein (HMW

-map) composition. The HMW-map composition was isolated from a D. farinae

homogenate by gel filtration, with each fraction being analysed for the

presence of proteins that bound to IGE present in mite-allergic dog

antiserum. The HMW-map composition comprises mapA (a 109 kd protein) and

mapB (98 kd). Mite allergenic proteins and peptides, and nucleic acids

encoding them, may be used in therapeutic compositions to modify an

animal's hypersensitivity reaction to mite allergens. Animals that may be

treated include mammals and birds, especially felines, canines, equines,

humans, other pets, and work or domestic animals. The proteins or

fragments may also be used to diagnose allergies via a skin test. The

proteins and peptides can also be used to raise antibodies, which have a

variety of potential uses. For example, they can be used as vaccines to

passively immunise animals against dust mite hypersensitivity, as

positive controls in test kits and as tools to recover desired dust mite

allergens from a mixture of proteins

Sequence 12 AA;

SQ

Query Match

Best Local Similarity 100.0%; Score 67; DB 3; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DEKNSPECTILGP 12

1 DEKNSPECTILGP 12

DB

1 DEKNSPECTILGP 12

RESULT 2

AAU96318 standard; peptide; 12 AA.

AAU96318;

15-JUL-2002 (first entry)

Der HMW-map polypeptide #5.

Der HMW-map; American house dust mite; anti-allergic; mite; IGE;

mite allergenic protein; immunoglobulin E; hypersensitivity;

immunocomplex formation.

Dermatophagoides farinae.

WO200222807-A2.

21-MAR-2002.

14-SEP-2001; 2001WO-US028730.

PR 14-SEP-2000; 2000US-00662293.

(HESK-) HESKA CORP.

Mccall CA, Hunter SW, Weber ER;

WPI; 2002-351888/38.

New mite allergenic protein isolated from Dermatophagoides, designated

Der HMW-map protein, useful as a vaccine for treating mite allergy.

Claim 12; Page 70; 161pp; English.

The invention relates to an isolated mite allergenic protein of

Dermatophagoides, designated Der HMW-map protein, and its related nucleic

acid. The Der HMW-map protein is useful for eliciting an immune response

against Der HMW-map protein. The protein or a reagent comprising a non-

proteinaceous epitope is useful for identifying an animal (e.g., dog,

cat) susceptible to or having an allergic response to a mite. A

therapeutic composition is useful for desensitising a host animal to an

allergic response to a mite. The DNA and protein can be used in the

detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

of immunoglobulin (Ig) E or Der HMW-map protein activity associated with a

disease. Antibodies that bind to Der HMW-map are useful for inhibiting

binding of proteins to IGE, to prevent immunocomplex formation, thus

reducing hypersensitivity responses to mite allergens, and as vaccines

against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

represent Der HMW-map polypeptides of the invention

Sequence 12 AA;

SQ

Query Match

Best Local Similarity 100.0%; Score 67; DB 5; Length 12;

Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY

1 DEKNSPECTILGP 12

1 DEKNSPECTILGP 12

DB

1 DEKNSPECTILGP 12

RESULT 3

AAV26547

AAV26547 standard; peptide; 20 AA.

AAV26547;

06-SEP-1999 (first entry)

Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX Synthetic.
 OS
 PN WO640749-A1.
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009910.
 XX
 PR 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.
 XX
 PA (JOHN) JOHNSON & JOHNSON CORP.
 PA (AFY-) AFYMAX TECHNOLOGIES NV.
 XX
 PI Wighton NC, Dower WJ, Chang RS, Kaehny AK, Jolliffe LK;
 PI Johnson D, Mulcahy L;
 XX
 DR WPI, 1997-052225/05.
 XX
 PT Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 XX
 PS Disclosure; Page 26; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS; autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptide can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AY6352-548 are representative peptides
 CC falling within the above peptide motif and isolated during the affinity
 CC selection process
 CC
 CC Sequence 20 AA;
 SO
 Query Match 50.7%; Score 34; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 95;
 Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 Oy 3 KNSPECTLGP 12
 Db 2 KNNYRCQFEP 11
 RESULT 4
 ABG66059
 ID ABG66059 standard; peptide; 18 AA.
 XX
 AC ABG66059;
 XX
 DT 29-AUG-2002 (first entry)
 XX
 DE IGB Receptor RI binding peptide from phage displayed g8 library #9.
 XX
 KW IGB receptor; immunoglobulin; ReceptorRI; antagonist; phage display;
 KW protein co-ordinate data; IGB-mediated disease; allergic rhinitis;
 KW asthma; allergic asthma; atopic dermatitis; urticaria-angioedema;

KW parasitic infection; IGB myeloma; immune-related disorder;
 KW inflammatory disorder; diabetes mellitus; reperfusion injury; stroke;
 KW IGB-mediated gastrointestinal inflammatory disease; burn;
 KW immune rejection of graft; myocardial infarction; atherosclerosis;
 KW acute lung injury; haemorrhagic shock; septic shock;
 KW acute tubular necrosis; endometriosis; degenerative joint disease;
 KW pancreatitis.
 XX
 OS Synthetic.
 OS
 PN WO200226781-A2.
 PD 04-APR-2002.
 XX
 PF 26-SEP-2001; 2001WO-US030289.
 XX
 PR 26-SEP-2000; 2000US-0235353P.
 PR 23-MAR-2001; 2001US-0278540P.
 XX
 PA (GETH) GENENTECH INC.
 PA
 XX Lowman HB, Reynolds ME, Nakamura GR, Starovashnik MA;
 PI WPI, 2002-444016/47.
 XX
 DR A peptide useful for treating a IGB-mediated disease or disorder in a
 PT host e.g. allergic rhinitis, asthma, which competes with immunoglobulin B
 PT for binding to high affinity IGB receptor in an in vitro assay.
 XX
 PS Example 1; Page 79; 328pp; English.
 XX
 CC The invention relates to a peptide which competes with immunoglobulin
 CC (Ig) B 134 comprising a sequence (S1), for binding the high affinity IGB
 CC receptor (ReceptorRI) in an in vitro assay and having a formula given in
 CC the specification. Also included are a fusion protein comprising the
 CC peptide, a pharmaceutical composition (C) comprising the peptide,
 CC designing a compound that mimics the three-dimensional surface structure
 CC of the peptide, a compound with a solvent accessible surface that mimics
 CC the solvent accessible surface defined by the side chains of residues (R)
 CC Pro4, Phe6, Pro16, Cys3, Cys7, Cys15 and Cys19 of IGB134, a peptide with
 CC structural coordinates as given in the specification, selecting a peptide
 CC mimetic which binds to ReceptorRI and blocks binding of IGB and a
 CC peptide mimetic which mimics the coordinates of IGB134 residues (R). (C)
 CC is useful for inhibiting the binding of IGB to high affinity IGB receptor
 CC (ReceptorRI). Peptides of the formula given in the specification are
 CC useful for inhibiting the binding of an IGB to high affinity IGB
 CC receptor. The peptide is useful for selecting a molecule which blocks the
 CC interaction of IGB with high affinity IGB receptor. The peptide is also
 CC useful for inhibiting the activation of high affinity IGB receptor. The
 CC peptide is useful for treating an IGB-mediated disease or disorder in a
 CC host. (C) is useful in research, diagnostic, therapeutic and prophylactic
 CC methods. The peptide is also useful for inhibiting IGB-mediated or
 CC associated processes such as IGB-dependent activation and degranulation
 CC of mast cells and basophils, as well as consequent release of
 CC inflammatory mediators such as histamine. (C) is useful for treating
 CC allergic rhinitis, asthma (e.g. allergic asthma), atopic dermatitis,
 CC urticaria-angioedema, parasitic infection, IGB myeloma, immune-related
 CC disorders, inflammatory disorders, diabetes mellitus, IGB-mediated
 CC gastrointestinal inflammatory disease, immune rejection of grafts,
 CC reperfusion injury, stroke, myocardial infarction, atherosclerosis, acute
 CC lung injury, haemorrhagic shock, burn, septic shock, acute tubular
 CC necrosis, endometriosis, degenerative joint disease and pancreatitis. The
 CC present sequence is a peptide of the invention expressed from a phage
 CC display library
 CC
 CC Sequence 18 AA;
 SO
 Query Match 49.3%; Score 33; DB 5; Length 18;
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 Oy 4 NSPECTLGP 12
 I | | | | |

Db 1 NYECCWGP 9

RESULT 5
ADC42730
ID ADC42730 standard; peptide; 13 AA.
XX
AC ADC42730;
XX
DT 18-DEC-2003 (first entry)
XX
DE Peptide with potential MHC classII binding activity #15.
XX
KW human factor IX; FIX; human.
XX
OS Homo sapiens.
XX
PN WO2003020764-A2.
XX
PD 13-MAR-2003.
XX
PF 30-AUG-2002; 2002WO-EP009717.
XX
PX 04-SEP-2001; 2001EP-00121154.
XX
PA (MERB) MERCK PATENT GMBH.
XX
PI Carr FU, Carter G;
XX
DR WPI; 2003-300864/29.
XX
PT Novel modified human factor IX molecule for therapeutic use, is
PT substantially non-immunogenic or less immunogenic than any non-modified
PT molecule having the same biological activity when used in vivo.
XX
PS Disclosure; SEQ ID NO 16; 49pp; English.
XX
CC The invention relates to a modified molecule having the biological
CC activity of human factor IX (FIX) and being substantially non-immunogenic
CC or less immunogenic than any non-modified molecule having the same
CC biological activity when used in vivo. The present sequence represents a
CC peptide from FIX with potential MHC class II binding activity.
XX
SQ Sequence 13 AA;

Query Match 47.8%; Score 32; DB 7; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 1 DEKNSPEC 8
| : ||| |
1 DDINSYEC 8

Db 1 DDINSYEC 8

RESULT 6
AD237865
ID AD237865 standard; peptide; 13 AA.
XX
AC AD237865;
XX
DT 30-JUN-2005 (first entry)
XX
DE Human kinase substrate peptide SEQ ID 795.
XX
KW kinase; substrate; drug delivery; cancer; restenosis; osteoporosis;
KW rheumatoid arthritis; asthma; psoriasis; inflammatory bowel disease;
KW systemic lupus erythematosus; multiple sclerosis; transplant rejection;
KW neoplasm; cytostatic; vasotropic; cardiovascular disease; osteopathic;
KW degeneration; endocrine disease; musculoskeletal disease;
KW antiinflammatory; inflammation; autoimmune disease; immunosuppressive;
KW immune disorder; antiarthritic; antirheumatic; antiasthmatic;
KW respiratory disease; antipsoriatic; dermatological disease;
KW gastrointestinal-gen.; gastrointestinal disease; neuroprotective;

KW neurological disease; dermatological; dermatological disease.
XX
OS Homo sapiens.
XX
PN WO2005035003-A2.
XX
PD 21-APR-2005.
XX
PF 22-SEP-2004; 2004WO-US031148.
XX
PX 22-SEP-2003; 2003US-0505325P.
XX
PR 04-MAY-2004; 2004US-0568340P.
XX
PR 22-JUN-2004; 2004US-0581835P.
XX
PA (DIHE-) DIHEDRON CORP.
XX
PI Ballatore C, Gaetellino AJ, Desharnais J, Guo Z, Li Q, Newman MJ;
PI Sun C;
XX
DR WPI; 2005-315493/32.
XX
PT New conjugate used for treating aberrant cellular activation, migration,
PT proliferation or survival condition such as cancer, comprises drug and
PT substrate for protein or lipid kinase linked to protein, optionally by
PT non-releasable linker.
XX
PS Disclosure; SEQ ID NO 795; 407pp; English.
XX
CC The invention relates to a conjugate (I) comprising a drug and a
CC substrate for a protein kinase or a lipid kinase non-releasably linked to
CC it, optionally by a non-releasable linker. Also included are preparing
CC pacitaxel C10 carbamate of formula (8a) (which comprises reacting a
CC pacitaxel compound of formula (5a) with a carbodiimide compound and
CC reacting the obtained compound of formula (6a) with an amine of formula
CC X, all formulae given in the specification), a pharmaceutical composition
CC (PCI) comprising (I) and a carrier, an article (comprising packaging
CC material, (I) or its derivatives, for treatment/prevention/amelioration
CC of one or more symptoms (associated with aberrant cellular activation,
CC migration, proliferation or survival (ACMPs) and a label that indicates
CC that (I) is used for treatment, prevention or amelioration of one or more
CC symptoms associated with ACMPs), and a peptide comprising an kinase
CC substrate peptide. The conjugate has improved cytotoxic selectivity index
CC as compared to an unconjugated drug. The conjugate is useful for treating
CC conditions caused by ACMPs characterized by undesirable or aberrant
CC activation, migration, proliferation or survival of tumor cells,
CC endothelial cells, B cells, T cells, macrophages, neutrophils, other
CC eosinophils, basophils, monocytes, platelets, fibroblasts, other
CC connective tissue cells, osteoblasts, osteoclasts and progenitors of
CC these cell types. The ACMPs condition is a cancer, coronary restenosis,
CC osteoporosis, chronic inflammation or autoimmune disease. The
CC autoimmune disease is rheumatoid arthritis, asthma, psoriasis,
CC inflammatory bowel disease, systemic lupus erythematosus, systemic
CC dermatomyositis, inflammatory ophthalmic diseases, autoimmune hematologic
CC disorders, multiple sclerosis, vasculitis, idiopathic nephrotic syndrome,
CC transplant rejection or graft versus host disease. The cancer is non-
CC small cell lung cancer, head squamous cancer, neck squamous cancer,
CC colorectal cancer, prostate cancer, breast cancer, acute lymphocytic
CC leukemia, adult acute myeloid leukemia, adult non-Hodgkin's lymphoma,
CC brain tumor, cervical cancer, childhood cancer, childhood sarcoma,
CC chronic lymphocytic leukemia, chronic myeloid leukemia, esophageal
CC cancer, hairy cell leukemia, kidney cancer, liver cancer, multiple
CC myeloma, neuroblastoma, oral cancer, pancreatic cancer, primary central
CC nervous system lymphoma, skin cancer or small-cell lung cancer. The
CC cancer is brain stem glioma, cerebellar astrocytoma, cerebral
CC astrocytoma, ependymoma, Ewing's sarcoma, germ cell tumor, Hodgkin's
CC disease, acute myelogenous leukemia, acute lymphoblastic leukemia, liver
CC cancer, medulloblastoma, neuroblastoma, non-Hodgkin's lymphoma,
CC osteosarcoma, malignant fibrous histiocytoma of bone, retinoblastoma,
CC rhabdomyo sarcoma, soft tissue sarcoma, supratentorial primitive
CC neuroectodermal and pineal tumors, visual pathway and hypothalamic
CC glioma, Wilms' tumor or other childhood kidney tumor. The cancer is
CC originated from or has metastasized to the bone, brain, breast, digestive
CC and gastrointestinal system, endocrine system, blood, lung, respiratory

CC system, thorax, musculoskeletal system, or skin. The cancer is selected
CC from breast cancer, lung cancer, prostate cancer, ovarian cancer,
CC esophageal cancer, bladder cancer, hepatoma, neuroblastoma, lymphoma,
CC testicular cancer, renal cancer, leukemia, colorectal cancer and head
CC neck cancer. The conjugate is useful for identifying kinase substrates
CC capable of selectively accumulating in a target system. The conjugate is
CC useful for identifying conjugates capable of exhibiting selective
CC toxicity against a target system. The conjugate is useful for enhancing
CC drug efficiency. The present sequence is kinase substrate peptide useful
CC in the conjugate of the invention.

Sequence 13 AA;

Query Match	47.8%	Score 32	DB 9	Length 13
Best Local Similarity	62.5%	Pred. NO.	1.4e+02	
Matches	5	Conservative	2	Mismatches 1
				Indels 0
				Gaps 0

QY	1	DEKNSPEC	8
		: :	
Db	4	DDINSYEC	11

RESULT 7
AAAY26489
ID AAAY26489 standard; peptide; 19 AA
...

AC AY26489

DT 06-SEP-1999 (first entry)

DE Erythropoietin receptor (EPO-R) binding peptide

KM Erythropoietin; EPO, receptor; EPO deficiency; renal failure; AIDS;
KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KM malignancy; beta-thalassaemia; cystic fibrosis; prematurity; blood loss
KM spinal cord injury; aging; neoplastic disease; erythropoietin; EPO-R.

Synthetic

PN WO9640749-A1

PD 19-DEC-1996

PF 07-JUN-1996; 96WO-US009810.

PR 07-JUN-1995; 95US-00484631.

XX

PA (AFY-) AFYMAX TECHNOLOGIES NV.

PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;

XX

PT Erythropoietin receptor binding peptide - useful for treating disorders
PT characterised by deficiency of EPO, or low or defective red blood cell
PT population.

P8 Disclosure; Page 23; 95pp; English.

The invention describes a peptide of 10-40 amino acid residues which binds to erythropoietin (EPO) receptor and which includes the amino acid sequence Cys-Xaa1-Xaa2-Gly-Thr-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg, His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally, the peptide may be cyclised or dimerised. The peptide can be used to treat a patient having a disorder characterised by a deficiency of EPO or a low or defective red blood cell population. It can be used to treat end stage renal failure or dialysis; anaemia associated with AIDS, autoimmune disease, chronic inflammatory diseases or malignancy; beta-thalassaemia; cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute

CC blood loss, aging, and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAY6332-548 are representative peptides
 CC falling within the above peptide motif and isolated during the affinity
 CC selection process
 CC

SQ Sequence 19 AA;

Query Match	47.8%	Score 32	DB 2	Length 19
Best Local Similarity	40.0%	Pred. No. 2e+02		
Matches 4	Conservative 3	Mismatches 3	Indels 0	Gaps 0

```

QY      3 KNSFECILGP 12
        |  ::|  ::||
Db      2 KTKYKCYMGP 11

```

RESULT 8
ABP83269
ID ABP83269 standard; peptide; 20 AA

AC ABP83269;

DT 04-MAR-2003 (first entry)

DB G protein-coupled receptor (GPCR) antigenic peptide SEQ ID NO:1942.

KW G protein-coupled receptor; GPCR; antigenic peptide; gene therapy;

KW growth-related disease; cell regeneration-related disease; AIDS; cancer

KW Alzheimer's disease; atherosclerosis; infection; osteoarthritis; allergy;

KW graft versus host disease; Parkinson's disease; multiple sclerosis; pain;

KW mental retardation; epilepsy; asthma; tuberculosis; obesity; nausea;

KW ulcer.

Homo sapiens.

PN W0200261087-A2.

PD 08-AUG-2002.

PF 19-DEC-2001; 2001WO-US050107.

PR 19-DEC-2000; 2000US-0257144P

PA (LIFB-) LIFESPAN BIOSCIENCES INC.

PI Butner GC, Roush CL, Brown JP;

DR WPI; 2003-046718/04

PT New isolated antigenic peptides e.g., for G protein-coupled receptors
PT (GPCR), useful for diagnosing and designing drugs for treating conditions
PT in which GPCRs are involved, e.g. AIDS, Alzheimer's disease, cancer or
PT autoimmune diseases.

PS Claim 1; Fig 2; 523pp; English.

The invention describes antigenic peptides (1) comprising: (a) any one of 1601 sequences (see ABB82019 to ABB83619) of 12-24 amino acids. Also described: (1) an assay for the detection of a particular G protein-coupled receptor (GPCR) or a candidate polypeptide in a sample; and (2) an isolated antibody having high specificity and high affinity or avidity for a particular GPCR. (1) can be used as GPCR modulators and in gene therapy. The antigenic peptides for GPCRs are useful in detecting an antibody against a particular GPCR, and in the production of specific antibodies. The peptides and antibodies are also useful for detecting the presence or absence of corresponding GPCRs. The antigenic peptides for

CC GPCRs and antibodies are useful for diagnosing and designing drugs for
CC creating immune-related diseases, growth-related diseases, cell
CC regeneration-related disease, immunological-related cell proliferative
CC diseases, or autoimmune diseases, e.g. AIDS, Alzheimer's disease,
CC atherosclerosis, bacterial, fungal, protozoan or viral infections,
CC osteoarthritis, osteoporosis, cancer, cardiomyopathy, chronic and acute
CC inflammation, allergies, Crohn's disease, diabetes, graft versus host
CC disease, Parkinson's disease, multiple sclerosis, pain, psoriasis,
CC anxiety, depression, schizophrenia, dementia, mental retardation, memory
CC loss, epilepsy, asthma, tuberculosis, obesity, nausea, hypertension,
CC hypotension, renal disorders, rheumatoid arthritis, trauma, ulcers, or
CC any other disorder in which GPCRs are involved. The antibodies may be
CC used in immunoassays and immunodiagnoses. AB242523 to AB242869 encode
CC GPCR proteins given in ABP81675 to ABP82018, which are used in the
CC exemplification of the present invention
XX
SQ Sequence 20 AA;

Query Match 46.3%; Score 31; DB 6; Length 20;
Best Local Similarity 62.5%; Pred. No. 3.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSFEC 8
|||:|
DB 13 DEKNTRKC 20

RESULT 9
ABJ15265
ID ABJ15265 standard; peptide; 18 AA.
XX
AC ABJ15265;
XX
DT 16-JUN-2003 (first entry)
XX
DE IGF related native phage peptide SEQ ID No 41.
XX
KW Cytostatic; antidiabetic; osteopathic; vasotropic; tranquiliser; IGF-1;
KW vulnerary; antiasphatic; ophthalmological; antagoise; ischemic injury;
KW insulin-like growth hormone 1; IGF; cancer; diabetic; nephropathy;
KW diabetic retinopathy; acromegaly; macular degeneration; trauma; asthma;
KW restenosis.
XX
OS Unidentified.
XX
PN MO200272780-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007606.
XX
PR 14-MAR-2001; 2001US-0275904P.
XX
PA (GETH) GENENTECH INC.
XX
PI Deshayes K, Lowman HB, Schaffer ML, Sidhu SS;
XX
DR WPI; 2002-732826/79.
XX
XX New peptide antagonizing insulin-like growth factor (IGF), useful for
XX treating disorder such as cancer, diabetic complication exacerbated by
XX IGF-1, acromegaly, age-related macular degeneration, ischemic injury,
XX trauma, asthma.
XX
PS Example 1; Page 42; 86pp; English.
XX
CC The invention relates to novel peptides that can antagonise the
CC interaction of insulin-like growth hormone 1 (IGF-1). The peptides are
CC useful for treating disorders such as cancer, diabetic complication
CC exacerbated by IGF-1, e.g. diabetic retinopathy or nephropathy,
CC acromegaly, age-related macular degeneration, ischemic injury or trauma.
CC Other disorders that can be treated by the peptide include restenosis or
CC asthma. This sequence represents a peptide relating to the IGF antagonist

CC peptides of the invention
XX
SQ Sequence 18 AA;

Query Match 44.8%; Score 30; DB 5; Length 18;
Best Local Similarity 33.3%; Pred. No. 4.4e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSFECILP 12
:::|:|
DB 1 DAMDCVGP 9

RESULT 10
AAJ01776
ID AAJ01776 standard; peptide; 19 AA.
XX
AC AAJ01776;
XX
DT 28-JUN-1999 (first entry)
XX
DE Active fragment of Brushtail possum ZP-2 protein.
XX
KW Zona pellucida protein; ZP-2; vaccine; female marsupial; contraceptive;
KW conception; Brushtail possum; koala; kangaroo; wallaroo; wallaby;
KW Pademelon.
XX
OS Trichosurus vulpecula.
XX
PN AU9878554-A.
XX
PD 11-FEB-1999.
XX
PP 29-JUL-1998; 98AU-00078554.
XX
PR 31-JUL-1997; 97AU-00008354.
XX
PR 12-FEB-1998; 98AU-00001800.
XX
PA (MARS-) MARSUPIAL CRC LTD.
XX
PI Mate K, McCartney C, Duckworth J, Bradley M;
XX
DR WPI; 1999-229776/20.
XX
PT New marsupial zona pellucida (ZP2 and ZP3) polypeptides for use in
PT contraceptive vaccines.
XX
PS Claim 23; Page 40; 43pp; English.
XX
CC AAJ01775-81 represent active fragments of the Brushtail possum zona
CC pellucida protein-2 (ZP-2). The ZP-2 polypeptides or polynucleotides
CC encoding them are administered as vaccines to female marsupials to raise
CC an immune response against ZP-2 proteins and prevent conception. The
CC population of koalas is growing which can cause death of food trees, and
CC the Brushtail possum is New Zealand's number one vertebrate pest and can
CC adversely affect the environment, animal health and the economy. Use of
CC the new polypeptides as contraceptives can help control the population
CC numbers of these and the Eastern grey and Western grey kangaroos, the Red
CC kangaroo, the common wallaroo, Bennett's (or red necked) wallaby, the
CC Tamar wallaby, the Whiptail wallaby, the Swamp wallaby, the Agile
XX
SQ Sequence 19 AA;

Query Match 44.8%; Score 30; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 4.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILGP 12
|||
DB 11 CILGP 15

RESULT 11
 ADD29120 standard; peptide; 19 AA.
 AC ADD29120;
 DT 15-JAN-2004 (first entry)
 DE MTN-13/I KDR binding peptide SEQ ID NO:55.
 KM display vector library; binding peptide; modular phage display library;
 KM recombinatorial phage display library.
 OS Synthetic.
 PN WO2003074678-A2.
 PD 12-SEP-2003.
 PF 03-MAR-2003; 2003WO-US006582.
 PR 01-MAR-2002; 2002US-0361121P.
 PA (DYAX-) DYAX CORP.
 PI Ladner RC;
 DR WPI; 2003-779023/73.
 PT New modular recombinatorial display libraries comprising a plurality of
 PT DNA molecules, useful for isolating binding polypeptides for a target
 PT molecule.
 PS Example 2; SEQ ID NO 55; 53bp; English.
 XX
 CC The present invention describes a library of display vectors comprising a
 CC plurality of DNA molecules that comprise a general structure: R1-2-R2,
 CC where R1 and R2 are independently variable regions; and Z is a constant
 CC region that includes a cleavage site for a restriction endonuclease. Also
 CC described: (1) obtaining a binding peptide, comprising: (a) selecting for
 CC phage in the above library, where a displayed peptide binds to a target
 CC of interest; (b) obtaining RF DNA for the selected phage; (c) cleaving
 CC the library RF DNA at the first and second restriction sites; (d) mixing
 CC the selected RF DNA fragments and the library RF DNA fragments; (e)
 CC ligating the mixed fragments; (f) introducing the ligated fragments into
 CC cells, such that phage displaying a new library are produced; and (g)
 CC selecting and sequencing binding phage from the new library, and so
 CC obtaining the binding peptide; (2) producing a modular phage display
 CC library; and (3) producing a recombinatorial phage display library. The
 CC methods are useful for obtaining a binding peptide, producing a modular
 CC phage display library, and producing a recombinatorial phage display
 CC library. The library of display vectors is useful in isolating binding
 CC polypeptides for a target molecule. The present sequence is used in the
 CC exemplification of the present invention.
 CC
 SO Sequence 19 AA;
 Query Match 44.8%; Score 30; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NSPEC 8
 DB 12 NSPEC 16
 RESULT 12
 ADK40569 standard; peptide; 19 AA.
 AC ADK40569;
 XX
 DT 06-MAY-2004 (first entry)

XX
 DE KDR & VEGF/KDR complex binding peptide of an MTN13 peptide library ID220.
 KM endothelial cell; vascular endothelial growth factor; VEGF;
 KM receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;
 KM foetal liver kinase-1; flk-1; VEGF/KDR complex; angiogenesis;
 KM neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;
 KM simian haemorrhagic fever virus;
 KM enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;
 KM virucidal; antibacterial; cytostatic.
 OS Synthetic.
 PN WO2003074005-A2.
 PD 12-SEP-2003.
 PF 03-MAR-2003; 2003WO-US006731.
 PR 01-MAR-2002; 2002US-0360851P.
 PR 15-JAN-2003; 2003US-0440411P.
 PA (DYAX-) DYAX CORP.
 PA (BRAC) BRACCO INT BV.
 PI Sato AK, Sexton DJ, Ladner RC, Dransfield DT, Swenson RE;
 PI Marinelli ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;
 PI Pochon S, Bussat P, Arbogast C, Pillal R, Fan H, Linder KE, Song B;
 PI Nanjappa P;
 DR WPI; 2003-779009/73.
 XX
 PT New polypeptide that binds to vascular endothelial growth factor receptor
 PT -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates
 PT with therapeutic or imaging agents.
 XX
 PS Claim 79; SEQ ID NO 220; 350bp; English.
 XX
 CC This invention relates to novel peptides useful for detecting and
 CC targeting primary receptors on endothelial cells that bind vascular
 CC endothelial growth factor (VEGF). Specifically, it refers to detecting
 CC the receptor tyrosine kinase identified as VEGF-2, which is also known as
 CC kinase domain region (KDR) and foetal liver kinase-1 (flk-1). The present
 CC invention describes the involvement of the VEGF/KDR complex as important
 CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding
 CC polypeptides can be used for imaging neoplastic tumours. Furthermore,
 CC these compositions are useful for targeting radiotherapeutics to specific
 CC sites for treating diseases associated with KDR activation, which include
 CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and
 CC enterohaemorrhagic Escherichia coli infection. Accordingly, these
 CC compositions exhibit various activities including protozoacidal, anti-
 CC HIV, virucidal, antibacterial and cytostatic. This peptide sequence is a
 CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of
 CC the MTN13 peptide library of the invention.
 CC
 SO Sequence 19 AA;
 Query Match 44.8%; Score 30; DB 7; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 NSPEC 8
 DB 12 NSPEC 16
 RESULT 13
 ADK40787 standard; peptide; 19 AA.
 AC ADK40787;
 XX
 DT 21-OCT-2004 (first entry)

XX Cyclic KDR/ VEGF binding peptide of the secondary MTN13 library Seq 220.
 XX
 DE kinase domain region; KDR: vascular endothelial growth factor; VEGF;
 XX VEGF receptor 2; VEGFR2; foetal liver kinase 1, flk-1; angiogenesis;
 KM neoplastic tumour; malaria; HIV infection; SIV infection;
 KM simian haemorrhagic fever virus infection;
 KM enterohaemorrhagic Escherichia coli infection; cytotoxic;
 KM antiangiogenic; antimalarial; anti-HIV, virucidal; antibacterial;
 KM MTN13 library; cyclic.
 XX
 OS Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Disulfide-bond 4. 16
 XX
 PN MO2004065621-A1.
 XX
 PD 05-AUG-2004.
 XX
 PF 11-SEP-2003; 2003WO-US028787.
 XX
 PR 15-JAN-2003; 2003US-0440411P.
 PR 03-MAR-2003; 2003US-00382082.
 PR 03-MAR-2003; 2003WO-US006731.
 XX
 PA (DYAX-) DYAX CORP.
 PA (BRAC) BRACCO INT BV.
 XX
 PI Sato AK, Sexton DJ, Dransfield DT, Ladhner RC, Arbogast C,
 PI Busse P, Fan H, Kuran S, Linder KE, Marinelli ER, Nanjappan P,
 PI Nunn A, Pallal R, Pochon S, Ramalingam K, Shrivastava A, Song B,
 PI Swenson RE, Von Wronski MA;
 XX
 DR WPI; 2004-580734/56.
 XX
 PT Novel isolated polypeptide having ability to bind to kinase domain region
 PT or vascular endothelial growth factor/kinase domain region complex,
 PT useful in inhibiting vascular endothelial growth factor activation of
 PT kinase domain region.
 XX
 PS Claim 11; SEQ ID NO 220; 470pp; English.
 XX
 CC This invention relates to novel isolated peptides that can bind to a
 CC kinase domain region (KDR) or vascular endothelial growth factor
 CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide
 CC dimers and multimeric complexes that bind with high affinity to KDR (also
 CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (flk-1))
 CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and
 CC KDR in angiogenesis these binding peptides can be used for imaging
 CC important sites of angiogenesis, as well as in targeting therapeutics to
 CC such sites. The present invention describes these peptides as useful for
 CC promoting or inhibiting angiogenesis and pathogenic conditions associated
 CC thereof such as neoplastic tumours. Furthermore, these binding peptides
 CC are useful for treating malaria, HIV infection, SIV infection, simian
 CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia
 CC coli infection. Accordingly, they exhibit cytotoxic, antiangiogenic,
 CC antimalarial, anti-HIV, virucidal and antibacterial activities. In
 CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and
 CC enable efficient detection, imaging and localisation of activated
 CC endothelial cells exhibiting upregulated KDR expression. This peptide
 CC sequence is a high affinity KDR and VEGF/KDR cyclic binding peptide
 CC belonging to the secondary MTN13 library of the invention.
 XX
 SQ Sequence 19 AA;

Query Match 44.8%; Score 30; DB 8; Length 19;
 Best Local Similarity 100.0%; Pred. No. 4.7e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8
 DB 12 NSPEC 16

RESULT 14
 AA26357
 ID AAY26357 standard; peptide, 20 AA.
 XX
 AC AAY26357;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KM Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX
 OS Synthetic.
 XX
 PN MO9640749-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009810.
 XX
 PR 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.
 XX
 PA (JOHJ) JOHNSON & JOHNSON CORP.
 PA (APFY-) APFYMEX TECHNOLOGIES NV.
 XX
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
 PI Johnson D, Mulcahy L;
 XX
 DR WPI; 1997-052225/05.
 XX
 PT Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 XX
 PS Disclosure; Page 16; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AA26352-548 are representative peptides
 CC falling within the above peptide motif and isolated during the affinity
 CC selection process
 XX
 SQ Sequence 20 AA;

Query Match 44.8%; Score 30; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FRCIIGP 12
 DB 4 YKCIIMGP 10

RESULT 15
 AAY13684

ID AAV13684 standard; peptide; 20 AA.
 AC AAV13684;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KM Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX
 OS Synthetic.
 XX
 PN MO9640749-A1.
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96MO-US009810.
 XX
 PR 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.
 XX
 PA (JOHN) JOHNSON & JOHNSON CORP.
 PA (AFRY-) AFRYMAX TECHNOLOGIES NV.
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
 PI Johnson D, Mulcahy L;
 XX
 DR WPI; 1997-052225/05.
 XX
 PT Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 XX
 PS Disclosure; Fig 2; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS; autoimmune
 CC disease; chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptide can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAV13682-735 are representative peptides of
 CC the invention
 CC
 SQ Sequence 20 AA;
 XX

Query Match 44.8%; Score 30; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PFCILGP 12
 ::||:|
 DB 4 YKCLMGP 10

RESULT 16
 AAW26998
 ID AAW26998 standard; peptide; 20 AA.
 XX
 AC AAW26998;
 XX
 DT 11-NOV-1997 (first entry)

XX
 DE Monomer subunit of erythropoietin receptor binding dimer.
 XX
 KM Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
 KM treatment; disorder; deficiency; low; defective; red blood cell;
 KM erythrocyte; population; cell surface; agonist; end stage; renal;
 KM failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;
 KM rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.
 XX
 OS Synthetic.
 XX
 PN MO9640772-A2.
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96MO-US009469.
 XX
 PR 07-JUN-1995; 95US-00484135.
 XX
 PA (JOHN) JOHNSON & JOHNSON.
 PA Johnson DL, Zivin RA;
 PI WPI; 1997-099920/09.
 XX
 DR
 XX
 PT Activating cell surface receptors using peptide dimer agonists - also,
 PT new dimers of erythropoietin receptor binding peptide(s) useful for
 PT treating patient having disorder characterised by EPO deficiency.
 XX
 PS Disclosure; Fig 9; 110pp; English.
 XX
 CC The present peptide is a specific example of a claimed generic monomer
 CC subunit of an erythropoietin (EPO) receptor binding dimer, which
 CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and
 CC activates or improves the bioactivity of the EPO cell surface receptor.
 CC The dimer can be used to treat disorders resulting from EPO deficiency by
 CC improving the activity of its cell surface receptor, e.g. end stage renal
 CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory
 CC diseases such as rheumatoid arthritis and chronic bowel inflammation and
 CC autoimmune disease. It can also be used to boost the red cell count of a
 CC patient prior to surgery or as pretreatment to transfusion. The dimer
 CC peptide exhibits increased biological potency in vitro and in vivo
 CC relative to its component monomeric agonists. Dimerisation may also
 CC convert cell surface receptor antagonists into agonists
 CC
 SQ Sequence 20 AA;
 XX

Query Match 44.8%; Score 30; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 4.9e+02;
 Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PFCILGP 12
 ::||:|
 DB 4 YKCLMGP 10

RESULT 17
 AAU05347
 ID AAU05347 standard; peptide; 20 AA.
 XX
 AC AAU05347;
 XX
 DT 24-OCT-2001 (first entry)
 XX
 DE R1 and R2 peptide #41 useful as erythropoietin receptor agonist.
 XX
 KM Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
 KM renal failure; anaemia; chronic inflammatory disease; autoimmune disease;
 KM malignancy; red blood count.
 XX
 OS Homo sapiens.
 XX
 PN WO200138342-A2.

```
XX 31-MAY-2001.
PD
XX
XX 24-NOV-2000; 2000WO-US032224.
XX
XX 24-NOV-1999; 99US-00449064.
XX
XX (GLAXO ) GLAXO GROUP LTD.
XX
XX Balu P;
XX
XX WPI; 2001-417749/44.
XX
XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by
XX binding linking group with functional groups as initiation sites for
XX peptide synthesis to support and synthesizing peptide segments.
XX
XX Disclosure; Fig 1; 43pp; English.
XX
XX The present sequence for potential R1 and R2 peptide #41 can be used to
XX form a peptide dimer that binds and activates the erythropoietin receptor
XX (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-
XX AAU05393) are described in the present invention. Also described is a
XX method for synthesizing such peptide dimers which act as EPO-R agonists.
XX The method is useful for synthesizing peptide dimers which are useful, in
XX vitro, as tools for understanding the biological role of EPO, in the
XX development of other compounds that bind to EPO-R, as commercial research
XX reagents for various medical research and diagnostic applications, for
XX detecting EPO receptors on living cells, for treatment of disorders
XX associated with a deficiency of EPO, such as end-stage renal
XX failure/dialysis, anemia associated with AIDS and chronic inflammatory
XX diseases, autoimmune diseases and malignancies, and for boosting the red
XX blood count of a patient prior to surgery
XX
XX Sequence 20 AA;

Query Match          44.8%; Score 30; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 4.9e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PECTIIGP 12
   :::::
DB 4 YKCLMGP 10

RESULT 18
AAG88114
ID AAG88114 standard; peptide; 10 AA.
XX
XX AAG88114;
XX
XX 11-SEP-2001 (first entry)
XX
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 3063.
XX
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX drug discovery; drug design.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200142276-A1.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004773.
XX
XX 13-DEC-1999; 99GB-00029471.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-367863/38.
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XX
XX Identifying complementary peptides by analysis of protein and nucleotide
XX sequence databases, useful in drug design.
XX
XX Example 5; Page 452; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides by
XX analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and plants. The specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents and
XX drugs for drug discovery and as lead ligands for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae
XX
XX Sequence 10 AA;

Query Match          43.3%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSPECTL 10
   :::::
DB 2 KNAPESVL 9

RESULT 19
AAG88115
ID AAG88115 standard; peptide; 10 AA.
XX
XX AAG88115;
XX
XX 11-SEP-2001 (first entry)
XX
XX Saccharomyces cerevisiae peptide, SEQ ID NO: 3064.
XX
XX Saccharomyces cerevisiae; complementary peptide; peptide identification;
XX drug discovery; drug design.
XX
XX Saccharomyces cerevisiae.
XX
XX WO200142276-A1.
XX
XX 14-JUN-2001.
XX
XX 13-DEC-2000; 2000WO-GB004773.
XX
XX 13-DEC-1999; 99GB-00029471.
XX
XX (PROT-) PROTEOM LTD.
XX
XX Roberts GW, Heal JR;
XX
XX WPI; 2001-367863/38.
XX
XX Identifying complementary peptides by analysis of protein and nucleotide
XX sequence databases, useful in drug design.
XX
XX Example 5; Page 452; 488pp; English.
XX
XX The invention relates to the identification of complementary peptides by
XX analysis of protein and nucleotide sequence databases from higher
XX eukaryotic genomes, excluding human and plants. The specific
XX complementary peptides interact with their relevant target proteins
XX encoded in the eukaryote genome. The peptides may be used as reagents and
XX drugs for drug discovery and as lead ligands for drug design and
XX development. The present sequence is a complementary peptide from
XX Saccharomyces cerevisiae
XX
XX Sequence 10 AA;

Query Match          43.3%; Score 29; DB 4; Length 10;
Best Local Similarity 62.5%; Pred. No. 3.7e+02;
```

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSPECTL 10
:|:|:|:
Db 2 KNAFBSVL 9

RESULT 20
ADT40845
ID ADT40845 standard; peptide; 10 AA.

AC ADT40845;

DT 30-DEC-2004 (first entry)

DE hSARS virus peptide, SEQ ID 1834.

XX virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.

OS SARS coronavirus.

XX MO2004085650-A1.

XX 07-OCT-2004.

PF 24-MAR-2004; 2004MO-CN000246.

XX 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-045730P.

PR 02-APR-2003; 2003US-045931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-046486P.

PR 25-APR-2003; 2003US-0465738P.

PR 14-MAY-2003; 2003US-0470935P.

XX (UYHK-) UNIV HONG KONG.

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

PI Leung PC;

DR MPI; 2004-737326/72.

XX New nucleic acid molecule encoding nucleocapsid- or spike-gene protein of

PT a human Severe Acute Respiratory Syndrome (hSARS) virus, useful for

PT diagnosing and treating SARS.

XX Example; SEQ ID NO 1834; 200pp; English.

PS The present invention relates to novel human Severe Acute Respiratory

CC Syndrome (hSARS) viral nucleic acid and protein sequences derived from a

CC hSARS virus having China Center for Type Culture Collection Deposit

CC Accession No. CCTCC-V200303. The present invention also relates to novel

CC nucleic acid molecules (I; ADT41483 or ADT41485) encoding a nucleocapsid-

CC (N) or spike (S)-gene protein of a hSARS virus. Also disclosed are

CC methods for detecting the presence of a N- or S-gene of the hSARS virus

CC or of the protein in a biological sample and identifying a subject

CC infected with the hSARS virus. The hSARS virus, nucleic acid and protein

CC sequences are useful as vaccines for diagnosing or treating SARS. They

CC are also useful in clinical and scientific research applications. The

CC hSARS virus genome (ADT30027) was obtained and the amino acid sequences

CC of all three reading frames were deduced from the complementary strand.

CC ADT40120 is the full-length protein encoded by the first reading frame of

CC the complementary strand and ADT40121-ADT40601 are the peptides from the

CC first reading frame protein. ADT40602 is the full-length protein encoded

CC by the second reading frame of the complementary strand and ADT40603-

CC ADT40976 are the peptides from the second reading frame protein. ADT40977

CC is the full-length protein encoded by the third reading frame of the

CC complementary strand and ADT40978-ADT41482 are the peptides from the

CC third reading frame protein.

XX Sequence 10 AA;

Query Match 43.3%; Score 29; DB 8; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECTL 10
:|:|:|:
Db 2 KKNSDHCVL 10

RESULT 21

ADS80262

ID ADS80262 standard; protein; 10 AA.

AC ADS80262;

DT 30-DEC-2004 (first entry)

DE SARS virus complementary DNA strand reading frame 2 protein #244.

XX virucide; vaccine; detection; severe acute respiratory syndrome;

XX real-time quantitative polymerase chain reaction; SARS.

OS SARS coronavirus.

XX MO2004085455-A1.

XX 07-OCT-2004.

PF 24-MAR-2004; 2004MO-CN000247.

XX 24-MAR-2003; 2003US-0457031P.

PR 26-MAR-2003; 2003US-045730P.

PR 02-APR-2003; 2003US-045931P.

PR 03-APR-2003; 2003US-0460357P.

PR 08-APR-2003; 2003US-0461265P.

PR 14-APR-2003; 2003US-0462805P.

PR 23-APR-2003; 2003US-046486P.

PR 25-APR-2003; 2003US-0468139P.

PR 16-MAY-2003; 2003US-0471200P.

XX (UYHK-) UNIV HONG KONG.

PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;

PI MPI; 2004-737292/72.

XX New isolated nucleic acid molecule useful for detecting, treating,

PT ameliorating, or preventing the virus causing severe acute respiratory

PT syndrome in humans using a real-time quantitative polymerase chain

XX Example; SEQ ID NO 1834; 183pp; English.

PS The invention relates to an isolated nucleic acid molecule consisting

CC essentially of, and/or hybridizes under stringent conditions to a fully

CC defined nucleotide sequence of 16-25 base pairs (bp); SEQ ID NO: 2471-

CC 2476), or its complement. The methods and compositions of the present

CC invention are useful for the detection of the virus causing Severe Acute

CC Respiratory Syndrome (SARS) in humans using a real-time quantitative

CC polymerase chain reaction (PCR) assay. They can also be used in treating,

CC ameliorating, managing or preventing SARS. This sequence corresponds to a

CC partial SARS protein sequence from the complementary reading frame 2.

XX Sequence 10 AA;

Query Match 43.3%; Score 29; DB 8; Length 10;

Best Local Similarity 55.6%; Pred. No. 3.7e+02;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECTL 10
:|:|:|:
Db 2 KKNSDHCVL 10

RESULT 22
ADT38375
ID ADT38375 standard; peptide, 10 AA.
XX
AC ADT38375;
XX
DT 30-DEC-2004 (first entry)
XX
DE hsSARS virus peptide, SEQ ID 1834.
XX
KW Virucide; Severe Acute Respiratory Syndrome; SARS; vaccine.
XX
OS SARS coronavirus.
XX
PN WO2004085633-A1.
XX
PD 07-OCT-2004.
XX
PF 24-MAR-2004; 2004WO-CN000248.
XX
PR 24-MAR-2003; 2003US-0457031P.
XX
PR 26-MAR-2003; 2003US-0457730P.
XX
PR 02-APR-2003; 2003US-0459931P.
XX
PR 03-APR-2003; 2003US-0460357P.
XX
PR 08-APR-2003; 2003US-0461265P.
XX
PR 14-APR-2003; 2003US-0462805P.
XX
PR 23-APR-2003; 2003US-0464866P.
XX
PA (UYHK-) UNIV HONG KONG.
XX
PI Chan K, Guan Y, Nicholls JM, Peiris JSM, Poon L, Yuen K;
PI Leung PC;
XX
DR WPI; 2004-728736/71.
XX
PT New isolated human severe acute respiratory syndrome (hsSARS) virus,
PT useful as vaccine for diagnosing or treating SARS or in clinical and
PT scientific research applications.
XX
PS Example; SEQ ID NO 1834; 176pp; English.
XX
XX The present invention relates to novel human Severe Acute Respiratory
CC Syndrome (hsSARS) viral nucleic acid and protein sequences derived from a
CC hsSARS virus having China Center for Type Culture Collection Deposit
CC Accession No. CCTCC-V200303. The hsSARS virus, nucleic acid and protein
CC sequences are useful as vaccines for diagnosing or treating SARS. They
CC are also useful in clinical and scientific research applications. The
CC hsSARS virus genome (ADT38357) was obtained and the amino acid sequences
CC of all three reading frames were deduced from the complementary strand.
CC ADT37650 is the full-length protein encoded by the first reading frame of
CC the complementary strand and ADT37651-ADT38131 are the peptides from the
CC first reading frame protein. ADT38132 is the full-length protein encoded
CC by the second reading frame of the complementary strand and ADT38133-
CC ADT38506 are the peptides from the second reading frame protein. ADT38507
CC is the full-length protein encoded by the third reading frame of the
CC complementary strand and ADT38508-ADT39012 are the peptides from the
CC third reading frame protein.
CC
SQ Sequence 10 AA;
XX
Query Match 43.3%; Score 29; DB 8; Length 10;
Best Local Similarity 55.6%; Pred. No. 3.7e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
QY 2 EKNSFECIL 10
:|||||:|
Db 2 KKNSDHCVL 10
RESULT 23
ABB77729

ID ABB77729 standard; peptide, 15 AA.
XX
XX ABB77729;
XX
AC ABB77729;
XX
DT 30-JUL-2002 (first entry)
XX
DE N-terminal of human class III MHC 61.
XX
DE Human, class III MHC 61; immunological disease; inflammation;
KW organ transplantation; gene therapy.
XX
XX Homo sapiens.
OS
XX
PN WO200226828-A1.
XX
PD 04-APR-2002.
XX
PF 02-JUL-2001; 2001WO-CN001116.
XX
PR 07-JUL-2000; 2000CN-00117015.
XX
PA (BIOW-) BIOWINDOW GENE DEV INC SHANGHAI.
XX
PI Mao Y, Xie Y;
XX
DR WPI; 2002-281324/32.
XX
PT Human class III MHC 61 and encoding polynucleotide, used in diagnosis and
PT treatment of immunological diseases and inflammation and in organ
PT transplantation.
XX
PS Example 6; Page 14; 40pp; Chinese.
XX
CC The present sequence is derived from class III MHC 61. The polypeptide
CC and polynucleotide are used in diagnosis and treatment of immunological
CC diseases and inflammation and in organ transplantation. The
CC polynucleotide may also be used for gene therapy
XX
SQ Sequence 15 AA;
XX
Query Match 43.3%; Score 29; DB 5; Length 15;
Best Local Similarity 80.0%; Pred. No. 5.6e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 8 CILGP 12
:|||||
Db 7 CVLGP 11
RESULT 24
ADU91959
ID ADU91959 standard; peptide, 17 AA.
XX
XX ADU91959;
AC
XX
DT 10-FEB-2005 (first entry)
XX
XX EPO-R agonist SEQ ID NO 100.
DE
XX
KW erythropoietin receptor; EPO-R; erythropoietin; renal failure;
KW autoimmune disease; cystic fibrosis; anemia; inflammation;
KW spinal cord injury; aging; neurological disease; nephrotropic;
KW antianemic; immunosuppressive; CNS-Gen.; neuroprotective;
KW respiratory-Gen.; antiinflammatory; vulnary; nootropic; cyrostatic;
XX hemostatic; cyclic.
OS
XX
XX Synthetic.
FH Key Location/Qualifiers
FT Modified-site 1
FT Disulfide-bond 4. .13
FT Modified-site 17

/note= "C-terminal amide"

FT XX WO2004101611-A2.
 PN XX
 XX XX
 PD 25-NOV-2004.
 PF 12-MAY-2004; 2004WO-US014886.
 XX XX
 PR 12-MAY-2003; 2003US-0470245P.
 XX XX
 PA (AFY-) AFFYMAX INC.
 PI yin K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumelty D;
 XX WPI; 2005-039329/04.
 DR
 XX
 XX
 PT New peptide comprising specified sequence of amino acid is erythropoietin
 PT receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal
 PT disorders.
 XX
 XX
 PS Disclosure; SEQ ID NO 100; 83pp; English.
 XX
 XX
 CC This invention describes a novel peptide which is an erythropoietin
 CC receptor (EPO-R) activator. The peptide forms a dimer comprising a
 CC linking moiety connecting two peptide chains composed of ADU91861. The N-
 CC terminal of the peptide is acetylated. The EPO-R activator further
 CC comprises at least one water soluble polymer, preferably polyethylene
 CC glycol (PEG) covalently bound to the peptide and a spacer moiety. The
 CC products of the invention are used for treating disorders associated with
 CC deficiency of erythropoietin or low or defective red blood cell
 CC population, end stage renal failure or dialysis, anemia associated with
 CC AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic
 CC fibrosis, early anemia of prematurity, anemia associated with chronic
 CC inflammatory disease, spinal cord injury, acute blood loss, aging and
 CC neoplastic disease states accompanied by abnormal erythropoiesis. The
 CC peptide compounds are potent agonists of erythropoietin receptor and have
 CC nephrotropic, antianemic, immunosuppressive, CNS-Gen., neuroprotective,
 CC respiratory-Gen., antiinflammatory, vulnerary, nootropic, cyostatic and
 CC hemostatic activity. This sequence represents a peptide which acts as an
 CC erythropoietin receptor (EPO-R) agonist.
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 43.3%; Score 29; DB 9; Length 17;
 Best Local Similarity 57.1%; Pred. No. 6.3e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FRCILGP 12
 : : : : :
 Db 2 YRCRMGP 8
 RESULT 25
 ADU91965
 ID ADU91965 standard; peptide; 17 AA.
 XX
 AC ADU91965;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE EPO-R agonist SEQ ID NO 106.
 XX
 XX erythropoietin receptor; EPO-R; erythropoietin; renal failure;
 KW autoimmune disease; cystic fibrosis; anemia; inflammation;
 KW spinal cord injury; aging; neurological disease; nephrotropic;
 KW antianemic; immunosuppressive; CNS-Gen.; neuroprotective;
 KW respiratory-Gen.; antiinflammatory; vulnerary; nootropic; cyostatic;
 KW hemostatic; cyclic.
 XX
 XX Synthetic.
 OS
 XX Key Location/Qualifiers
 FT Modified-site 1

/note= "Acetylated residue"

FT FT Disulfide-bond 4. .13
 FT FT Modified-site 17
 FT FT /note= "C-terminal amide"
 XX
 PN XX WO2004101611-A2.
 XX XX
 PD 25-NOV-2004.
 PF 12-MAY-2004; 2004WO-US014886.
 XX XX
 PR 12-MAY-2003; 2003US-0470245P.
 XX XX
 PA (AFY-) AFFYMAX INC.
 PI yin K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumelty D;
 XX WPI; 2005-039329/04.
 DR
 XX
 XX
 PT New peptide comprising specified sequence of amino acid is erythropoietin
 PT receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal
 PT disorders.
 XX
 XX
 PS Disclosure; SEQ ID NO 106; 83pp; English.
 XX
 XX
 CC This invention describes a novel peptide which is an erythropoietin
 CC receptor (EPO-R) activator. The peptide forms a dimer comprising a
 CC linking moiety connecting two peptide chains composed of ADU91861. The N-
 CC terminal of the peptide is acetylated. The EPO-R activator further
 CC comprises at least one water soluble polymer, preferably polyethylene
 CC glycol (PEG) covalently bound to the peptide and a spacer moiety. The
 CC products of the invention are used for treating disorders associated with
 CC deficiency of erythropoietin or low or defective red blood cell
 CC population, end stage renal failure or dialysis, anemia associated with
 CC AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic
 CC fibrosis, early anemia of prematurity, anemia associated with chronic
 CC inflammatory disease, spinal cord injury, acute blood loss, aging and
 CC neoplastic disease states accompanied by abnormal erythropoiesis. The
 CC peptide compounds are potent agonists of erythropoietin receptor and have
 CC nephrotropic, antianemic, immunosuppressive, CNS-Gen., neuroprotective,
 CC respiratory-Gen., antiinflammatory, vulnerary, nootropic, cyostatic and
 CC hemostatic activity. This sequence represents a peptide which acts as an
 CC erythropoietin receptor (EPO-R) agonist.
 XX
 SQ Sequence 17 AA;
 XX
 Query Match 43.3%; Score 29; DB 9; Length 17;
 Best Local Similarity 42.9%; Pred. No. 6.3e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FRCILGP 12
 : : : : :
 Db 2 YRCRMGP 8
 RESULT 26
 ADU92009
 ID ADU92009 standard; peptide; 17 AA.
 XX
 AC ADU92009;
 XX
 DT 10-FEB-2005 (first entry)
 XX
 DE EPO-R agonist SEQ ID NO 150.
 XX
 XX erythropoietin receptor; EPO-R; erythropoietin; renal failure;
 KW autoimmune disease; cystic fibrosis; anemia; inflammation;
 KW spinal cord injury; aging; neurological disease; nephrotropic;
 KW antianemic; immunosuppressive; CNS-Gen.; neuroprotective;
 KW respiratory-Gen.; antiinflammatory; vulnerary; nootropic; cyostatic;
 KW hemostatic; cyclic.
 XX
 XX Synthetic.
 OS

```

XX Key Location/Qualifiers
FH Modified-site 1
PT Disulfide-bond 4, .13
PT Modified-site 17
PT Modified-site /note="C-terminal amide"
XX
XX MO2004101611-A2.
XX
XX 25-NOV-2004.
XX
XX 12-MAY-2004; 2004WO-US014886.
XX
XX 12-MAY-2003; 2003US-0470245P.
XX
XX (AFPMY-) AFPMYMAX INC.
XX
XX Yin K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tynnelly D,
XX WPI; 2005-039329/04.
XX
XX New peptide comprising specified sequence of amino acid is erythropoietin
XX receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal
XX disorders.
XX
XX Disclosure; SEQ ID NO 150; 83pp; English.
XX
XX This invention describes a novel peptide which is an erythropoietin
XX receptor (EPO-R) activator. The peptide forms a dimer comprising a
XX linking moiety connecting two peptide chains composed of AD91861. The N-
XX terminal of the peptide is acetylated. The EPO-R activator further
XX comprises at least one water soluble polymer, preferably polyethylene
XX glycol (PEG) covalently bound to the peptide and a spacer moiety. The
XX products of the invention are used for treating disorders associated with
XX deficiency of erythropoietin or low or defective red blood cell
XX population, end stage renal failure or dialysis, anemia associated with
XX AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic
XX fibrosis, early anemia of prematurity, anemia associated with chronic
XX inflammatory disease, spinal cord injury, acute blood loss, aging and
XX neoplastic disease states accompanied by abnormal erythropoiesis. The
XX peptide compounds are potent agonists of erythropoietin receptor and have
XX nephroprotective, anti-anemic, immunosuppressive, CNS-Gen., neuroprotective,
XX respiratory-Gen., anti-inflammatory, vulnerary, nociceptive, cytoprotective,
XX and hemostatic activity. This sequence represents a peptide which acts as an
XX erythropoietin receptor (EPO-R) agonist.
XX
XX Sequence 17 AA;
XX
XX Query Match 43.3%; Score 29; DB 9; Length 17;
XX Best Local Similarity 42.9%; Pred. No. 6.3e+02;
XX Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
XX QY 6 PEGCIIIGP 12
XX : ||:|
XX 2 YSCLMGP 8
XX
XX DB
XX
XX RESULT 27
XX ID AAY26490 standard; peptide; 19 AA.
XX
XX AC AAY26490;
XX
XX XX
XX DT 06-SEP-1999 (first entry)
XX
XX DE Erythropoietin receptor (EPO-R) binding peptide.
XX
XX KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
XX dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
XX malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
XX spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX

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OS Synthetic.
XX
XX MO9640749-A1.
XX
XX 19-DEC-1996.
XX
XX
XX 07-JUN-1996; 96WO-US009810.
XX
XX 07-JUN-1995; 95US-00484631.
XX
XX 07-JUN-1995; 95US-00484635.
XX
XX (JOHJ) JOHNSON & JOHNSON CORP.
XX (AFPMY-) AFPMYMAX TECHNOLOGIES NV.
XX
XX Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
XX Johnson D, Mulcahy L;
XX WPI; 1997-052225/05.
XX
XX Erythropoietin receptor binding peptide - useful for treating disorders
XX characterised by deficiency of EPO, or low or defective red blood cell
XX population.
XX
XX Disclosure; Page 23; 95pp; English.
XX
XX The invention describes a peptide of 10-40 amino acid residues which
XX binds to erythropoietin (EPO) receptor and which includes the amino acid
XX sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trip-Xaa4-Cys, where Xaa1 = Arg,
XX His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
XX coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
XX the peptide may be cyclised or dimerised. The peptide can be used to
XX treat a patient having a disorder characterised by a deficiency of EPO or
XX a low or defective red blood cell population. It can be used to treat end
XX stage renal failure or dialysis; anemia associated with AIDS, autoimmune
XX disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
XX cystic fibrosis; early anaemia or prematurity; spinal cord injury; acute
XX blood loss; aging; and neoplastic disease states accompanied by abnormal
XX erythropoiesis. The peptides can also be used as reagents for detecting
XX EPO receptors on living cells, in biological fluids, in tissue
XX homogenates, etc. Sequences AAY26352-548 are representative peptides
XX falling within the above peptide motif and isolated during the affinity
XX selection process
XX
XX Sequence 19 AA;
XX
XX Query Match 43.3%; Score 29; DB 2; Length 19;
XX Best Local Similarity 40.0%; Pred. No. 7e+02;
XX Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
XX
XX QY 3 KNSPFCIIIGP 12
XX : ||:|
XX 2 KTKYRCGMGP 11
XX
XX DB
XX
XX RESULT 28
XX ID ADS33404 standard; peptide; 19 AA.
XX
XX AC ADS33404;
XX
XX XX
XX DT 02-DEC-2004 (first entry)
XX
XX DE CMET-HGF binding peptide #57.
XX
XX KW cytostatic; hepatocyte growth factor receptor; CMET; HGF; tumor;
XX glioblastoma; malignant mesothelioma; colorectal tumor;
XX hepatocellular tumor; hepatobiliary tumor; renal tumor; osteosarcoma;
XX cervical tumors; diagnostic imaging; cellular proliferation;
XX angiogenesis; hyperproliferation; cancer; solid phase matrix;
XX chromatography.
XX
XX Synthetic.
XX

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PN WO2004078778-A2.
 XX 16-SEP-2004.
 PD
 XX 03-MAR-2004, 2004WO-US006473.
 PF
 XX 03-MAR-2003, 2003US-0451588P.
 PR
 XX (DYAX-) DYAX CORP.
 PA (BRAC) BRACCO INT BV.
 XX
 PI Sato AK, Dransfield DT, Ladner RC, Shrivastava A, Nanjappan P;
 XX WPI, 2004-668601/65.
 DR
 XX Hepatocyte growth factor receptor (cmet) binding polypeptide or
 PT multimeric peptide construct, useful for diagnostic imaging of sites of
 PT cellular proliferation and/or angiogenesis, and for treating cancer.
 XX
 PS Claim 7, SEQ ID NO 57, 174pp; English.
 XX
 CC The invention relates to a novel polypeptide or multimeric peptide
 CC construct (I) which binds hepatocyte growth factor receptor (cmet) or a
 CC complex comprising cmet and hepatocyte growth factor (HGF). (I) is useful
 CC for detecting cmet or a complex of cmet and HGF in an animal or human
 CC subject which involves providing (I), where (I) is labelled,
 CC administering to the subject the labelled (I), and detecting labelled (I)
 CC in the subject. The label is radioactive or paramagnetic. (I) is useful
 CC for purifying cmet or a cmet and HGF complex from a solution containing
 CC it which involves contacting the solution with at least one (I), and
 CC separating the polypeptide or multimeric polypeptide from the solution.
 CC (M1) is useful for treating conditions involving activation of cmet. The
 CC disease is a solid tumor chosen from breast, thyroid, glioblastoma,
 CC prostate, malignant mesothelioma, colorectal, hepatocellular,
 CC hepatobiliary, renal, osteosarcoma and cervical tumors. (I) is useful for
 CC diagnostic imaging of sites of cellular proliferation and/or
 CC angiogenesis, thus useful in diagnosis of such hyperproliferative-related
 CC and/or angiogenesis-related disorders. (I) is useful for targeting
 CC therapeutic agents or delivering vehicles for therapeutics to sites of
 CC hyperproliferation and/or angiogenesis or other tissue expressing cmet.
 CC (I) is useful for detection and/or imaging of cmet in vitro or in vivo.
 CC (I) is useful for treating cancer. (I) is used in gene therapy for
 CC treating hyper proliferative disorders. cmet binding peptides were
 CC synthesized on a solid phase matrix using 9-fluorenylmethoxycarbonyl
 CC protocols. The peptides were purified with reverse chromatography. This
 CC sequence corresponds to a peptide of the invention.
 CC
 XX SQ Sequence 19 AA;
 Query Match 43.3%; Score 29; DB 8; Length 19;
 Best Local Similarity 83.3%; Pred. No. 7e+02;
 Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SPECIL 10
 :|||
 Db 11 TPECIL 16
 RESULT 29
 ID AAY13694
 AAY13694 standard; peptide, 20 AA.
 AC AAY13694,
 XX
 XX 06-SRP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KM Erythropoietin, EPO, receptor; EPO deficiency; renal failure; AIDS;
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX

OS Synthetic.
 XX
 PN WO9640749-A1.
 XX
 PD 19-DEC-1996.
 XX
 XX 07-JUN-1996; 96WO-US009810.
 PF
 XX 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.
 XX
 XX (JOHN) JOHNSON & JOHNSON CORP.
 PA (AFFY-) AFFYMAX TECHNOLOGIES NV.
 XX
 PI Wighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
 PT Johnson D, Mulcahy L;
 XX WPI, 1997-052225/05.
 DR
 XX Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 XX
 PS Disclosure; Fig 2; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAY13662-735 are representative peptides of
 CC the invention
 XX
 SO Sequence 20 AA;
 Query Match 43.3%; Score 29; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 7.4e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FRCILGP 12
 :|||
 Db 4 YECRMGP 10
 RESULT 30
 ID AAY13720
 AAY13720 standard; peptide, 20 AA.
 AC AAY13720;
 XX
 XX 06-SRP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KM Erythropoietin, EPO, receptor; EPO deficiency; renal failure; AIDS;
 KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX
 OS Synthetic.
 OS
 PN WO9640749-A1.
 XX 19-DEC-1996.
 PD

XX 07-JUN-1996; 96WO-US009810.
 XX
 XX 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.
 XX
 PA (JOHN J) JOHNSON & JOHNSON CORP.
 PA (AFRY-) AFRYMAX TECHNOLOGIES NV.
 XX
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
 PI Johnson D, Mulcahy L;
 DR WPI; 1997-052225/05.
 XX
 XX Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 PS Disclosure; Fig 2; 95pp; English.
 XX
 XX The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAY13662-735 are representative peptides of
 CC the invention
 CC
 SQ Sequence 20 AA;

Query Match 43.3%; Score 29; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 7.4e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRCILGP 12
 : ||:|
 Db 4 YSCLMGP 10

RESULT 31
 AAY13685
 ID AAY13685 standard; peptide; 20 AA.
 XX
 AC AAY13685;
 XX

DT 06-SEP-1999 (first entry)

DE Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX

OS Synthetic.

XX WO9640749-A1.

PD 19-DEC-1996.

PP 07-JUN-1996; 96WO-US009810.

XX 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.

XX (JOHN J) JOHNSON & JOHNSON CORP.
 PA (AFRY-) AFRYMAX TECHNOLOGIES NV.
 XX
 XX Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
 PI Johnson D, Mulcahy L;
 DR WPI; 1997-052225/05.
 XX
 XX Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 PS Disclosure; Fig 2; 95pp; English.
 XX
 XX The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAY13662-735 are representative peptides of
 CC the invention
 CC
 SQ Sequence 20 AA;

Query Match 43.3%; Score 29; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 7.4e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PRCILGP 12
 : ||:|
 Db 4 YSCLMGP 10

RESULT 32
 AAY26375
 ID AAY26375 standard; peptide; 20 AA.
 XX
 AC AAY26375;
 XX

DT 06-SEP-1999 (first entry)

DE Erythropoietin receptor (EPO-R) binding peptide.

XX Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX

OS Synthetic.

XX WO9640749-A1.

PD 19-DEC-1996.

PP 07-JUN-1996; 96WO-US009810.

XX 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.

XX (JOHN J) JOHNSON & JOHNSON CORP.
 PA (AFRY-) AFRYMAX TECHNOLOGIES NV.
 XX
 XX Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;

PI Johnson D, Mulcahy L;
 XX WPI, 1997-052225/05.
 XX
 PT Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 XX
 PS Disclosure; Page 17; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAY26352-548 are representative peptides
 CC falling within the above peptide motif and isolated during the affinity
 CC selection process
 CC
 SQ Sequence 20 AA;
 XX
 XX
 Query Match 43.3%; Score 29; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 7.4e+02;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FRCILGP 12
 : : : : :
 Db 4 YSCIMGP 10
 XX
 XX
 RESULT 33
 AAY26374
 ID AAY26374 standard; peptide; 20 AA.
 XX
 AC AAY26374;
 XX
 DT 06-SEP-1999 (first entry)
 XX
 DE Erythropoietin receptor (EPO-R) binding peptide.
 XX
 KW Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
 KW dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
 KW malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
 KW spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
 XX
 OS Synthetic.
 XX
 PN WO9640749-A1.
 XX
 PD 19-DEC-1996.
 XX
 PF 07-JUN-1996; 96WO-US009810.
 XX
 PR 07-JUN-1995; 95US-00484631.
 PR 07-JUN-1995; 95US-00484635.
 XX
 PA (JOHN J) JOHNSON & JOHNSON CORP.
 PA (APFY-) APFYMEX TECHNOLOGIES NV.
 XX
 PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Jolliffe LK;
 PI Johnson D, Mulcahy L;
 XX
 XX WPI, 1997-052225/05.
 XX

PT Erythropoietin receptor binding peptide - useful for treating disorders
 PT characterised by deficiency of EPO, or low or defective red blood cell
 PT population.
 XX
 PS Disclosure; Page 17; 95pp; English.
 XX
 CC The invention describes a peptide of 10-40 amino acid residues which
 CC binds to erythropoietin (EPO) receptor and which includes the amino acid
 CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Tyr-Xaa4-Cys, where Xaa1 = Arg,
 CC His, Leu or Tyr, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
 CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
 CC the peptide may be cyclised or dimerised. The peptide can be used to
 CC treat a patient having a disorder characterised by a deficiency of EPO or
 CC a low or defective red blood cell population. It can be used to treat end
 CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
 CC disease, chronic inflammatory diseases or malignancy; beta-thalassemia;
 CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
 CC blood loss; aging; and neoplastic disease states accompanied by abnormal
 CC erythropoiesis. The peptides can also be used as reagents for detecting
 CC EPO receptors on living cells, in biological fluids, in tissue
 CC homogenates, etc. Sequences AAY26352-548 are representative peptides
 CC falling within the above peptide motif and isolated during the affinity
 CC selection process
 CC
 SQ Sequence 20 AA;
 XX
 XX
 Query Match 43.3%; Score 29; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 7.4e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 6 FRCILGP 12
 : : : : :
 Db 4 YRCRMGP 10
 XX
 XX
 RESULT 34
 AAW27034
 ID AAW27034 standard; peptide; 20 AA.
 XX
 AC AAW27034;
 XX
 DT 11-NOV-1997 (first entry)
 XX
 DE Monomer subunit of erythropoietin receptor binding dimer.
 XX
 KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
 KW treatment; disorder; deficiency; low; defective; red blood cell;
 KW erythrocyte; population; cell surface; agonist; end stage; renal;
 KW failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;
 KW rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.
 XX
 OS Synthetic.
 XX
 PN WO9640772-A2.
 XX
 PD 19-DEC-1996.
 XX
 PF 06-JUN-1996; 96WO-US009469.
 XX
 PR 07-JUN-1995; 95US-00484135.
 XX
 PA (JOHN J) JOHNSON & JOHNSON.
 PA Johnson DL, Zivin RA;
 XX
 PI WPI, 1997-099920/09.
 XX
 XX
 PT Activating cell surface receptors using peptide dimer agonists - also,
 PT new dimers of erythropoietin receptor binding peptide(s) useful for
 PT treating patient having disorder characterised by EPO deficiency.
 XX
 PS Disclosure; Fig 9; 110pp; English.
 XX

CC The present peptide is a specific example of a claimed generic monomer
CC subunit of an erythropoietin (EPO) receptor binding dimer, which
CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and
CC activates or improves the bioactivity of the EPO cell surface receptor.
CC The dimer can be used to treat disorders resulting from EPO deficiency by
CC improving the activity of its cell surface receptor, e.g. end stage renal
CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory
CC diseases such as rheumatoid arthritis and chronic bowel inflammation and
CC autoimmune disease. It can also be used to boost the red cell count of a
CC patient prior to surgery or as pretreatment to transfusion. The dimer
CC peptide exhibits increased biological potency in vitro and in vivo
CC relative to its component monomeric agonists. Dimerisation may also
CC convert cell surface receptor antagonists into agonists
XX
SQ Sequence 20 AA;
XX
Query Match 43.3%; Score 29; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 PECTIGP 12
: || : ||
Db 4 YECRMGP 10
XX
RESULT 35
AAW27008
ID AAW27008 standard; peptide; 20 AA.
XX
AC AAW27008;
XX
DT 11-NOV-1997 (first entry)
XX
DE Monomer subunit of erythropoietin receptor binding dimer.
XX
KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
KW treatment; disorder; deficiency; low; defective; red blood cell;
KW erythrocyte; population; cell surface; agonist; end stage; renal;
KW failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;
KW rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.
XX
OS Synthetic.
XX
PN WO9640772-A2.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US009469.
XX
PR 07-JUN-1995; 95US-00484135.
XX
PA (JOHN) JOHNSON & JOHNSON.
XX
PI Johnson DL, Zivin RA;
XX
DR WPI; 1997-099920/09.
XX
PT Activating cell surface receptors using peptide dimer agonists - also,
PT new dimers of erythropoietin receptor binding peptide(s) useful for
PT treating patient having disorder characterised by EPO deficiency.
XX
PS Disclosure; Fig 9; 110pp; English.
XX
SQ The present peptide is a specific example of a claimed generic monomer
CC subunit of an erythropoietin (EPO) receptor binding dimer, which
CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and
CC activates or improves the bioactivity of the EPO cell surface receptor.
CC The dimer can be used to treat disorders resulting from EPO deficiency by
CC improving the activity of its cell surface receptor, e.g. end stage renal
CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory
CC diseases such as rheumatoid arthritis and chronic bowel inflammation and
CC autoimmune disease. It can also be used to boost the red cell count of a
CC patient prior to surgery or as pretreatment to transfusion. The dimer

CC peptide exhibits increased biological potency in vitro and in vivo
CC relative to its component monomeric agonists. Dimerisation may also
CC convert cell surface receptor antagonists into agonists
XX
SQ Sequence 20 AA;
XX
Query Match 43.3%; Score 29; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
XX
QY 6 PECTIGP 12
: || : ||
Db 4 YECRMGP 10
XX
RESULT 36
AAW26999
ID AAW26999 standard; peptide; 20 AA.
XX
AC AAW26999;
XX
DT 11-NOV-1997 (first entry)
XX
DE Monomer subunit of erythropoietin receptor binding dimer.
XX
KW Monomer; erythropoietin; EPO; receptor; binding; dimer; activation;
KW treatment; disorder; deficiency; low; defective; red blood cell;
KW erythrocyte; population; cell surface; agonist; end stage; renal;
KW failure; dialysis; anaemia; anemia; AIDS; chronic; inflammatory; disease;
KW rheumatoid arthritis; bowel inflammation; autoimmune; transfusion.
XX
OS Synthetic.
XX
PN WO9640772-A2.
XX
PD 19-DEC-1996.
XX
PF 06-JUN-1996; 96WO-US009469.
XX
PR 07-JUN-1995; 95US-00484135.
XX
PA (JOHN) JOHNSON & JOHNSON.
XX
PI Johnson DL, Zivin RA;
XX
DR WPI; 1997-099920/09.
XX
PT Activating cell surface receptors using peptide dimer agonists - also,
PT new dimers of erythropoietin receptor binding peptide(s) useful for
PT treating patient having disorder characterised by EPO deficiency.
XX
PS Disclosure; Fig 9; 110pp; English.
XX
SQ The present peptide is a specific example of a claimed generic monomer
CC subunit of an erythropoietin (EPO) receptor binding dimer, which
CC comprises 2 EPO receptor binding monomers of 10 to 40 amino acids, and
CC activates or improves the bioactivity of the EPO cell surface receptor.
CC The dimer can be used to treat disorders resulting from EPO deficiency by
CC improving the activity of its cell surface receptor, e.g. end stage renal
CC failure/dialysis, anaemia associated with AIDS or chronic inflammatory
CC diseases such as rheumatoid arthritis and chronic bowel inflammation and
CC autoimmune disease. It can also be used to boost the red cell count of a
CC patient prior to surgery or as pretreatment to transfusion. The dimer
CC peptide exhibits increased biological potency in vitro and in vivo
CC relative to its component monomeric agonists. Dimerisation may also
CC convert cell surface receptor antagonists into agonists
XX
SQ Sequence 20 AA;
XX
Query Match 43.3%; Score 29; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTILGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 37
AAU05356
ID AAU05356 standard; peptide; 20 AA.
XX
AC AAU05356;
XX
DT 24-OCT-2001 (first entry)
XX
DE R1 and R2 peptide #50 useful as erythropoietin receptor agonist.
XX
KM Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
KW renal failure; anaemia; chronic inflammatory disease; autoimmune disease;
KM malignancy; red blood count.
XX
OS Homo sapiens.
XX
PN WO200138342-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032224.
XX
PR 24-NOV-1999; 99US-00449064.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Balu P;
XX
DR WPI; 2001-417749/44.
XX
PT Synthesizing peptide dimer useful as erythropoietin receptor agonist by
PT binding linking group with functional groups as initiation sites for
PT peptide synthesis to support and synthesizing peptide segments.
XX
PS Disclosure; Fig 1; 43pp; English.

XX
CC The present sequence for potential R1 and R2 peptide #50 can be used to
CC form a peptide dimer that binds and activates the erythropoietin receptor
CC (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-
CC AAU05393) are described in the present invention. Also described is a
CC method for synthesizing such peptide dimers which act as EPO-R agonists.
CC The method is useful for synthesizing peptide dimers which are useful, in
CC vitro, as tools for understanding the biological role of EPO, in the
CC development of other compounds that bind to EPO-R, as commercial research
CC reagents for various medical research and diagnostic applications, for
CC detecting EPO receptors on living cells, for treatment of disorders
CC associated with a deficiency of EPO, such as end-stage renal
CC failure/dialysis, anaemia associated with AIDS and chronic inflammatory
CC diseases, autoimmune diseases and malignancies, and for boosting the red
CC blood count of a patient prior to surgery
XX
SO Sequence 20 AA;

Query Match 43.3%; Score 29; DB 4; Length 20;
Best Local Similarity 57.1%; Pred. No. 7.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTILGP 12
: ||: ||
Db 4 YECRMGP 10

RESULT 38
AAU05348
ID AAU05348 standard; peptide; 20 AA.
XX
AC AAU05348;
XX

DT 24-OCT-2001 (first entry)
XX
DE R1 and R2 peptide #42 useful as erythropoietin receptor agonist.
XX
KM Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
KW renal failure; anaemia; chronic inflammatory disease; autoimmune disease;
KM malignancy; red blood count.
XX
OS Homo sapiens.
XX
PN WO200138342-A2.
XX
PD 31-MAY-2001.
XX
PF 24-NOV-2000; 2000WO-US032224.
XX
PR 24-NOV-1999; 99US-00449064.
XX
PA (GLAX) GLAXO GROUP LTD.
XX
PI Balu P;
XX
DR WPI; 2001-417749/44.
XX
PT Synthesizing peptide dimer useful as erythropoietin receptor agonist by
PT binding linking group with functional groups as initiation sites for
PT peptide synthesis to support and synthesizing peptide segments.
XX
PS Disclosure; Fig 1; 43pp; English.

XX
CC The present sequence for potential R1 and R2 peptide #42 can be used to
CC form a peptide dimer that binds and activates the erythropoietin receptor
CC (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-
CC AAU05393) are described in the present invention. Also described is a
CC method for synthesizing such peptide dimers which act as EPO-R agonists.
CC The method is useful for synthesizing peptide dimers which are useful, in
CC vitro, as tools for understanding the biological role of EPO, in the
CC development of other compounds that bind to EPO-R, as commercial research
CC reagents for various medical research and diagnostic applications, for
CC detecting EPO receptors on living cells, for treatment of disorders
CC associated with a deficiency of EPO, such as end-stage renal
CC failure/dialysis, anaemia associated with AIDS and chronic inflammatory
CC diseases, autoimmune diseases and malignancies, and for boosting the red
CC blood count of a patient prior to surgery
XX
SQ Sequence 20 AA;

Query Match 43.3%; Score 29; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTILGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 39
AAU05381
ID AAU05381 standard; peptide; 20 AA.
XX
AC AAU05381;
XX
DT 24-OCT-2001 (first entry)
XX
DE R1 and R2 peptide #75 useful as erythropoietin receptor agonist.
XX
KM Human; erythropoietin receptor; EPO-R; EPO agonist; EPO deficiency;
KW renal failure; anaemia; chronic inflammatory disease; autoimmune disease;
KM malignancy; red blood count.
XX
OS Homo sapiens.
XX
PN WO200138342-A2.

XX 31-MAY-2001.
PD
XX
XX 24-NOV-2000; 2000WO-US032224.
PF
XX
XX 24-NOV-1999; 99US-00449064.
PR
XX
PA (GLAXO) GLAXO GROUP LTD.
XX
PI Balu P;
XX
XX WPI; 2001-417749/44.
DR
XX
XX
XX Synthesizing peptide dimer useful as erythropoietin receptor agonist by
PT binding linking group with functional groups as initiation sites for
PT peptide synthesis to support and synthesizing peptide segments.
XX
XX Disclosure; Fig 1; 43pp; English.
XX
XX The present sequence for potential R1 and R2 peptide #75 can be used to
CC form a peptide dimer that binds and activates the erythropoietin receptor
CC (EPO-R). Various possible peptide sequences for R1 and R2 (AAU05301-
CC AAU05393) are described in the present invention. Also described is a
CC method for synthesizing such peptide dimers which act as EPO-R agonists.
CC The method is useful for synthesizing peptide dimers which are useful, in
CC vitro, as tools for understanding the biological role of EPO, in the
CC development of other compounds that bind to EPO-R, as commercial research
CC reagents for various medical research and diagnostic applications, for
CC detecting EPO receptors on living cells, for treatment of disorders
CC associated with a deficiency of EPO, such as end-stage renal
CC failure/dialysis, anaemia associated with AIDS and chronic inflammatory
CC diseases, autoimmune diseases and malignancies, and for boosting the red
CC blood count of a patient prior to surgery
XX
SQ Sequence 20 AA;

Query Match 43.3%; Score 29; DB 4; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.4e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PFCILGP 12
: : : : :
DB 4 YSCILMGP 10

RESULT 40
ABB83243
ID ABB83243 standard; peptide; 9 AA.
XX
XX ABB83243;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Human ETV6/AML1 fusion protein peptide Y9W.
DE
XX
XX Human; TEL/AML1 fusion protein; cytostatic; immunogenic peptide;
KW lymphoblastic tumour; B-type acute lymphoblastic leukaemia; TEL;
KW Translocation ETS Leukaemia; AML1; Acute Myeloid Leukaemia-1.
XX
XX Homo sapiens.
OS
XX
XX WO200244202-A2.
PN
XX
XX 06-JUN-2002.
PD
XX
XX 29-NOV-2001; 2001WO-FR003779.
PF
XX
XX 01-DEC-2000; 2000CA-02325666.
PR
XX
XX (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX

PI Firat H, Langlade-Demoyan P, Vilmer E, Lemonnier F, Rohrllich P;
PI Yotnda P;
XX
XX WPI; 2002-471825/50.
DR
XX
XX New mutated peptide from fusion protein TEL/AML1, useful for vaccination
PT against acute lymphoblastic leukemia, also related nucleic acid and
PT transfected tumor cells.
XX
XX Example 1; Page 20; 47pp; French.
XX
XX The present invention relates to mutated immunogenic peptides (ABB83233-
CC ABB83238), derived from wild-type human fusion protein TEL/AML1 peptide
CC R9W (TEL: Translocation ETS Leukaemia; AML1: Acute Myeloid Leukaemia-1.
CC ABB83232). The mutated immunogenic peptides can induce an immune response
CC against development of lymphoblastic tumour cells, specifically B-type
CC acute lymphoblastic leukaemia (ALL) cells associated with the t(12;21)
CC translocation (TEL is located on chromosome 12 and AML1 is located on
CC chromosome 21). The present peptide was used in an example from the
CC invention
XX
SQ Sequence 9 AA;

Query Match 41.8%; Score 28; DB 5; Length 9;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECILG 11
: : : : :
DB 4 ECILG 8

RESULT 41
ABB83232
ID ABB83232 standard; peptide; 9 AA.
XX
XX ABB83232;
AC
XX
XX 19-AUG-2002 (first entry)
DT
XX
XX Wild-type human TEL/AML1 fusion protein peptide R9W.
DE
XX
XX Human; TEL/AML1 fusion protein; cytostatic; immunogenic peptide;
KW lymphoblastic tumour; B-type acute lymphoblastic leukaemia; TEL;
KW Translocation ETS Leukaemia; AML1; Acute Myeloid Leukaemia-1.
XX
XX Homo sapiens.
OS
XX
XX WO200244202-A2.
PN
XX
XX 06-JUN-2002.
PD
XX
XX 29-NOV-2001; 2001WO-FR003779.
PF
XX
XX 01-DEC-2000; 2000CA-02325666.
PR
XX
XX (INSP) INST PASTEUR.
PA (INRM) INSERM INST NAT SANTE & RECH MEDICALE.
PA (ASSI-) ASSISTANCE PUBLIQUE HOPITAUX PARIS.
XX
XX Firat H, Langlade-Demoyan P, Vilmer E, Lemonnier F, Rohrllich P;
PI Yotnda P;
XX
XX WPI; 2002-471825/50.
DR
XX
XX N-PSDB; ABB83397.
DR
XX
XX New mutated peptide from fusion protein TEL/AML1, useful for vaccination
PT against acute lymphoblastic leukemia, also related nucleic acid and
PT transfected tumor cells.
XX
XX Claim 1; Page 6; 47pp; French.
XX
XX The present invention relates to mutated immunogenic peptides (ABB83233-

CC ABB83238), derived from the present peptide: wild-type human fusion
 CC protein TEL/AML1 peptide R9M (TEL: Translocation B15 Leukaemia; AML1:
 CC Acute Myeloid Leukemia-1). The mutated immunogenic peptides can induce
 CC an immune response against development of lymphoblastic tumour cells,
 CC specifically B-type acute lymphoblastic leukaemia (ALL) cells associated
 CC with the t(12;21) translocation (TEL is located on chromosome 12 and AML1
 CC is located on chromosome 21)

XX Sequence 9 AA;

Query Match 41.8%; Score 28; DB 5; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECTIG 11
 |||||
 DB 4 ECTIG 8

RESULT 42

ADCS9364
 ID ADCS9364 standard; peptide; 9 AA.

AC ADCS9364;
 XX
 DT 18-DEC-2003 (first entry)
 XX
 DE GST binding peptide #11.
 XX
 XX Glutathione-S-transferase pI, GST pI; GST pI inhibitory peptide;
 KM inhibitory peptide; drug metabolising enzyme; GST binding protein;
 KM drug resistance; cancer; cytotoxic effect; cytostatic.

OS Unidentified.

XX JP2002371100-A.

XX 26-DEC-2002.

XX 11-JUN-2001; 2001JP-00176265.

XX 11-JUN-2001; 2001JP-00176265.

XX (TAMA-) TAMA TLO KK.

XX WPI; 2003-472866/45.

XX Glutathione-S-transferase (GST) binding peptides and a process for their
 PT preparation for GST-pai inhibitors without substantial adverse reaction.
 PT

PS Claim 2; Page 2; 6pp; Japanese.

XX The invention discloses glutathione-S-transferase (GST) pI inhibitory
 CC peptides which are useful as drug metabolising enzymes. The GST binding
 CC proteins are prepared by culture of a transformant obtained from GST
 CC plasmid and purification of resultant GST binding peptide,
 CC preparation of a peptide library, recovery of a phage expressing GST
 CC binding peptide, purification of the phage from single plaque and
 CC determination of the peptide sequence of GST binding phage. The agents
 CC overcome drug resistance of cancers. The peptides improvement of drug
 CC sensitivity of cancer cells providing elevated cytotoxic effect. The
 CC sequence presented is a GST binding peptide of the invention.

XX Sequence 9 AA;

Query Match 41.8%; Score 28; DB 7; Length 9;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILGP 12
 |||||
 DB 1 CILGP 5

RESULT 43

ADG20335
 ID ADG20335 standard; peptide; 9 AA.

XX ADG20335;

XX 11-MAR-2004 (first entry)

XX Antigenic peptide SEQ ID NO:11.

XX double-chimeric beta 2-microglobulin; antigenic peptide;
 KM antigen-presenting cell; beta 2-microglobulin;
 KM major histocompatibility complex class I epitope; MHC class I epitope;
 KM cytotoxic; antibacterial; virucide; fungicide; protozoacide; vaccine;
 KM cytotoxic T lymphocyte induction; cancer; pathogenic organism;
 KM tumour associated antigen; pathogenic antigen.

XX Synthetic.

XX WO2003106616-A2.

XX 24-DEC-2003.

XX 12-JUN-2003; 2003WO-11000501.

XX 12-JUN-2002; 2002US-0388273P.

XX (GAVI-) GAVISH-GALILEE BIO APPL LTD.

XX Gross G, Margalit A;

XX WPI; 2004-071554/07.

XX Novel double-chimeric beta2-microglobulin polynucleotide useful for
 PT treating cancer, comprising sequence encoding polypeptide capable of
 PT presentation of antigenic peptides.

PS Claim 16; SEQ ID NO 11; 86pp; English.

XX The present invention describes a double-chimeric beta 2-microglobulin
 CC polynucleotide (I) comprising a sequence encoding a polypeptide (II) that
 CC is capable of high level presentation of antigenic peptides on antigen-
 CC presenting cells, where (II) comprising a beta 2-microglobulin molecule
 CC that is linked through its carboxyl terminal to a polypeptide stretch
 CC which allows the anchorage of the beta 2-microglobulin molecule to the
 CC cell membrane, and through its amino terminal to an antigenic peptide
 CC comprising major histocompatibility complex (MHC) class I epitope. The
 CC antigenic peptide is not related to an autoimmune disease. Also
 CC described: (1) an expression vector (III) comprising (I) and is a
 CC recombinant viral vector; (2) an antigen-presenting cell (IV) transfected
 CC with (I); (3) a DNA vaccine (V) comprising a (I) or (III); (4) a cellular
 CC vaccine (VI) for the prevention or treatment of cancer comprising (IV)
 CC which express (I) or tumour cells transfected with (I), where the cells
 CC have been pulsed with an antigenic peptide derived from one tumour
 CC associated antigen; and (5) a pharmaceutical composition (VII) comprising
 CC (I), (III) or (IV) as an active ingredient and carrier. (I) has
 CC cytotoxic, antibacterial, virucide, fungicide and protozoacide
 CC activities, and can be used in vaccines, and for inducing cytotoxic T
 CC lymphocytes. (I) and (V) can be used for the prevention or treatment of
 CC cancer or for a disease caused by a pathogenic organism. (VI) is useful
 CC for prevention or treatment of cancer, or disease caused by a pathogenic
 CC organism, where (VI) presents one tumour associated antigen, or
 CC pathogenic antigen. (VI) is also useful for immunising a mammal against a
 CC tumour-associated antigen or a disease caused by a pathogenic organism,
 CC which involves immunising the mammal with (VI). (I) is useful for
 CC inducing class I-restricted CTL response in a mammal. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 9 AA;

Query Match 41.8%; Score 28; DB 8; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECTIG 11
 |||||
 Db 4 ECTIG 8

RESULT 44
 ADX08674
 ID ADX08674 standard; peptide; 9 AA.

AC ADX08674;
 XX
 DT 21-APR-2005 (first entry)
 XX

DE HLA class I restricted epitope (derived from fusion protein) peptide #10.
 XX
 KW vaccine; infection; viral infections; virucide; bacterial infection;
 KW antibacterial; yeast infection; fungicide; fungal infection;
 KW protozoal infection; protozoacide; cancer; cytostatic; melanoma;
 KW lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
 KW multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
 KW antineumatic; systemic lupus erythematosus; antiinflammatory;
 KW dermatological; immunosuppressive.
 XX
 OS Unidentified.
 XX
 PN WO2005011730-A1.
 XX
 PD 10-FEB-2005.
 XX
 PF 30-JUL-2004; 2004WO-GB003285.
 XX
 PR 01-AUG-2003; 2003GB-00018096.
 XX

(UNIO) QUEEN MARY & WESTFIELD COLLEGE.
 PA
 PI Wang P, Li S;
 XX
 PI
 XX
 DR WPI; 2005-152360/16.

PT New vaccine composition comprises inverted microsomes from animal cells
 PT with an externally disposed peptide antigen and a protein of the Major
 PT Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
 PT cancer.
 XX
 PS Disclosure; Page 60; 83pp; English.
 XX
 CC The invention comprises a vaccine composition that consists of isolated
 CC inverted microsomes from an animal cell (or its membrane fragments). In
 CC association with an externally disposed peptide antigen and a protein of
 CC the MHC. The vaccine composition of the invention is useful for the
 CC prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
 CC fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
 CC cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
 CC sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
 CC present amino acid sequence represents an HLA class I restricted epitope
 CC derived from a fusion protein.
 XX
 SQ Sequence 9 AA;

Query Match 41.8%; Score 28; DB 9; Length 9;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECTIG 11
 |||||
 Db 4 ECTIG 8

RESULT 45
 AAW98996
 ID AAW98996 standard; peptide; 10 AA.

XX AAW98996;
 AC
 XX
 DT 11-MAY-1999 (first entry)
 XX
 DE I domain peptide P1.
 XX
 KW Cyclic integrin binding peptide; integrin alpha-2i domain; inhibitor;
 KW collagen IV; collagen IV; laminin-1; cell migration; cancer;
 KW cardiovascular disease; periodontal disease.
 XX
 OS Synthetic.
 XX
 PN WO9902551-A1.
 XX
 PD 21-JAN-1999.
 XX
 PF 09-JUL-1998; 98WO-FI000579.
 XX
 PR 11-JUL-1997; 97US-00893526.
 XX
 PA (HEIN/) HEINO J.
 PA (IVAS/) IVASKA J.
 PA (KASP/) KAPRYLAE J.
 XX
 PI Heino J, Ivaaka J, Kaepylae J;
 XX
 DR WPI; 1999-120775/10.

PT Cyclic integrin binding peptides - used to inhibit integrin-dependant
 PT cell migration.
 XX
 PS Example 3; Page 24; 59pp; English.
 XX
 CC The present sequence invention describes cyclic integrin binding peptides
 CC comprising the amino acid sequence RKK, preferably RKKH. Also described
 CC in the present invention are: (1) a cyclic peptide comprising the amino
 CC acid sequence XIRKKHX2Xn where X is any amino acid and n=1-4; (2) a
 CC cyclic integrin binding peptide comprising the amino acid sequence
 CC CTRKKHNC or CTRKKHNAQC; (3) a pharmaceutical composition comprising one
 CC of the above integrin binding peptides; and (4) a binding assay for
 CC identifying integrin binding agents, comprising: (a) biotinylating the
 CC integrin binding agent to be assayed; (b) reacting the biotinylated agent
 CC with an immobilised recombinant alpha 2i domain or domain-derived
 CC peptides in conditions suitable for binding; (c) washing the solid
 CC support carrying the bound agent; (d) adding a labelled biotin-binding
 CC agent; and (e) detecting any bound integrin binding agent. The integrin
 CC binding peptides can be used for inhibiting integrins. They can also be
 CC used for inhibiting integrin-dependent cell migration, such as associated
 CC with cancer, cardiovascular disease or a periodontitis condition. They can
 CC also be used for inhibiting the adhesion of platelets to collagen or
 CC collagen induced platelet aggregation in a patient. The present sequence
 CC represents a peptide from the present invention
 XX
 SQ Sequence 10 AA;

Query Match 41.8%; Score 28; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 5.6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSFEC 8
 |||||
 Db 3 DESNSIYC 10

RESULT 46
 ABR91275
 ID ABR91275 standard; peptide; 13 AA.

AC ABR91275;
 XX
 DT 10-SEP-2003 (first entry)
 XX

DE P. papataei salivary polypeptide immunogenic peptide SEQ ID NO:109.
 XX Phlebotomus papataei; salivary polypeptide; antigenic; immunogenic;
 KM protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.
 XX OS
 OS Phlebotomus papataei.
 XX Synthetic.
 XX WO2002102324-A2.
 XX PD
 PD 27-DEC-2002.
 XX PF
 PF 18-JUN-2002; 2002WO-US019663.
 XX PR
 PR 19-JUN-2001; 2001US-0299391P.
 XX (US98) US DEPT HEALTH & HUMAN SERVICES.
 XX Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;
 PI WPI; 2003-157000/15.
 XX DR
 DR Novel isolated salivary polypeptide of Phlebotomus papataei, useful for
 PT producing an immune response in a subject or for preventing Leishmaniasis
 PT in a subject.
 XX PS
 PS Claim 10; Page 93; 279pp; English.
 XX The present invention describes an isolated salivary polypeptide (I), of
 CC Phlebotomus papataei. Also described: (1) an isolated nucleic acid (II)
 CC encoding (I); (2) an isolated fragment (III) of (II), where the fragment
 CC encodes the polypeptide fragment specific for a polypeptide such as
 CC Phlebotomus papataei salivary polypeptide (PSP) 12, PSP14, PSP15,
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
 CC immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridizes
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or
 CC (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)
 CC or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide
 CC and immunostimulant activities, and can be used in vaccines. (VII) is
 CC useful for producing an immune response in a subject or for preventing
 CC Leishmaniasis in a subject. (II) is also useful for preventing
 CC Leishmaniasis in a subject. (VI) is also useful as a vaccine. ACC79987 to
 CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the
 CC exemplification of the present invention
 XX SQ
 SQ Sequence 13 AA;
 Query Match 41.8%; Score 28; DB 6; Length 13;
 Best Local Similarity 100.0%; Pred. No. 7.3e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

KM dermatological; antiinflammatory; cardiant; ophthalmological; uropathic;
 XX antidiabetic; antithyroid; antidepressant; hepatotropic.
 XX OS
 OS Unidentified.
 XX WO200216411-A2.
 XX PN
 PN 28-FEB-2002.
 XX PD
 PD 17-AUG-2001; 2001WO-US025850.
 XX PF
 PF 18-AUG-2000; 2000US-0226700P.
 XX PR
 PR (HDMA-) HUMAN GENOME SCI INC.
 XX PA
 PA Beltez JP, Potter DM, Fleming TL, Rosen CA;
 PI WPI; 2002-499775/53.
 XX DR
 DR The treatment of various diseases e.g. rheumatoid arthritis, comprises
 PT administering B lymphocyte stimulator binding polypeptide.
 PT
 XX PS
 PS Claim 70; Page 192; 387pp; English.
 XX The present invention relates to the treatment, prevention or
 CC amelioration of a disease or disorder associated with: aberrant B
 CC lymphocyte stimulator (Blys), Blys receptor expression or activity; cells
 CC of hematopoietic origin; or proliferative disease; and reducing,
 CC inhibiting or stimulating immunoglobulin production, B cell proliferation
 CC and graft rejection involving administration of Blys binding polypeptide.
 CC The Blys binding polypeptides are used in the treatment, prevention or
 CC amelioration of diseases such as immune system diseases, proliferative
 CC diseases, diseases of cells of hematopoietic origin, graft rejection,
 CC allergies, infectious diseases, arteriosclerosis, inflammatory disorders,
 CC hypergammaglobulinaemia, blood clotting disorders, ischaemia, and
 CC neurodegenerative diseases. The present sequence is a B lymphocyte
 CC stimulator protein binding peptide
 XX SQ
 SQ Sequence 14 AA;
 Query Match 41.8%; Score 28; DB 5; Length 14;
 Best Local Similarity 57.1%; Pred. No. 7.8e+02;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPCIL 10
 Db 5 FPCIL 9
 RESULT 47
 AB000601
 ID AB000601 standard; peptide; 14 AA.
 XX
 XX AB000601,
 XX
 DT 05-SEP-2002 (first entry)
 XX
 XX B lymphocyte stimulator protein binding peptide #45.
 XX
 KM B lymphocyte stimulator protein binding protein; Blys; immune disease;
 KM allergy; proliferative disease; infectious disease; arteriosclerosis;
 KM inflammatory disorder; hypergammaglobulinaemia; blood clotting;
 KM ischaemia; graft-versus-host disease; neurodegenerative disease;
 KM immunosuppressive; nephrotropic; antineumatic; antiarthritic;
 KM neuroprotective; cytotoxic; immunostimulant; antitumour; anti-HIV;
 KM antiaesthetic; antiallergic; thyromimetic; antianemic; haemostatic;

QY 6 FPCIL 12
 Db 2 FPCIL 8
 RESULT 48
 ABG33462
 ID ABG33462 standard; peptide; 14 AA.
 XX
 XX ABG33462;
 XX
 DT 15-UTL-2002 (first entry)
 XX
 XX B lymphocyte stimulator (Blys) binding peptide #50.
 DE
 KM B lymphocyte stimulator protein; B lymphocyte stimulator binding peptide;
 KM Blys; biological fluid; serum; plasma; lymph; blood; urine; spinal fluid;
 KM synovial fluid; saliva; mucus.
 XX
 XX Synthetic.
 XX
 PN WO200216412-A2.
 XX
 PD 28-FEB-2002.
 XX
 PF 17-AUG-2001; 2001WO-US025891.
 XX
 PR 18-AUG-2000; 2000US-0226489P.
 XX

CC heart defects, etc), neovascularisation disorders, wound healing and
 CC epithelial cell proliferation, neurological diseases (such as Alzheimer's
 CC disease, Parkinson's disease, Huntington's disease, mania, dementia,
 CC etc), infectious diseases caused by virus, bacteria, fungi, etc. The
 CC present sequence represents the amino acid sequence of a novel human
 CC secreted protein associated polypeptide.

SO Sequence 14 AA;

Query Match 41.8%; Score 28; DB 7; Length 14;
 Best Local Similarity 55.6%; Pred. No. 7.8e+02;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

OY 3 KNSPECTIG 11
 DB 3 KQDLHCILG 11

RESULT 50

ADJ55612 standard; protein; 14 AA.

ADJ55612;

06-MAY-2004 (first entry)

Novel human secreted protein fragment #136.

neuroprotective; nootropic; antiparkinsonian; anticonvulsant;
 antiarthritis; antirheumatic; antiarthritic; dermatological;
 antiinflammatory; immunosuppressive; antithyroid; antianemic;
 antiparasitic; anti-HIV; hepatotropic; vitruclide; antibacterial; fungicide;
 antidiabetic; muscular; gynecological; gastrointestinal; respiratory;
 cardiovascular; litholytic; cytoskeletal; antiarrhythmic; cardiac;
 nephrotropic; litholytic; cytoskeletal; gene therapy; neural disorder;
 Alzheimer's disease; Parkinson's disease; Huntington's chorea;
 amyotrophic lateral sclerosis; multiple sclerosis;
 immune system disorder; diabetes; rheumatoid arthritis;
 systemic lupus erythematosus; autoimmune thyroiditis; haemolytic anemia;
 inflammatory bowel disease; Crohn's disease; infectious disease;
 infection; muscular disorder; reproductive disorder;
 gastroenteroal disorder; pulmonary disorder; cardiovascular disorder;
 atherosclerosis; arrhythmia; myocarditis; renal disorder;
 acute glomerulonephritis; pyelonephritis; renal lithiasis;
 hyperproliferative disorder; cancer; human.

Homo sapiens.

US2004023283-A1.

05-FEB-2004.

18-JUL-2003; 2003US-00621363.

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 PR 19-AUG-199

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DE 63B internal peptide.
XX
XX 63B protein; formicidal; toxin; carpenter; fire; argentine; pharaoh ant.
XX
XX Bacillus thuringiensis.
OS
XX EP1065275-A1.
XX
XX 03-JAN-2001.
XX
XX 22-MAY-1992; 2000EP-00114196.
XX
XX 22-MAY-1991; 91US-00703997.
XX
XX 25-NOV-1991; 91US-00797645.
XX
XX 22-MAY-1992; 92EP-00913802.
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX Payne JM, Kennedy MK, Randall JB, Meier H, Vick HJ,
XX
XX WPI; 1992-400664/49.
XX
XX Controlling hymenopteran insect pests - comprises contacting insect with
XX
XX new Bacillus thuringiensis and their mutants, useful for killing partic.
XX
XX pharaoh ants.
XX
XX Example 2; Page 16; 55pp; English.
XX
XX
XX The present invention relates to toxins from Bacillus thuringiensis (see
XX
XX AAF23793-AAF23797 and AAB59881-AAB59885). The toxins have activity
XX
XX against hymenopteran pests e.g. carpenter, fire, argentine and pharaoh
XX
XX ants. The toxins can therefore be used to produce formicidal compositions
XX
XX for controlling ants, which are a better alternative to chemical
XX
XX insecticides. The present sequence is an internal peptide from one toxin
XX
XX (63B) identified in the present invention
XX
XX
XX Sequence 15 AA;
SQ
XX
XX
XX Query Match 41.8%; Score 28; DB 2; Length 15;
XX
XX Best Local Similarity 66.7%; Pred. No. 8.4e+02;
XX
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1 DEKNSPECT 9
XX
XX |||||:|
XX
XX 6 DEKLSFQLI 14
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XX
XX RESULT 52
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XX AAR63075
XX
XX ID AAR63075 standard; peptide; 15 AA.
XX
XX
XX AAR63075;
XX
XX
XX 16-OCT-2003 (revised)
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 12-AUG-1995 (first entry)
XX
XX
XX B.t. PS63B toxin internal peptide.
XX
XX
XX Delta-endotoxin; crystal protein; biological control agent; Calliphorida;
XX
XX screw-worm; sheep blowfly; Lucilia; Phormia; Calliphora; insecticide;
XX
XX pesticide; B.t.
XX
XX
XX Bacillus thuringiensis; isolate PS63B.
XX
XX
XX WO9502694-A2.
XX
XX PN
XX
XX 26-JAN-1995.
XX
XX
XX 13-JUL-1994; 94WO-US007902.
XX
XX PF
XX
XX 15-JUL-1993; 93US-00093199.
XX
XX

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PA (MYCO ) MYCOGEN CORP.
XX
XX
XX Hickle LA, Payne J;
XX
XX WPI; 1995-067338/09.
XX
XX
XX Method for controlling Calliphoridae pests - specifically utilizes
XX
XX Bacillus thuringiensis isolates or toxins.
XX
XX
XX Example 2; Page 15; 50pp; English.
XX
XX
XX N-terminal sequences of proteins from parasporal inclusion bodies of
XX
XX CC Bacillus thuringiensis (B.t.) isolates PS86Q3, PS63B, PS52A1 and PS33F2,
XX
XX CC and an internal peptide of the 63B protein, are given in AAR63071-75, and
XX
XX CC were used to design probes and primers (AA081159-77) for the isolation
XX
XX CC and cloning of B.t. genes encoding delta-endotoxins, used to control e.g.
XX
XX CC screw-worm and sheep blowfly. (updated on 25-MAR-2003 to correct PN
XX
XX CC field.) (updated on 16-OCT-2003 to standardise OS field)
XX
XX
XX Sequence 15 AA;
SQ
XX
XX
XX Query Match 41.8%; Score 28; DB 2; Length 15;
XX
XX Best Local Similarity 66.7%; Pred. No. 8.4e+02;
XX
XX Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
XX
XX
XX 1 DEKNSPECT 9
XX
XX |||||:|
XX
XX 6 DEKLSFQLI 14
XX
XX
XX RESULT 53
XX
XX AAM13880
XX
XX ID AAM13880 standard; protein; 15 AA.
XX
XX
XX AAM13880;
XX
XX
XX 17-OCT-2003 (revised)
XX
XX DT 25-MAR-2003 (revised)
XX
XX DT 14-MAY-1997 (first entry)
XX
XX
XX N-terminal peptide of protein 63B(2).
XX
XX
XX Toxin; ant; Bacillus thuringiensis; hymenopteran pest; pharaoh ant;
XX
XX KM biological control; Monomorium pharaonis; delta-endotoxin; Lepidoptera;
XX
XX KM insect; N-terminal peptide.
XX
XX
XX Bacillus thuringiensis; isolate PS63B.
XX
XX
XX US5596071-A.
XX
XX PN
XX
XX 21-JAN-1997.
XX
XX
XX 24-NOV-1993; 93US-00158232.
XX
XX PF
XX
XX 22-MAY-1991; 91US-00703977.
XX
XX PR 25-NOV-1991; 91US-00797645.
XX
XX PR 22-MAY-1992; 92US-00887980.
XX
XX
XX (MYCO ) MYCOGEN CORP.
XX
XX
XX Vick HJ, Meier H, Payne JM, Schwab GE, Fu J, Foncerra L;
XX
XX Kennedy MK, Schnepf HJ, Randall JB;
XX
XX WPI; 1997-107615/10.
XX
XX
XX Bacillus thuringiensis toxin - active against hymenopteran pests.
XX
XX
XX Example 2; Col 19; 64pp; English.
XX
XX
XX AAM13873-W13881 represent N-terminal peptides for the proteins of the
XX
XX CC invention (see AAM13872, and AAM13884-W13887). The peptides were all
XX
XX CC isolated from different Bacillus thuringiensis (B.t.) isolates. B.t. is a
XX
XX CC gram-positive, spore forming, soil bacterium, characterised by parasporal

```

CC crystalline protein inclusions. These proteins can be highly toxic to
 CC pests, and have been used to produce insect resistant plants. The
 CC previously isolated B.t. delta-endotoxins were mainly active against
 CC lepidopteran insects, however the proteins of the invention are active
 CC against hymenopteran insects. The sequences represented by AAM13888 and
 CC AAM13871 represent the generic formulae for the toxins of the invention.
 CC As the toxins of the invention are active against hymenopteran pests,
 CC they can be used for the biological control of ants, particularly pharaoh
 CC ants (Monomorium pharaonis) (Updated on 25-MAR-2003 to correct PR
 CC field.) (Updated on 17-OCT-2003 to standardise OS field)

XX Sequence 15 AA;

Query Match 41.8%; Score 28; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 8.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 DB 6 DEKLSFOLI 14

RESULT 54
 ID AAM73115 standard; protein; 15 AA.

XX AAM73115;

DT 06-JAN-1999 (first entry)

DE B.t. toxin protein N-terminal fragment.

XX B.t. toxin; hymenopteran pest; pesticide; ant; insecticide;
 KM paraaporal crystalline protein inclusion.

XX Bacillus thuringiensis.

PN US5824792-A.

PD 20-OCT-1998.

PF 06-MAR-1996; 96US-00611928.

PR 22-MAY-1991; 91US-00703977.

PR 25-NOV-1991; 91US-00797645.

PR 22-MAY-1992; 92US-00887980.

PR 24-NOV-1993; 93US-00158232.

XX (MYCO) MYCOGEN CORP.

XX Payne JM, Meier H, Fonceerrada L, Schwab GE, Fu J, Vick HJ;

PI Kennedy MK, Schnepf HE, Randall JB;

DR WPI; 1998-582628/49.

XX Bacillus thuringiensis toxin proteins - useful for insecticidal activity

PT against hymenopteran pests i.e. ants.

XX Example 2; Col 19; 65pp; English.

CC This sequence is a fragment of a *Bacillus thuringiensis* (B.t.) toxin of
 CC the invention. The toxins are lethal to a hymenopteran pest. The DNA
 CC sequences are useful for the recombinant production of B.t. toxins. These
 CC toxins in turn are useful as pesticides against hymenopteran (ant) pests,
 CC especially fire, carpenter, argentine and pharaoh ants. The toxins are
 CC paraaporal crystalline protein inclusions that are highly specific
 CC to pests. The toxins are highly specific against ants, rather than e.g.
 CC toxic chemicals used as insecticides which can be harmful to humans and
 CC the environment in general

XX Sequence 15 AA;

Query Match 41.8%; Score 28; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 8.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 DB 6 DEKLSFOLI 14

RESULT 55
 ID AAB13902 standard; peptide; 15 AA.

XX AAB13902;

DT 13-NOV-2000 (first entry)

DE Internal peptide of *Bacillus thuringiensis* 63B protein.

XX Hymenopteran; ant; pest control; 86Q3a; 17a; 17b; 33P2; 63B.

XX *Bacillus thuringiensis*.

OS *Bacillus thuringiensis*.

PN US6077937-A.

PD 20-JUN-2000.

PF 16-OCT-1998; 98US-00173891.

PR 22-MAY-1991; 91US-00703977.

PR 25-NOV-1991; 91US-00797645.

PR 22-MAY-1992; 92US-00887980.

PR 24-NOV-1993; 93US-00158232.

PR 06-MAR-1996; 96US-00611928.

XX (MYCO) MYCOGEN CORP.

XX Meier H, Kennedy MK, Schwab GE, Fu J, Payne JM, Vick HJ;

PI Fonceerrada L, Schnepf HE, Randall JB;

DR WPI; 2000-450980/39.

XX N-PSDB; AAM65095.

XX New *Bacillus thuringiensis* toxins with activity against hymenopteran

PT pests such as fire ants and carpenter ants, conform to a specific generic

PT formula and have a specific amino acid sequence.

XX Example 2; Col 20; 67pp; English.

CC The present invention relates to novel *Bacillus thuringiensis* toxins with

CC hymenopteran activity. Preparations containing protein from *Bacillus*

CC *thuringiensis* were tested for toxicity to ants. The N-terminal amino

CC acids of toxic proteins were then sequenced. The present sequence is an

CC internal peptide of the 65B protein. These sequences were used to design

CC oligonucleotide probes. The probes were used to clone ant-active toxin

CC genes. The toxic proteins can be used to control pests such as fire ants,

CC carpenter ants, argentine ants and pharaoh ants. The proteins can also be

CC used for producing transgenic plants that are resistant to attack by

CC ants. The proteins are a safe and effective biological control agent

XX Sequence 15 AA;

Query Match 41.8%; Score 28; DB 3; Length 15;
 Best Local Similarity 66.7%; Pred. No. 8.4e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 DB 6 DEKLSFOLI 14

RESULT 56
 AAM10365

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ID AAU10365 standard; peptide; 15 AA.
XX
XX AAU10365;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Bacillus thuringiensis delta-endotoxin PS63B, internal sequence.
DE
XX
XX Delta-endotoxin; nematode-active toxin; PS63B; antihelminthic; nematocidal;
KW fluke.
XX
XX Bacillus thuringiensis.
OS
XX
XX EP1143004-A2.
PN
XX
XX 10-OCT-2001.
PD
XX
XX 04-JUN-1991; 2001BP-00102789.
PF
XX
XX 11-JUN-1990; 90US-00535810.
PR 24-JUL-1990; 90US-00557246.
PR 27-JUL-1990; 90US-00558738.
PR 10-AUG-1990; 90US-00565544.
PR 14-MAR-1991; 91US-00669126.
PR 27-MAR-1991; 91US-00675772.
PR 03-MAY-1991; 91US-00693018.
PR 04-JUN-1991; 91BP-00305047.
XX
XX (MYCO ) MYCOGEN CORP.
PA
XX
XX Narva KE, Payne JM, Schwab GR, Hickie LA, Galasan T, Sick AJ;
PI MPI; 2002-043040/06.
XX
XX Bacillus thuringiensis isolate encoding a toxin active against nematodes.
DR
XX
XX Claim 2; Page 47; 47pp; English.
XX
XX The invention relates to a Bacillus thuringiensis isolate (I) active
CC against nematodes, selected from strains PS167P, PS158D5, PS169B,
CC PS177F1, PS177G, PS204G4, and PS204G6. (I) comprises a toxin encoded by
CC (II). Contacting nematodes with (I), where the DNA (II) has been
CC transformed into a plant or other host cell, may be used to control
CC nematodes. In addition, administering a toxin, from a wild-type Bacillus
CC thuringiensis DNA, to a host harbouring a fluke, or directly to a fluke
CC may also be useful for controlling flukes. The present sequence
CC represents an internal amino acid sequence of B. thuringiensis PS63B, a
CC nematode-active delta-endotoxin as described in the invention
XX
XX
SQ Sequence 15 AA;

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```

Query Match 41.8%; Score 28; DB 5; Length 15;
Best Local Similarity 66.7%; Pred. No. 8.4e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 DEKNSPECTI 9
   |||||:|
Db 6 DEKLSFOLI 14

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RESULT 57
ABR30097
ID ABR30097 standard; peptide; 15 AA.
XX
XX ABR30097;
AC
XX
XX 19-MAY-2003 (first entry)
DT
XX
XX Human cancer-related protein 74P3B3 HLA peptide #2941.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX

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OS Homo sapiens.
XX
XX WO200283921-A2.
XX
XX 24-OCT-2002.
XX
XX 10-APR-2002; 2002WO-US011654.
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
XX (AGEN-) AGENSYS INC.
PA
XX
XX Jakobovits A, Challita-Eid PM, Faris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
XX MPI; 2003-075555/07.
XX
XX New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
XX Claim 13; Page 468; 1021pp; English.
XX
XX The present invention relates to novel human cancer-related genes and
CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
XX
SQ Sequence 15 AA;

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```

Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DEKNSPECTICP 12
   |||||:|
Db 2 DELISFEBHVP 13

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RESULT 58
ABR30031
ID ABR30031 standard; peptide; 15 AA.
XX
XX ABR30031;
AC
XX
XX 19-MAY-2003 (first entry)
DT
XX
XX Human cancer-related protein 74P3B3 HLA peptide #2875.
DE
XX
XX Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
XX Homo sapiens.
OS
XX
XX WO200283921-A2.
PN
XX
XX 24-OCT-2002.
PD
XX
XX 10-APR-2002; 2002WO-US011654.
PF
XX
XX 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR

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PR    25-APR-2001; 2001US-0286630P.
XX
PA    (AGEN-) AGENSYS INC.
XX
PI    Jakobovits A, Challita-Eld PM, Paris M, Ge W, Hubert RS;
PI    Morrison K, Morrison RK, Raitano AB;
XX
DR    MPI; 2003-075555/07.
XX
PT    New composition comprising a substance that modulates the structure of
PT    proteins and polynucleotides, useful for therapeutic, prognostic and
PT    diagnostic reagents for eliciting cellular or humoral immune response in
XX    cancer patients.
XX
PS    Claim 13, Page 467; 1021pp; English.
XX
CC    The present invention relates to novel human cancer-related genes and
CC    proteins (ABZ78120-ABZ78168 and ABR01789-ABR01961). The genes and
CC    proteins are useful for eliciting a humoral or cellular immune response.
CC    The genes are useful as probes and primers for the amplification and/or
CC    detection of genes, mRNAs or their fragments, as reagents for the
CC    diagnosis and/or prognosis of cancer, as coding sequences capable of
CC    inhibiting the expression of the protein, as tools for modulating or
CC    inhibiting the expression of genes and/or translation of transcripts, and
CC    as therapeutic agents. The proteins and peptides are useful as
CC    chemopreventive, prognostic and diagnostic reagents for cancer. The present
CC    sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC    from the invention
XX
SQ    Sequence 15 AA;

Query Match          41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY      1 DEKNSFECILAP 12
        ||||| :|||
DB       2 DELISFESEHVP 13

RESULT 59
ABR30127 standard; peptide; 15 AA.
XX
AC     ABR30127;
XX
DT     19-MAY-2003 (first entry)
XX
DE     Human cancer-related protein 74PB3 HLA peptide #2971.
XX
KW     Human; cytosolic; vaccine; cancer; immune response; HLA;
KW     human leukocyte antigen.
XX
OS     Homo sapiens.
XX
PN     WO200283921-A2.
XX
PD     24-OCT-2002.
XX
PF     10-APR-2002; 2002WO-US011654.
XX
PR     10-APR-2001; 2001US-0282739P.
PR     10-APR-2001; 2001US-0283112P.
PR     25-APR-2001; 2001US-0286630P.
XX
PA     (AGEN-) AGENSYS INC.
XX
PI     Jakobovits A, Challita-Eld PM, Paris M, Ge W, Hubert RS;
PI     Morrison K, Morrison RK, Raitano AB;
XX
DR     MPI; 2003-075555/07.
XX
New composition comprising a substance that modulates the structure of

```

PT	proteins and polynucleotides; useful for therapeutic,
PT	diagnostic reagents for eliciting cellular or humoral immune response in
PT	cancer patients.
PS	Claim 13; Page 469; 1021pp; English.
XX	
CC	The present invention relates to novel human cancer-related genes and
CC	proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC	proteins are useful for eliciting a humoral or cellular immune response.
CC	The genes are useful as probes and primers for the amplification and/or
CC	detection of genes, mRNAs or their fragments, as reagents for the
CC	diagnosis and/or prognosis of cancer, as coding sequences capable of
CC	directing the expression of the protein, as tools for modulating or
CC	inhibiting the expression of genes and/or translation of transcripts, and
CC	as therapeutic agents. The proteins and peptides are useful as
CC	therapeutic, prognostic and diagnostic reagents for cancer. The present
CC	sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC	from the invention
XX	
SQ	Sequence 15 AA;
Query Match	41.8%; Score 28; DB 6; Length 15;
Best Local Similarity	58.3%; Pred. NO. 8.4e+02;
Matches	7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
Oy	1 DENKSPFICIGP 12 : 2 DELISFEHVGVP 13
Db	
RESULT 60	
ABR30078	
ID	ABR30078 standard; peptide; 15 AA.
XX	
AC	ABR30078;
XX	
DT	19-MAY-2003 (first entry)
DS	Human cancer-related protein 74P3B HLA peptide #2922.
XX	
KM	Human; cytostatic; vaccine; cancer; immune response; HLA;
KW	human leukocyte antigen.
OS	Homo sapiens.
PX	WO200283921-A2.
XX	
PD	24-OCT-2002.
PF	10-APR-2002; 2002MO-USO11654.
PR	10-APR-2001; 2001US-0282739P.
PR	10-APR-2001; 2001US-0283112P.
XX	25-APR-2001; 2001US-0286630P.
PA	(AGEN-) AGENSYS INC.
PI	Jakovovics A, Chalilita-Bid PM, Faris M, Ge W, Hubert RS;
PI	Morrison K, Morrison RK, Raitano AB;
DR	WPI; 2003-075555/07.
XX	
XX	New composition comprising a substance that modulates the structure of
PT	proteins and polynucleotides; useful for therapeutic, prognostic and
PT	diagnostic reagents for eliciting cellular or humoral immune response in
PT	cancer patients.
XX	
XX	Claim 13; Page 468; 1021pp; English.
CC	
CC	The present invention relates to novel human cancer-related genes and
CC	proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and
CC	proteins are useful for eliciting a humoral or cellular immune response.
CC	The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;

Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSFECITLGP 12
|||
DB 1 DELISFEEHVGVP 12

RESULT 61

ABR29975
ID ABR29975 standard; peptide, 15 AA.

AC ABR29975;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 74P3B3 HLA peptide #2819.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

PN 24-OCT-2002.

PD 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Chailita-Eld PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX MPI; 2003-075555/07.

DR MPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and

PT diagnostic reagents for eliciting cellular or humoral immune response in

PT cancer patients.

XX Claim 13; Page 466; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention

CC Sequence 15 AA;

Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSFECITLGP 12
|||
DB 1 DELISFEEHVGVP 12

RESULT 62

ABR30106
ID ABR30106 standard; peptide, 15 AA.

AC ABR30106;

DT 19-MAY-2003 (first entry)

DE Human cancer-related protein 74P3B3 HLA peptide #2950.

XX Human; cytostatic; vaccine; cancer; immune response; HLA;

KW human leukocyte antigen.

XX Homo sapiens.

OS WO200283921-A2.

PN 24-OCT-2002.

PD 10-APR-2002; 2002WO-US011654.

XX 10-APR-2001; 2001US-0282739P.

PR 10-APR-2001; 2001US-0283112P.

PR 25-APR-2001; 2001US-0286630P.

XX (AGEN-) AGENSYS INC.

XX Jakobovits A, Chailita-Eld PM, Faris M, Ge W, Hubert RS;

PI Morrison K, Morrison RK, Raitano AB;

XX MPI; 2003-075555/07.

DR MPI; 2003-075555/07.

XX New composition comprising a substance that modulates the structure of

PT proteins and polynucleotides, useful for therapeutic, prognostic and

PT diagnostic reagents for eliciting cellular or humoral immune response in

PT cancer patients.

XX Claim 13; Page 468; 1021pp; English.

XX The present invention relates to novel human cancer-related genes and

CC proteins (ABZ78120-ABZ78168 and ABR01789-ABR01861). The genes and

CC proteins are useful for eliciting a humoral or cellular immune response.

CC The genes are useful as probes and primers for the amplification and/or

CC detection of genes, mRNAs or their fragments, as reagents for the

CC diagnosis and/or prognosis of cancer, as coding sequences capable of

CC directing the expression of the protein, as tools for modulating or

CC inhibiting the expression of genes and/or translation of transcripts, and

CC as therapeutic agents. The proteins and peptides are useful as

CC therapeutic, prognostic and diagnostic reagents for cancer. The present

CC sequence is a human leukocyte antigen (HLA) peptide, used in an example

CC from the invention

CC Sequence 15 AA;

Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSFECITLGP 12
|||
DB 1 DELISFEEHVGVP 12

RESULT 63
ABR30059 standard; peptide; 15 AA.
XX ABR30059;
AC ABR30059;
OS
DT 19-MAY-2003 (first entry)
XX
DE Human cancer-related protein 74P3B3 HLA peptide #2903.
XX
KW Human; cytostatic; vaccine; cancer; immune response; HLA;
KW human leukocyte antigen.
XX
OS Homo sapiens.
OS
PN WO200283921-A2.
XX
PD 24-OCT-2002.
XX
PF 10-APR-2002; 2002WO-US011654.
XX
PR 10-APR-2001; 2001US-0282739P.
PR 10-APR-2001; 2001US-0283112P.
PR 25-APR-2001; 2001US-0286630P.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Jakobovits A, Chailita-Bid PM, Paris M, Ge W, Hubert RS;
PI Morrison K, Morrison RK, Raitano AB;
XX
DR WPI; 2003-07555/07.
XX
PT New composition comprising a substance that modulates the structure of
PT proteins and polynucleotides, useful for therapeutic, prognostic and
PT diagnostic reagents for eliciting cellular or humoral immune response in
PT cancer patients.
XX
PS Claim 13; Page 467; 1021pp; English.
XX
CC The present invention relates to novel human cancer-related genes and
CC proteins (AB278120-AB278168 and ABR01789-ABR01861). The genes and
CC proteins are useful for eliciting a humoral or cellular immune response.
CC The genes are useful as probes and primers for the amplification and/or
CC detection of genes, mRNAs or their fragments, as reagents for the
CC diagnosis and/or prognosis of cancer, as coding sequences capable of
CC directing the expression of the protein, as tools for modulating or
CC inhibiting the expression of genes and/or translation of transcripts, and
CC as therapeutic agents. The proteins and peptides are useful as
CC therapeutic, prognostic and diagnostic reagents for cancer. The present
CC sequence is a human leukocyte antigen (HLA) peptide, used in an example
CC from the invention
XX
SQ Sequence 15 AA;
XX

Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 58.3%; Pred. No. 8.4e+02;
Matches 7; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 1 DENRSEFCILGP 12
|||
DB 1 DELISFEBHVG 12
|||

RESULT 64
ABR91283 standard; peptide; 15 AA.
XX ABR91283;
AC ABR91283;
OS
DT 10-SEP-2003 (first entry)
XX
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:117.
XX

KW Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;
KW protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.
XX
XX Phlebotomus papatasi.
OS
OS Synthetic.
XX
PN WO2002102324-A2.
XX
PD 27-DEC-2002.
XX
PF 18-JUN-2002; 2002WO-US019663.
XX
PR 19-JUN-2001; 2001US-0299391P.
XX
PA (USSH) US DBPT HEALTH & HUMAN SERVICES.
XX
PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;
XX
DR WPI; 2003-157000/15.
XX
PT Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for
PT producing an immune response in a subject or for preventing Leishmaniasis
PT in a subject.
XX
PS Claim 10; Page 95; 279pp; English.
XX
CC The present invention describes an isolated salivary polypeptide (I), of
CC Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)
CC encoding (I); (2) an isolated fragment (III) of (II), where the fragment
CC encodes the polypeptide fragment specific for a polypeptide such as
CC Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,
CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
CC immunogenic fragment (IV) of (I); (4) a nucleic acid (V) that hybridises
CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or
CC (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)
CC or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide
CC and immunostimulant activities, and can be used in vaccines. (VII) is
CC useful for producing an immune response in a subject or for preventing
CC Leishmaniasis in a subject. (II) is also useful for preventing
CC Leishmaniasis in a subject. (VII) is useful as a vaccine. ACC79987 to
CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the
CC exemplification of the present invention
XX
SQ Sequence 15 AA;
XX

Query Match 41.8%; Score 28; DB 6; Length 15;
Best Local Similarity 100.0%; Pred. No. 8.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 6 FFCIL 10
|||
DB 5 FFCIL 9
|||

RESULT 65
ABR91282 standard; peptide; 15 AA.
XX ABR91282;
AC ABR91282;
OS
DT 10-SEP-2003 (first entry)
XX
DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:116.
XX
KW Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;
KW protozoacide; immunostimulant; vaccine; immune response; Leishmaniasis.
XX
OS Phlebotomus papatasi.
OS Synthetic.
XX
PN WO2002102324-A2.
XX
PD 27-DEC-2002.
XX

XX 18-JUN-2002; 2002WO-US019663.
 XX
 XX
 PR 19-JUN-2001; 2001US-0299391P.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;
 XX WPI; 2003-157000/15.
 DR
 XX Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for
 PT producing an immune response in a subject or for preventing Leishmaniasis
 PT in a subject.
 XX
 PS Claim 10; Page 95; 279pp; English.
 XX
 CC The present invention describes an isolated salivary polypeptide (I), of
 CC Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)
 CC encoding (i); (2) an isolated fragment (III) of (II), where the fragment
 CC encodes the polypeptide fragment specific for a polypeptide such as
 CC Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
 CC immunogenic fragment (IV) of (i); (4) a nucleic acid (V) that hybridizes
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or
 CC (III); and (6) a composition (VII) comprising (i) or its fragment, (IV)
 CC or (VI), and a pharmaceutically acceptable carrier. (I) has protozoacide
 CC and immunostimulant activities, and can be used in vaccines. (VII) is
 CC useful for producing an immune response in a subject or for preventing
 CC Leishmaniasis in a subject. (II) is also useful for preventing
 CC Leishmaniasis in a subject. (VII) is useful as a vaccine. ACC79987 to
 CC exemplification of the present invention
 CC
 SQ Sequence 15 AA;
 Query Match 41.8%; Score 28; DB 6; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 FCITL 10
 DB 7 FCITL 11
 RESULT 66
 ADX08687
 ID ADX08687 standard; peptide; 15 AA.
 XX
 AC ADX08687;
 XX
 DT 21-APR-2005 (first entry)
 XX
 DE HLA class II restricted epitope (derived from fusion protein) peptide 13.
 XX
 XX vaccine; infection; viral infections; virucide; bacterial infection;
 KW antibacterial; yeast infection; fungicide; fungal infection;
 KW protozoal infection; protozoacide; cancer; cytostatic; melanoma;
 KW lung tumor; colon tumor; breast tumor; leukemia; autoimmune disease;
 KW multiple sclerosis; neuroprotective; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; systemic lupus erythematosus; antiinflammatory;
 KW dermatological; immunosuppressive.
 XX
 OS Unidentified.
 XX
 PN WO2005011730-A1.
 XX
 PD 10-FEB-2005.
 XX
 PF 30-JUL-2004; 2004WO-GB003285.
 XX
 PR 01-AUG-2003; 2003GB-00018096.
 XX

PA (UNLO) QUEEN MARY & WESTFIELD COLLEGE.
 XX
 XX Wang P, Li S;
 PI
 DR WPI; 2005-152360/16.
 XX
 PT New vaccine composition comprises inverted microsomes from animal cells
 PT with an externally disposed peptide antigen and a protein of the Major
 PT Histocompatibility Complex (MHC), useful for treating or preventing, e.g.
 PT cancer.
 XX
 PS Disclosure; Page 61; 83pp; English.
 XX
 CC The invention comprises a vaccine composition that consists of isolated
 CC inverted microsomes from an animal cell (or its membrane fragments), in
 CC association with an externally disposed peptide antigen and a protein of
 CC the MHC. The vaccine composition of the invention is useful for the
 CC prophylaxis or treatment of: infection (e.g. viral, bacterial, yeast,
 CC fungal or protozoal), cancer (e.g. melanoma, lung adenocarcinoma, colon
 CC cancer, breast cancer or leukemia), autoimmune disease (e.g. multiple
 CC sclerosis, rheumatoid arthritis or systemic lupus erythematosus). The
 CC present amino acid sequence represents an HLA class II restricted epitope
 CC derived from a fusion protein.
 CC
 SQ Sequence 15 AA;
 Query Match 41.8%; Score 28; DB 9; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.4e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 7 FCITL 11
 DB 6 FCITL 10
 RESULT 67
 AAW81961
 ID AAW81961 standard; peptide; 16 AA.
 XX
 AC AAW81961;
 XX
 DT 05-FEB-1999 (first entry)
 XX
 DE Rat ENDO-I protein fragment.
 XX
 KW ENDO; endometriosis; reproductive age; peritoneal fluid; secreted;
 KW stromal cell; tissue inhibitor; metalloproteinases-1; TIMP-1.
 XX
 OS Rattus sp.
 XX
 PN US5843673-A.
 XX
 PD 01-DEC-1998.
 XX
 PF 07-JUN-1995; 95US-00474696.
 XX
 PR 25-OCT-1994; 94US-00328451.
 XX
 PA (UMOR) UNTV MISSOURI.
 XX
 PI Sharpe-Timms KL;
 XX
 DR WPI; 1999-044572/04.
 XX
 PT Diagnosis of endometriosis - based on reduced levels of tissue inhibitor
 PT of metalloproteinases-1 or related protein.
 XX
 PS Example 3; Col 23-24; 17pp; English.
 XX
 CC This sequence is a fragment of the rat ENDO-I protein used in a method to
 CC screen for endometriosis in a woman of reproductive age. The method
 CC involves determining if a protein is present in a peritoneal fluid or
 CC serum sample at a level below that of normal controls. The protein has a

CC molecular weight of 28-32 kD (by two-dimensional SDS-PAGE), has an
 CC isoelectric point of 7.0-9.0, is synthesized and secreted specifically by
 CC endometrial stromal cells and has the N-terminal amino acid sequence
 CC Cys Ser Cys Ala Pro Thr His Pro Gln Thr Ala Phe Cys Asn Ser Asp Leu Val
 CC Ile Arg Ala Lys Phe Met Gly or the protein is tissue inhibitor of
 CC metalloproteinases-1 (TIMP-1)
 CC
 XX

SO Sequence 16 AA;

Query Match 41.8%; Score 28; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
 DB 7 DAKGSFPC 14

RESULT 68

ABR91286
 ID ABR91286 standard; peptide; 16 AA.

AC ABR91286;

DT 10-SEP-2003 (first entry)

DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:120.

XX Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;
 KW protozoacide; immunostimulant; vaccine; immune response; leishmaniasis.
 XX
 OS Synthetic.

OS Phlebotomus papatasi.
 XX
 PN WO2002102324-A2.

PD 27-DEC-2002.

PP 18-JUN-2002; 2002WO-US019663.

PR 19-JUN-2001; 2001US-0299391P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;

DR WPI; 2003-157000/15.

XX Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for
 PT producing an immune response in a subject or for preventing leishmaniasis
 PT in a subject.
 PS
 XX

PS Claim 10; Page 96; 279pp; English.

CC The present invention describes an isolated salivary polypeptide (I), of
 CC Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)
 CC encoding (1); (2) an isolated fragment (III) of (II), where the fragment
 CC encodes the polypeptide fragment specific for a polypeptide such as
 CC Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
 CC immunogenic fragment (IV) of (1); (4) a nucleic acid (V) that hybridises
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or
 CC (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)
 CC or (VI); and a pharmaceutically acceptable carrier. (I) has protozoacide
 CC and immunostimulant activities, and can be used in vaccines. (VII) is
 CC useful for producing an immune response in a subject or for preventing
 CC leishmaniasis in a subject. (II) is also useful for preventing
 CC leishmaniasis in a subject. (VI) is useful as a vaccine. ACC79987 to
 CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the
 CC exemplification of the present invention
 XX
 SO Sequence 16 AA;

Query Match 41.8%; Score 28; DB 6; Length 16;
 Best Local Similarity 100.0%; Pred. No. 8.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FRCIL 10
 DB 8 FRCIL 12

RESULT 69

ABR91288
 ID ABR91288 standard; peptide; 17 AA.

AC ABR91288;

DT 10-SEP-2003 (first entry)

DE P. papatasi salivary polypeptide immunogenic peptide SEQ ID NO:122.

XX Phlebotomus papatasi; salivary polypeptide; antigenic; immunogenic;
 KW protozoacide; immunostimulant; vaccine; immune response; leishmaniasis.
 XX
 OS Synthetic.

OS Phlebotomus papatasi.
 XX
 PN WO2002102324-A2.

PD 27-DEC-2002.

PP 18-JUN-2002; 2002WO-US019663.

PR 19-JUN-2001; 2001US-0299391P.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Valenzuela JG, Belkaid Y, Kamhawi S, Sacks D, Ribeiro JMC;

DR WPI; 2003-157000/15.

XX Novel isolated salivary polypeptide of Phlebotomus papatasi, useful for
 PT producing an immune response in a subject or for preventing leishmaniasis
 PT in a subject.
 PS
 XX

PS Claim 10; Page 96; 279pp; English.

CC The present invention describes an isolated salivary polypeptide (I), of
 CC Phlebotomus papatasi. Also described: (1) an isolated nucleic acid (II)
 CC encoding (1); (2) an isolated fragment (III) of (II), where the fragment
 CC encodes the polypeptide fragment specific for a polypeptide such as
 CC Phlebotomus papatasi salivary polypeptide (PSP) 12, PSP14, PSP15,
 CC PSP30, PSP32, PSP36, PSP42 or PSP44; (3) an isolated antigenic or
 CC immunogenic fragment (IV) of (1); (4) a nucleic acid (V) that hybridises
 CC under stringent conditions to (II); (5) a vector (VI) comprising (II) or
 CC (III); and (6) a composition (VII) comprising (I) or its fragment, (IV)
 CC or (VI); and a pharmaceutically acceptable carrier. (I) has protozoacide
 CC and immunostimulant activities, and can be used in vaccines. (VII) is
 CC useful for producing an immune response in a subject or for preventing
 CC leishmaniasis in a subject. (II) is also useful for preventing
 CC leishmaniasis in a subject. (VI) is useful as a vaccine. ACC79987 to
 CC ACC79999 and ABR91176 to ABR92046 represent sequences used in the
 CC exemplification of the present invention
 XX
 SO Sequence 17 AA;

Query Match 41.8%; Score 28; DB 6; Length 17;
 Best Local Similarity 100.0%; Pred. No. 9.5e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FRCIL 10
 DB 7 FRCIL 11

RESULT 70
ADU92006
ID ADU92006 standard; peptide; 17 AA.
XX
AC ADU92006;
XX
DT 10-FEB-2005 (first entry)
XX
DE EPO-R agonist SEQ ID NO 147.
XX
KM erythropoietin receptor; EPO-R; erythropoietin; renal failure;
KM autoimmune disease; cystic fibrosis; anemia; inflammation;
KM spinal cord injury; aging; neurological disease; nephrotropic;
KM anti-neuritic; immunosuppressive; CNS-Gen.; neuroprotective;
KM respiratory-Gen.; anti-inflammatory; vulnary; nocotropic; cyostatic;
KM hemostatic; cyclic.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Modified-site 1 /note="Acetylated residue"
FT Disulfide-bond 4..13
FT Modified-site 17 /note="C-terminal amide"
XX
PN MO2004101611-A2.
XX
PD 25-NOV-2004.
XX
PF 12-MAY-2004; 2004WO-US014886.
XX
PR 12-MAY-2003; 2003US-0470245P.
XX
PA (AFPR-) APFYMIX INC.
XX
PI Yin K, Holmes C, Lalonde G, Balu P, Schatz PJ, Tumely D,
PI WPI; 2005-039329/04.
XX
DR WPI; 2005-039329/04.
XX
PT New peptide comprising specified sequence of amino acid is erythropoietin
PT receptor agonist useful for treating e.g. anemia, beta-thalassemia, renal
PT disorders.
XX
PS Disclosure; SEQ ID NO 147; 83pp; English.
XX
CC This invention describes a novel peptide which is an erythropoietin
CC receptor (EPO-R) activator. The peptide forms a dimer comprising a
CC linking moiety connecting two peptide chains composed of ADU91861. The N-
CC terminal of the peptide is acetylated. The EPO-R activator further
CC comprises at least one water soluble polymer, preferably polyethylene
CC glycol (PEG) covalently bound to the peptide and a spacer moiety. The
CC products of the invention are used for treating disorders associated with
CC deficiency of erythropoietin or low or defective red blood cell
CC population, and stage renal failure or dialysis, anemia associated with
CC AIDS, autoimmune disease or malignancy, beta-thalassemia, cystic
CC fibrosis, early anemia of prematurity, anemia associated with chronic
CC inflammatory disease, spinal cord injury, acute blood loss, aging and
CC neoplastic disease states accompanied by abnormal erythropoiesis. The
CC peptide compounds are potent agonists of erythropoietin receptor and have
CC nephrotropic, anti-neuritic, immunosuppressive, CNS-Gen., neuroprotective,
CC respiratory-Gen., anti-inflammatory, vulnary, nocotropic, cyostatic and
CC hemostatic activity. This sequence represents a peptide which acts as an
CC erythropoietin receptor (EPO-R) agonist.
XX
SQ Sequence 17 AA;

Query Match 41.8%; Score 28; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 9.5e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 5 SPECTIGP 12
|::|:|

DB 1 SWDCRIGP 8
RESULT 71
AA26517
ID AA26517 standard; peptide; 18 AA.
XX
AC AA26517;
XX
DT 06-SEP-1999 (first entry)
XX
DE Erythropoietin receptor (EPO-R) binding peptide.
XX
KM Erythropoietin; EPO; receptor; EPO deficiency; renal failure; AIDS;
KM dialysis; anaemia; autoimmune disease; chronic inflammatory disease;
KM malignancy; beta-thalassemia; cystic fibrosis; prematurity; blood loss;
KM spinal cord injury; aging; neoplastic disease; erythropoiesis; EPO-R.
XX
OS Synthetic.
XX
PN MO9640749-A1.
XX
PD 19-DEC-1996.
XX
PF 07-JUN-1996; 96WO-US009810.
XX
PR 07-JUN-1995; 95US-00484631.
XX
PR 07-JUN-1995; 95US-00484635.
XX
PA (JOHN J) JOHNSON & JOHNSON CORP.
XX
PA (AFPR-) APFYMIX TECHNOLOGIES NV.
XX
PI Wrighton NC, Dower WJ, Chang RS, Kashyap AK, Joliffe LK;
PI Johnson D, Mulcahy L;
XX
DR WPI; 1997-052225/05.
XX
PT Erythropoietin receptor binding peptide - useful for treating disorders
PT characterised by deficiency of EPO, or low or defective red blood cell
PT population.
XX
PS Disclosure; Page 25; 95pp; English.
XX
CC The invention describes a peptide of 10-40 amino acid residues which
CC binds to erythropoietin (EPO) receptor and which includes the amino acid
CC sequence Cys-Xaa1-Xaa2-Gly-Pro-Xaa3-Thr-Trp-Xaa4-Cys, where Xaa1 = Arg,
CC His, Leu or Trp, Xaa2 = Met, Phe or Ile, Xaa3 = 1 of the 20 genetically
CC coded L-amino acids, and Xaa4 = Asp, Glu, Ile, Leu or Val. Optionally,
CC the peptide may be cyclised or dimerised. The peptide can be used to
CC treat a patient having a disorder characterised by a deficiency of EPO or
CC a low or defective red blood cell population. It can be used to treat end
CC stage renal failure or dialysis; anaemia associated with AIDS, autoimmune
CC disease; chronic inflammatory diseases or malignancy; beta-thalassemia;
CC cystic fibrosis; early anaemia of prematurity; spinal cord injury; acute
CC blood loss; aging; and neoplastic disease states accompanied by abnormal
CC erythropoiesis. The peptides can also be used as reagents for detecting
CC EPO receptors on living cells, in biological fluids, in tissue
CC homogenates, etc. Sequences AA26517-548 are representative peptides
CC falling within the above peptide motif and isolated during the affinity
CC selection process
XX
SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 1e+03;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
QY 2 EKNSPECTIGP 12
|:|:|:|
DB 1 ERPRYKCRFGP 11

RESULT 72

AAW67525
 ID AAW67525 standard; peptide; 18 AA.
 XX
 AC AAW67525;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE IGF-1/IGFBP inhibitory peptide 23B3.7.
 XX
 KW Inhibition; interaction; insulin-like growth factor; IGF; receptor;
 binding protein; serum; tissue; insulin; plasma; growth hormone; glucose;
 secretion; blood; hyperglycaemia; obesity.
 XX
 OS Synthetic.
 XX
 PN MO9845427-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 31-MAR-1998; 98WO-US006514.
 XX
 PR 04-APR-1997; 97US-00825852.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark RG, Lowman HB, Robinson ICAF,
 XX
 DR WPI, 1998-583196/49.
 XX
 PT Inhibitors of interaction between insulin-like growth factor - useful
 for, e.g. treating or preventing hyperglycaemia, obesity and neurological
 disorders, and are optionally formulated with thiazolidinone.
 XX
 PS Example 7; Page 57; 133pp; English.
 XX
 CC The invention relates to the isolation of compounds, especially peptides,
 that: (a) inhibit interaction between an insulin-like growth factor (IGF)
 with any one of its binding proteins (IGFBP), and (b) do not bind to a
 human IGF receptor (hIGFR), e.g. see AAW67476-W67491 and AAW67503-W67565.
 CC The peptides are produced synthetically or are isolated from peptide
 libraries where the encoding sequence is generated so that the resulting
 peptide produced retains its structure in solution. This sequence
 CC represents a peptide isolated from a 98 display peptide library which
 CC binds the IGF-1 binding protein IGFBP-3. The compounds are used to
 CC increase serum and tissue levels of active IGF-1, preferably also to
 CC reduce insulin and plasma growth hormone (GH) secretion, and blood
 CC glucose levels, without direct stimulation of secretion or release of
 CC endogenous GH. Particularly the compounds are used to treat or prevent
 CC hyperglycaemia, obesity-related disorders, neurological, cardiac,
 CC anabolic, renal and immunological diseases
 CC
 SQ Sequence 18 AA;
 8Q

Query Match 41.8%; Score 28; DB 2; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12
 |||||
 DB 4 ECTIGP 9

RESULT 73
 AAW67523
 ID AAW67523 standard; peptide; 18 AA.
 XX
 AC AAW67523;
 XX
 DT 02-MAR-1999 (first entry)
 XX
 DE IGF-1/IGFBP inhibitory peptide 23B3.4.
 XX
 KW Inhibition; interaction; insulin-like growth factor; IGF; receptor;
 binding protein; serum; tissue; insulin; plasma; growth hormone; glucose;
 secretion; blood; hyperglycaemia; obesity.

KW binding protein; serum; tissue; insulin; plasma; growth hormone; glucose;
 secretion; blood; hyperglycaemia; obesity.
 XX
 OS Synthetic.
 XX
 PN MO9845427-A2.
 XX
 PD 15-OCT-1998.
 XX
 PF 31-MAR-1998; 98WO-US006514.
 XX
 PR 04-APR-1997; 97US-00825852.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark RG, Lowman HB, Robinson ICAF,
 XX
 DR WPI, 1998-583196/49.
 XX
 PT Inhibitors of interaction between insulin-like growth factor - useful
 for, e.g. treating or preventing hyperglycaemia, obesity and neurological
 disorders, and are optionally formulated with thiazolidinone.
 XX
 PS Example 7; Page 57; 133pp; English.
 XX
 CC The invention relates to the isolation of compounds, especially peptides,
 that: (a) inhibit interaction between an insulin-like growth factor (IGF)
 with any one of its binding proteins (IGFBP), and (b) do not bind to a
 human IGF receptor (hIGFR), e.g. see AAW67476-W67491 and AAW67503-W67565.
 CC The peptides are produced synthetically or are isolated from peptide
 libraries where the encoding sequence is generated so that the resulting
 peptide produced retains its structure in solution. This sequence
 CC represents a peptide isolated from a 98 display peptide library which
 CC binds the IGF-1 binding protein IGFBP-3. The compounds are used to
 CC increase serum and tissue levels of active IGF-1, preferably also to
 CC reduce insulin and plasma growth hormone (GH) secretion, and blood
 CC glucose levels, without direct stimulation of secretion or release of
 CC endogenous GH. Particularly the compounds are used to treat or prevent
 CC hyperglycaemia, obesity-related disorders, neurological, cardiac,
 CC anabolic, renal and immunological diseases
 CC
 SQ Sequence 18 AA;
 8Q

Query Match 41.8%; Score 28; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12
 |||||
 DB 4 ECTWGP 9

RESULT 74
 ABB38888
 ID ABB38888 standard; peptide; 18 AA.
 XX
 AC ABB38888;
 XX
 DT 04-FEB-2002 (first entry)
 XX
 DE Peptide #6394 encoded by human foetal liver single exon probe.
 XX
 KW Human; foetal liver; gene expression; single exon nucleic acid probe.
 XX
 OS Homo sapiens.
 XX
 PN MO200157277-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US000669.
 XX
 PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-483447/52.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human fetal liver.
 XX
 PS Claim 27; SEQ ID NO 31523; 639PP + Sequence Listing; English.
 XX
 CC The invention relates to a single exon nucleic acid probe for measuring
 CC human gene expression in a sample derived from human foetal liver. The
 CC single exon nucleic acid probes may be used for predicting, measuring and
 CC displaying gene expression in samples derived from human fetal liver. The
 CC present sequence is a peptide encoded by a single exon nucleic acid probe
 CC of the invention. Note: The sequence data for this patent did not form
 CC part of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pct_sequences
 CC
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 4; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SPECILGP 12
 ||: ||||
 Db 2 SFQGLGP 9

RESULT 75
 AAM32369
 ID AAM32369 standard; protein; 18 AA.
 XX
 AC AAM32369;
 XX
 DT 17-OCT-2001 (first entry)
 XX
 DE Peptide #6406 encoded by probe for measuring placental gene expression.
 KW Probe; microarray; human; placenta; antenatal diagnosis;
 KW genetic disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200157272-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US0000663.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488897/53.
 DR
 XX

PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human placenta.
 XX
 PS Claim 27; SEQ ID NO 32638; 654PP; English.
 XX
 CC The present invention relates to single exon nucleic acid probes (SENP;
 CC see AA131315-AA157546). The present sequence is a peptide encoded by one
 CC such probe. The probes are useful for producing a microarray for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from human placenta. The probes are useful for antenatal diagnosis of
 CC human genetic disorders
 CC
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 4; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 5 SPECILGP 12
 ||: ||||
 Db 2 SFQGLGP 9

RESULT 76
 AAM72107
 ID AAM72107 standard; protein; 18 AA.
 XX
 AC AAM72107;
 XX
 DT 06-NOV-2001 (first entry)
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32413.
 XX
 DE Human bone marrow expressed probe encoded protein SEQ ID NO: 32413.
 XX
 KW Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma.
 XX
 OS Homo sapiens.
 XX
 PN WO200157276-A2.
 XX
 PD 09-AUG-2001.
 XX
 PF 30-JAN-2001; 2001WO-US0000668.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX Penn SG, Hanzel DK, Chen W, Rank DR;
 XX WPI; 2001-488890/53.
 DR
 XX
 PT Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.
 XX
 PS Example 4; SEQ ID NO 32413; 658PP + Sequence Listing; English.
 XX
 CC The present invention provides a number of single exon nucleic acid
 CC probes which are derived from genomic sequences expressed in the human
 CC bone marrow. They can be used to measure gene expression in bone marrow
 CC samples, which may enable the improved diagnosis and treatment of cancers
 CC such as lymphoma, leukaemia and myeloma. The present sequence is a
 CC protein encoded by one of the probes of the invention
 CC
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 4; Length 18;

Best Local Similarity 62.5%; Pred. No. 1e+03; Indels 0; Gaps 0;
Matches 5; Conservative 2; Mismatches 1;

QY 5 SPECIILGP 12
||:||||
Db 2 SFGGLGIP 9

RESULT 77

AAMS9539 standard; protein; 18 AA.

AC AAMS9539;

DT 05-NOV-2001 (first entry)

XX Human brain expressed single exon probe encoded protein SEQ ID NO: 31644.

KM Human; brain expressed exon; gene expression analysis; probe; microarray;

XX Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer.

OS Homo sapiens.

PN MO200157275-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000667.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR,

XX WPI; 2001-483446/52.

PT Single exon nucleic acid probes for analyzing gene expression in human

PT brains.

PS Example 4; SEQ ID NO 31644; 650bp + Sequence Listing; English.

XX The present invention provides a number of single exon nucleic acid

CC probes which are derived from genomic sequences expressed in the human

CC brain. They can be used to measure gene expression in brain cell samples,

CC which may enable the diagnosis and improved treatment of nervous system

CC diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,

CC epilepsy and cancers. The present sequence is a protein encoded by one of

XX the probes of the invention

XX Sequence 18 AA;

XX

XX

XX

DT 25-FEB-2003 (first entry)

XX Human liver peptide, SEQ ID NO 32441.

KM Human; liver; cirrhosis; hyperlipoproteinaemia; hyperlipidaemia;

XX hypercholesterolaemia; coronary heart disease.

OS Homo sapiens.

PN MO200157273-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US000664.

PR 04-FEB-2000; 2000US-0180312P.

PR 26-MAY-2000; 2000US-0207456P.

PR 30-JUN-2000; 2000US-00608408.

PR 03-AUG-2000; 2000US-00632366.

PR 21-SEP-2000; 2000US-0234687P.

PR 27-SEP-2000; 2000US-0236359P.

PR 04-OCT-2000; 2000GB-00024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PI Penn SG, Hanzel DK, Chen W, Rank DR,

XX WPI; 2001-48898/53.

PT Human genome-derived single exon nucleic acid probes useful for analyzing

PT gene expression in human adult liver.

PS Claim 27; SEQ ID NO 32441; 658bp; English.

XX The invention relates to a single exon nucleic acid probe (SENP) (I) for

CC measuring human gene expression in a sample derived from human adult

CC liver, comprising one of 13109 defined nucleotide sequences given in the

CC specification (or complements/ fragments). The probe hybridizes at high

CC stringency to a nucleic acid molecule expressed in the human adult liver.

CC (I) may be used for predicting, measuring and displaying gene expression

CC in samples derived from human adult liver. The genes identified may be

CC involved in genetic liver diseases such as cirrhosis,

CC hyperlipoproteinaemia, hyperlipidaemia and hypercholesterolaemia which is

CC associated with coronary heart disease. ABG47348-ABG59330 represent human

CC liver single exon encoded peptides of the invention. Note: The sequence

CC information for this patent does not appear in the printed specification

CC but was obtained in electronic format directly from WIPO at

CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 18 AA;

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

XX

KW	immunological disorder; kidney regeneration; degenerative disorder;
KW	hypoxia; wound healing; cardiac regeneration; cancer; angiogenesis;
KW	metabolic stress; growth hormone deficiency; diabetes; short stature;
KW	osteoporosis; obesity.
XX	
OS	Synthetic.
XX	
FN	US6251865-B1.
XX	
PD	26-JUN-2001.
XX	
PF	31-MAR-1998; 98US-00052888.
XX	
PR	04-APR-1997; 97US-00825852.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Clark RG, Lowman HB, Robinson ICAF;
XX	
DR	WPI, 2001-520042/57.
XX	
PT	Isolated peptides used to increase serum and tissue levels of insulin-
PT	like growth factor in those with hyperglycemic, obesity-related,
PT	neurological, cardiac, anabolic, renal or immunological disorders.
XX	
PS	Example 7, Col 57, 108pp; English.
XX	
CC	The present sequence represents a synthetic peptide, which binds to an
CC	insulin-like growth factor (IGF)-1 binding protein. The specification
CC	describes IGF agonists. IGF agonist peptides are used to increase serum
CC	and tissue levels of IGF-1 in mammals with hyperglycemic, obesity-
CC	related, neurological, cardiac, anabolic, renal or immunological
CC	disorders. They may also be used to increase whole body, bone and muscle
CC	growth rate in normal and hypopituitary animals, to protect body weight
CC	and nitrogen loss during catabolic states, kidney regeneration, to treat
CC	peripheral and central nervous system (CNS) degenerative disorders and
CC	promote neuroprotection or repair following CNS damage or injury, to
CC	treat hypoxia, to promote wound healing, for cardiac regeneration, to
CC	reverse cancer cachexia, to inhibit angiogenesis, to regenerate the
CC	gastrointestinal tract, to stimulate mammary function, to counteract IGF-
CC	1-dependent actions of growth hormone such as metabolic stress, age-
CC	-related decline in growth hormone activity and adult growth hormone
CC	deficiency, to treat maturity onset diabetes and/or to treat specific IGF
CC	deficiency. They may also be used to treat growth-hormone resistant short
CC	stature, growth hormone insensitivity syndrome, osteoporosis and
CC	catabolic states, and reduce obesity
XX	
XX	
SQ	Sequence 18 AA;
XX	
Query Match	41.8%; Score 28; DB 4; Length 18;
Best Local Similarity	66.7%; Pred. No. 18+03;
Matches	4; Conservative 1; Mismatches 1; Indels 0; Gaps 0
QY	7 ECTIGP 12
	:
Db	4 BCWGP 9
XX	
RESULT 80	
AAAG63762	
ID	AAAG63762 standard; peptide; 18 AA.
XX	
AC	AAAG63762;
XX	
DT	29-OCT-2001 (first entry)
XX	
DE	Synthetic peptide which binds to IGF-1 binding protein IGFBP-3.
XX	
KW	Insulin-like growth factor; IGF, IGF-1; IGF binding protein; IGFBP-3;
KW	hyperglycemic disorder; obesity-related disorder; neurological disorder;
KW	cardiac disorder; anabolic disorder; renal disorder; neuroprotection;
KW	immunological disorder; kidney regeneration; degenerative disorder;
KW	hypoxia; wound healing; cardiac regeneration; cancer; angiogenesis;

KM		metabolic stress; growth hormone deficiency; diabetes; short stature;
KM		osteoporosis; obesity.
XX	OS	Synthetic.
XX	PM	US6251865-B1.
XX	PD	26-JUN-2001.
XX	PF	31-MAR-1998; 98US-00052888.
XX	PR	04-APR-1997; 97US-00825852.
XX	PA	(GETH) GENENTECH INC.
PI		Clark RG, Lowman HB, Robinson ICAF;
DR		WPI, 2001-520042/57.
XX		
PT		Isolated peptides used to increase serum and tissue levels of insulin-
PT		like growth factor in those with hyperglycemic, obesity-related,
PT		neurological, cardiac, anabolic, renal or immunological disorders.
PS		Example 7; Col 57; 108pp; English.
XX		
CC		The present sequence represents a synthetic peptide, which binds to an
CC		insulin-like growth factor (IGF)-1 binding protein. The specification
CC		describes IGF agonists. IGF agonist peptides are used to increase serum
CC		and tissue levels of IGF-1 in mammals with hyperglycemic, obesity-
CC		related, neurological, cardiac, anabolic, renal or immunological
CC		disorders. They may also be used to increase whole body, bone and muscle
CC		growth rate in normal and hypopituitary animals, to protect body weight
CC		and nitrogen loss during catabolic states, kidney regeneration, to treat
CC		peripheral and central nervous system (CNS) degenerative disorders and
CC		promote neuroprotection or repair following CNS damage or injury, to
CC		treat hypoxia, to promote wound healing, for cardiac regeneration, to
CC		reverse cancer cachexia, to inhibit angiogenesis, to regenerate the
CC		gastrointestinal tract, to stimulate mammary function, to counteract IGF-
CC		1-dependent actions of growth hormone such as metabolic stress, age-
CC		-related decline in growth hormone activity and adult growth hormone
CC		deficiency, to treat maturity onset diabetes and/or to treat specific IGF
CC		deficiency. They may also be used to treat growth-hormone resistant short
CC		stature, growth hormone insensitivity syndrome, osteoporosis and
CC		catabolic states, and reduce obesity
XX		
SEQ		Sequence 18 AA;
	Query Match	41.8%; Score 28; DB 4; Length 18;
	Best Local Similarity	83.3%; Pred. No. 1e+03;
	Matches 5; Conservative	0; Mismatches 1; Indels 0; Gaps 0;
QY	7 ECILGP 12	
Dd	4 ECIKCP 9	
RESULT 81		
ABG41921		
ID	ABG41921 standard; peptide; 18 AA.	
XX		
AC	ABG41921;	
XX		
DT	19-AUG-2002 (first entry)	
XX		
DE	Human peptide encoded by genome-derived single exon probe SEQ ID 31586.	
XX		
KM	Human; single exon probe; asthma; lung cancer; COPD; ILD;	
KM	chronic obstructive pulmonary disease; interstitial lung disease;	
KM	familial idiopathic pulmonary fibrosis; neurofibromatosis;	
KM	tuberous sclerosis; Gaucher's disease; Niemann-Pick disease;	
KM	Hemnansky-Pudlak syndrome; sarcoidosis; pulmonary haemosiderosis;	
KM	pulmonary histiocytosis; lymphangioleiomyomatosis; Kartagener syndrome;	
KM	pulmonary alveolar proteinosis; fibrocystic pulmonary dysplasia;	

KW primary ciliary dyskinesia; pulmonary hypertension;
 KM hyaline membrane disease.
 XX
 OS Homo sapiens.
 PN WO200186003-A2.
 PD 15-NOV-2001.
 PF 30-JAN-2001; 2001WO-US000665.
 XX
 PR 04-FEB-2000; 2000US-0180312P.
 PR 26-MAY-2000; 2000US-0207456P.
 PR 30-JUN-2000; 2000US-00608408.
 PR 03-AUG-2000; 2000US-00632366.
 PR 21-SEP-2000; 2000US-0234687P.
 PR 27-SEP-2000; 2000US-0236359P.
 PR 04-OCT-2000; 2000GB-00024263.
 XX
 PA (MOLE-) MOLECULAR DYNAMICS INC.
 XX
 PI Penn SG, Hanzel DK, Chen W, Rank DR;
 DR WPI; 2002-114183/15.
 XX
 PT Spatially-addressable set of single exon nucleic acid probes, used to
 PT measure gene expression in human lung samples.
 XX
 PS Claim 27, SEQ ID NO 31586; 634bp; English.
 XX
 CC The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human lung comprising single exon nucleic acid probes having one of
 CC 12614 nucleic acid sequences mentioned in the specification, or their
 CC complements or the 12387 open reading frames derived from the 12614
 CC probes. Also included are a microarray comprising the novel set of probes
 CC; the novel set of probes which hybridize at high stringency to a nucleic
 CC acid expressed in the human lung; measuring gene expression in a sample
 CC derived from human lung, comprising (a) contacting the array with a
 CC collection of detectably labeled nucleic acids derived from human lung
 CC mRNA, and (b) measuring the label detectably bound to each probe of the
 CC array; identifying exons in a eukaryotic genome, comprising (a)
 CC algorithmically predicting at least one exon from genomic sequences of
 CC the eukaryote; and (b) detecting specific hybridization of detectably
 CC labeled nucleic acids from eukaryote lung mRNA, to a single exon probe,
 CC having a fragment identical to the predicted exon, the probe is included
 CC in the above mentioned microarray; assigning exons to a single gene,
 CC comprising (a) identifying exons from genomic sequence by the method
 CC above and (b) measuring the expression of each of the exons in several
 CC tissues and/or cell types using hybridization to a single exon
 CC microarray having a probe with the exon, where a common pattern of
 CC expression of the exons in the tissues and/or cell types indicates that
 CC the exons should be assigned to a single gene; a peptide comprising one
 CC of 12011 sequences, mentioned in the specification, or encoded by the
 CC probes/open reading frames (ORF). The probes are used for gene expression
 CC analysis, and for identifying exons in a gene, particularly using human
 CC lung derived mRNA and for the study of lung diseases such as asthma, lung
 CC cancer, chronic obstructive pulmonary disease (COPD), interstitial lung
 CC disease (ILD), familial idiopathic pulmonary fibrosis, neurofibromatosis,
 CC tuberous sclerosis, Gaucher's disease, Niemann-Pick disease, Hermansky-
 CC Pudlak syndrome, sarcoidosis, pulmonary haemorrhoidosis, pulmonary
 CC histiocytosis, lymphangioleiomyomatosis, pulmonary alveolar proteinosis,
 CC Karsenger syndrome, fibrocystic pulmonary dysplasia, primary ciliary
 CC dyskinesia, pulmonary hypertension and hyaline membrane disease. The
 CC present sequence is a peptide/protein encoded by a single exon probe of
 CC the invention. Note: The sequence data for this patent did not form part
 CC of the printed specification, but was obtained in electronic format
 CC directly from WIPO at ftp.wipo.int/pub/published_pat_sequences
 XX
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 5; Length 18;
 Best Local Similarity 62.5%; Pred. No. 1e+03;

Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Qy 5 SPECILGP 12
 Db 2 SFQGLIGP 9
 RESULT 82
 ABB57684
 ID ABB57684 standard; peptide; 18 AA.
 XX
 AC ABB57684;
 XX
 DT 18-MAR-2002 (first entry)
 XX
 DE IGFBP-3 binding peptide #33.
 XX
 KM Antithrombotic; antiarthritic; osteopathic; cartilage disorder;
 KM Insulin-like growth factor; IGF; binding protein; IGFBP;
 KM rheumatoid arthritis; osteoarthritis.
 XX
 OS Synthetic.
 XX
 PN WO200187323-A2.
 PD 22-NOV-2001.
 XX
 PF 16-MAY-2001; 2001WO-US015904.
 XX
 PR 16-MAY-2000; 2000US-0204490P.
 PR 15-NOV-2000; 2000US-0248985P.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Dubaigle Y, Flvaroff BH, Lowman HB;
 DR WPI; 2002-082942/11.
 XX
 CC Treating cartilage disorders including cartilage damage by injury or
 CC degenerative cartilaginous disorders, by contacting cartilage with
 CC insulin-like growth factor analog with altered affinity for IGF-binding
 CC proteins.
 PT
 PS Example 1; Page 44; 136bp; English.
 XX
 CC The present invention relates to a method for treating cartilage
 CC disorders. The method comprises contacting cartilage with an active agent
 CC such as insulin-like growth factor (IGF-1) analog with a binding affinity
 CC preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1
 CC analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a
 CC IGFBP displacer peptide that prevents the interaction of IGF with an
 CC IGFBP and does not bind to human IGF receptor. The method is useful for
 CC treating cartilage disorders (CD), including degenerative CD, articular
 CC CD such as rheumatoid arthritis and osteoarthritis. The present sequence
 CC was used to illustrate the invention
 XX
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 5; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 ECIIGP 12
 Db 4 ECIIGP 9
 RESULT 83
 ABB57681
 ID ABB57681 standard; peptide; 18 AA.
 XX
 AC ABB57681;
 XX

DT		18-MAR-2002	(first entry)
XX			
DB		IGFBP-3 binding peptide #30.	
XX			
KW		Antirheumatic; antiarthritic; osteopathic; cartilage disorder;	
KM		insulin-like growth factor; IGF; binding protein; IGFBP;	
KW		rheumatoid arthritis; osteoarthritis.	
XX			
OS		Synthetic.	
XX			
PN		WO200187323-A2.	
XX			
PD		22-NOV-2001.	
XX			
PF		16-MAY-2001; 2001WO-US015904.	
XX			
PR		16-MAY-2000; 2000US-0204490P.	
PR		15-NOV-2000; 2000US-0248985P.	
XX			
PA		(GETH) GENENTECH INC.	
XX			
PI		Dubague Y, Filvaroff EH, Lowman HB;	
DR		WPI; 2002-082942/11.	
XX			
PT		Treating cartilage disorders including cartilage damage by injury or	
PT		degenerative cartilaginous disorders, by contacting cartilage with	
PT		insulin-like growth factor analog with altered affinity for IGF-binding	
PT		proteins.	
XX			
PS		Example 1, Page 44; 136pp; English.	
XX			
CC		The present invention relates to a method for treating cartilage	
CC		disorders. The method comprises contacting cartilage with an active agent	
CC		such as insulin-like growth factor (IGF-1) analog with a binding affinity	
CC		preference for IGF binding protein-3 (IGFBP-3) over IGFBP-1, an IGF-1	
CC		analog with a binding affinity preference for IGFBP-1 over IGFBP-3, or a	
CC		IGFBP displacer peptide that prevents the interaction of IGF with an	
CC		IGFBP and does not bind to human IGF receptor. The method is useful for	
CC		treating cartilage disorders (CD), including degenerative CD, articular	
CC		CD such as rheumatoid arthritis and osteoarthritis. The present sequence	
CC		was used to illustrate the invention	
XX			
SO		Sequence 18 AA;	
	Query Match	41.8%; Score 28; DB 5; Length 18;	
	Best Local Similarity	66.7%; Pred. No. 1e+03;	
	Matches	4; Conservative 1; Mismatches 1; Indels 0; Gaps 0	
OY			
	7 ECILGP 12		
	:		
	4 ECVGCP 9		
DB			
RESULT 84			
ADA03290			
ID	ADA03290	standard; peptide; 18 AA.	
XX			
AC	ADA03290;		
XX			
DT	06-NOV-2003	(first entry)	
XX			
DE	Angiotensin converting enzyme 2 binding peptide #88.		
XX			
KM	hypotensive; cardiac; cerebroprotective; antiatherosclerotic; analgesic;		
KM	antiinflammatory; nephrotropic; hypertensive; vasotropic; cytostatic;		
KM	antiallergic; neuroprotective; antiparkinsonian;		
KM	neurotropic; antirheumatic; antiarthritic; antigout; tranquilizer;		
KM	vulnerary; antidiabetic; dermatological; immunosuppressive; hepatotropic;		
KM	anti-HIV; antibacterial; angiotensin converting enzyme; ACE-2;		
KM	angiotensin converting enzyme; ACE-2; hypertension;		
KM	congestive heart failure; stroke; left ventricular failure;		
KM	atherosclerotic heart disease; stenosis; pain; inflammatory reaction;		

XX	histamine; vasoconstriction; epithios; aldosterone; cell proliferation;
KM	renal disorder; acute glomerulonephritis; immunophenotyping;
KM	cardiac myocyte; Bowman's capsule; hypotension; ischemia; asthma; allergy;
KM	multiple sclerosis; cancer; Parkinson's disease; Alzheimer's disease;
KM	rheumatoid arthritis; gout; trauma; dermatitis; diabetes mellitus;
KM	Sjogren's syndrome; Addison's disease; hepatitis; Crohn's disease;
KM	sarcoidosis; AIDS; sepsis.
XX	
OS	Synthetic.
XX	
XX	WO200298448-A1.
PN	
XX	12-DEC-2002.
PD	
XX	03-JUN-2002; 2002WO-US017199.
PP	
XX	04-JUN-2001; 2001US-0294976P.
PR	
XX	(HUMA-) HUMAN GENOME SCI INC.
PA	
XX	Parry TJ, Rosen CA, Albert VR, Sanyal I, Huang L, Wescott CR,
P1	Sekut LJ,
PI	
XX	WPI; 2003-140552/13.
DR	
XX	
XX	Novel angiotensin converting enzyme-2 binding polypeptide useful for
PT	treating, preventing or ameliorating hypertension, congestive heart
PT	failure, stroke, left ventricular failure and atherosclerotic heart
PT	disease.
XX	
XX	Example 1, Page 179; 246pp: English.
XX	
XX	The invention relates to novel isolated angiotensin converting enzyme
CC	(ACE)-2 binding polypeptides (1), which are useful for treating,
CC	preventing or ameliorating hypertension, congestive heart failure,
CC	stroke, left ventricular failure and atherosclerotic heart disease in an
CC	animal. The peptides are useful for detecting, isolating, or purifying
CC	ACE-2 proteins or ACE-2 like polypeptides in solutions, mixtures, or
CC	biological samples; for inhibiting or reducing stenosis, pain,
CC	inflammatory reactions, abnormal histamine release, vasoconstriction,
CC	diseases or disorders related to vasoconstriction, and diseases and/or
CC	disorders associated with aberrant action of ACE-2; to detect, isolate,
CC	or remove ACE-2 target proteins in solutions, and also to identify
CC	epitopes of ACE-2; to detect, diagnose, prognosis, or monitor
CC	cardiovascular diseases, and disorders associated with aberrant
CC	aldosterone activity, or cell proliferation; for preventing and treating
CC	renal disorders, e.g., acute glomerulonephritis, and diseases associated
CC	with it; to assay protein levels in a biological sample, for
CC	immunophenotyping of cell lines and biological samples by their ACE-2
CC	expression, and for identifying cells, such as cardiac myocytes,
CC	endothelial and epithelial cells of Bowman's capsule. The peptides are
CC	especially useful for treating, preventing, or ameliorating diseases or
CC	disorders associated with hypotension, ischemia, asthma, allergy, multiple
CC	sclerosis, cancers, Parkinson's and Alzheimer's diseases, rheumatoid
CC	arthritis, gout, trauma, dermatitis, diabetes mellitus, Sjogren's
CC	syndrome, Addison's disease, chronic active hepatitis, Crohn's disease,
CC	sarcoidosis, AIDS, and sepsis. In an example of the invention, ACE-2
CC	binding peptides were isolated from a number of peptide display
CC	libraries. Evaluation of the peptide sequences revealed a series of
CC	peptide families. This sequence represents a specific example of one of
CC	the ACE-2 binding peptides of the invention
XX	
XX	
SQ	Sequence 18 AA;
Query Match	41.8%; Score 28; DB 6; Length 18;
Best Local Similarity	71.4%; Pred. No. 1e+03;
Matches	5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY	6 PFCILGP 12
DB	2 PFCWMP 8

KW growth hormone secretagogue; growth hormone binding protein; IGF;
 KW IGF binding protein; insulin; plasma insulin secretion;
 KW blood glucose level; hyperglycaemic disorder; obesity-related disorder;
 KW neurological disorder; cardiac disorder; anabolic disorder;
 KW renal disorder; immunological disorder; anorectic; neuroprotective;
 KW cardiac; nephrotropic; immunomodulator; antidiabetic.
 XX
 OS Synthetic.
 XX
 PN US6632794-B1.
 XX
 PD 14-OCT-2003.
 XX
 PF 28-NOV-2000; 2000US-00723547.
 XX
 PR 04-APR-1997; 97US-00825852.
 PR 31-MAR-1998; 98US-00052888.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark RG, Lowman HB, Robinson ICAF;
 DR WPI; 2003-810559/76.
 XX
 PT Increasing serum and tissue levels of biologically active insulin-like
 PT growth factor (IGF)-I in a mammal for treating e.g. renal disorder, by
 PT administering IGF peptide.
 XX
 PS Example 7; SEQ ID NO 69; 117pp; English.
 XX
 CC The invention relates to a method for increasing serum and tissue levels
 CC of biologically active insulin-like growth factor I (IGF-I) in a mammal
 CC comprising administering a growth hormone, a growth hormone releasing
 CC peptide, a growth hormone releasing hormone, a growth hormone
 CC secretagogue, a growth hormone in combination with growth hormone binding
 CC protein, an IGF, an IGF in combination with an IGF binding protein, an
 CC IGF binding protein, insulin or a hypoglycaemic agent. The invention also
 CC relates to a method of reducing plasma insulin secretion and blood
 CC glucose levels in a mammal. The method is useful for increasing serum and
 CC tissue levels of biologically active IGF-I in a mammal for treating
 CC hyperglycaemic, obesity-related, neurological, cardiac, anabolic, renal
 CC or immunological disorders. This sequence represents a peptide used in
 CC the method of the invention.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 41.8%; Score 28; DB 7; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1e+03;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 7 ECLIGP 12
 DB 4 ECLIGP 9
 XX
 RESULT 88
 ADH48156
 ID ADH48156 standard; peptide; 18 AA.
 XX
 AC ADH48156;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE IGFBP-3 binding peptide #21.
 XX
 KW IGF-I serum level; IGF-I tissue level; insulin-like growth factor; IGF-I;
 KW hyperglycaemic disorder; obesity-related disorder; neurological disorder;
 KW cardiac disorder; anabolic disorder; renal disorder;
 KW immunological disorder; IGFBP-3.
 XX
 OS Synthetic.
 XX
 PN US6635619-B1.

XX
 PD 21-OCT-2003.
 XX
 PF 28-NOV-2000; 2000US-00724127.
 XX
 PR 04-APR-1997; 97US-00825852.
 PR 31-MAR-1998; 98US-00052888.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark RG, Lowman HB, Robinson ICAF;
 DR WPI; 2003-810569/76.
 XX
 PT Increasing serum and tissue levels of biologically active insulin-like
 PT growth factor (IGF)-I in a mammal for treating e.g., renal disorder by
 PT administering IGF peptide.
 XX
 PS Example 7; SEQ ID NO 67; 117pp; English.
 XX
 CC The invention relates to a method of increasing serum and tissue levels
 CC of biologically active insulin-like growth factor (IGF)-I in a mammal.
 CC The method is useful for increasing serum and tissue levels of
 CC biologically active IGF-I in a mammal for treating hyperglycaemic,
 CC obesity-related, neurological, cardiac, anabolic, renal or immunological
 CC disorder. The present sequence represents the amino acid sequence of an
 CC IGFBP-3 binding peptide.
 XX
 SQ Sequence 18 AA;
 XX
 Query Match 41.8%; Score 28; DB 7; Length 18;
 Best Local Similarity 66.7%; Pred. No. 1e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 7 ECLIGP 12
 DB 4 ECLWGP 9
 XX
 RESULT 89
 ADH48158
 ID ADH48158 standard; peptide; 18 AA.
 XX
 AC ADH48158;
 XX
 DT 25-MAR-2004 (first entry)
 XX
 DE IGFBP-3 binding peptide #23.
 XX
 KW IGF-I serum level; IGF-I tissue level; insulin-like growth factor; IGF-I;
 KW hyperglycaemic disorder; obesity-related disorder; neurological disorder;
 KW cardiac disorder; anabolic disorder; renal disorder;
 KW immunological disorder; IGFBP-3.
 XX
 OS Synthetic.
 XX
 PN US6635619-B1.
 XX
 PD 21-OCT-2003.
 XX
 PF 28-NOV-2000; 2000US-00724127.
 XX
 PR 04-APR-1997; 97US-00825852.
 PR 31-MAR-1998; 98US-00052888.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Clark RG, Lowman HB, Robinson ICAF;
 DR WPI; 2003-810569/76.
 XX
 PT Increasing serum and tissue levels of biologically active insulin-like
 PT growth factor (IGF)-I in a mammal for treating e.g., renal disorder by

PT administering IGF peptide.
XX
PS Example 7, SEQ ID NO 69, 117pp; English.
XX
CC The invention relates to a method of increasing serum and tissue levels
CC of biologically active insulin-like growth factor (IGF-I in a mammal.
CC The method is useful for increasing serum and tissue levels of
CC biologically active IGF-I in a mammal for treating hyperglycaemic,
CC obesity-related, neurological, cardiac, anabolic, renal or immunological
CC disorder. The present sequence represents the amino acid sequence of an
CC IGFBP-3 binding peptide.
XX
SQ Sequence 18 AA;
XX
Query Match 41.8%; Score 28; DB 7; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
XX
QY 7 ECIIGP 12
DB 4 ECIIGP 9
XX
RESULT 90
ID ADF47647 standard; peptide; 18 AA.
XX
AC ADF47647;
XX
DT 12-FEB-2004 (first entry)
XX
DE Insulin-like growth factor (IGF) inhibitory peptide #48.
XX
KW Insulin-like growth factor; IGF; inhibitory peptide; IGF binding protein;
KW hyperglycaemic disorder; diabetes; hyperlipidaemia;
KW obesity-related disease; neurological disorder; multiple sclerosis;
KW Alzheimer's disease; schizophrenia; depression; cardiac disorder;
KW congestive heart failure; renal disorder; chronic renal failure;
KW glomerulonephritis; glomerulosclerosis; interstitial nephritis;
KW immunological disorder; immunodeficiency; anabolic disorder;
KW osteoporosis.
XX
OS Synthetic.
XX
PN US6608031-B1.
XX
PD 19-AUG-2003.
XX
PF 28-NOV-2000; 2000US-00723890.
XX
PR 04-APR-1997; 97US-00825852.
PR 31-MAR-1998; 98US-00052888.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark RG, Lowman HB, Robinson ICAF;
XX
PT WPI; 2004-030477/03.
XX
DR New insulin-like growth factor agonist peptides, useful for treating or
XX preventing hyperglycaemic disorders such as diabetes or hyperlipidaemia,
XX obesity-related diseases, or neurological disorders such as multiple
XX sclerosis.
XX
PS Example 7, SEQ ID NO 67, 117pp; English.
XX
CC The invention relates to an insulin-like growth factor (IGF) inhibitory
CC peptide which inhibits the interaction of an IGF with one or more of its
CC binding proteins. The peptides of the invention are useful for increasing
CC serum and tissue levels of active insulin-like growth factor in a mammal,
CC and for treating or preventing hyperglycaemic disorders such as diabetes,
CC hyperlipidaemia, obesity-related diseases, neurological disorders such as
CC multiple sclerosis, Alzheimer's disease, schizophrenia or depression.

CC cardiac disorders such as congestive heart failure, renal disorders such
CC as end-stage chronic renal failure, glomerulonephritis,
CC glomerulosclerosis or interstitial nephritis and immunological disorders
CC such as immunodeficiencies, anabolic disorders or osteoporosis. This
CC sequence represents an inhibitory peptide of the invention.
XX
SQ Sequence 18 AA;
XX
Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
XX
QY 7 ECIIGP 12
DB 4 ECIIGP 9
XX
RESULT 91
ID ADF47649 standard; peptide; 18 AA.
XX
AC ADF47649;
XX
DT 12-FEB-2004 (first entry)
XX
DE Insulin-like growth factor (IGF) inhibitory peptide #50.
XX
KW Insulin-like growth factor; IGF; inhibitory peptide; IGF binding protein;
KW hyperglycaemic disorder; diabetes; hyperlipidaemia;
KW obesity-related disease; neurological disorder; multiple sclerosis;
KW Alzheimer's disease; schizophrenia; depression; cardiac disorder;
KW congestive heart failure; renal disorder; chronic renal failure;
KW glomerulonephritis; glomerulosclerosis; interstitial nephritis;
KW immunological disorder; immunodeficiency; anabolic disorder;
KW osteoporosis.
XX
OS Synthetic.
XX
PN US6608031-B1.
XX
PD 19-AUG-2003.
XX
PF 28-NOV-2000; 2000US-00723890.
XX
PR 04-APR-1997; 97US-00825852.
PR 31-MAR-1998; 98US-00052888.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark RG, Lowman HB, Robinson ICAF;
XX
PT WPI; 2004-030477/03.
XX
DR New insulin-like growth factor agonist peptides, useful for treating or
XX preventing hyperglycaemic disorders such as diabetes or hyperlipidaemia,
XX obesity-related diseases, or neurological disorders such as multiple
XX sclerosis.
XX
PS Example 7, SEQ ID NO 69; 117pp; English.
XX
CC The invention relates to an insulin-like growth factor (IGF) inhibitory
CC peptide which inhibits the interaction of an IGF with one or more of its
CC binding proteins. The peptides of the invention are useful for increasing
CC serum and tissue levels of active insulin-like growth factor in a mammal,
CC and for treating or preventing hyperglycaemic disorders such as diabetes,
CC hyperlipidaemia, obesity-related diseases, neurological disorders such as
CC multiple sclerosis, Alzheimer's disease, schizophrenia or depression,
CC cardiac disorders such as congestive heart failure, renal disorders such
CC as end-stage chronic renal failure, glomerulonephritis,
CC glomerulosclerosis or interstitial nephritis and immunological disorders
CC such as immunodeficiencies, anabolic disorders or osteoporosis. This
CC sequence represents an inhibitory peptide of the invention.

SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12

DB 4 ECTIGP 9

RESULT 92

ADG39595

ID ADG39595 standard; peptide; 18 AA.

AC ADG39595;

DT 26-FEB-2004 (first entry)

DE IGFBP-3 binding peptide seq id 69.

XX Insulin-like growth factor binding protein; IGFBP;

KM Insulin-like growth factor; IGF binding site; IGFBP antibody;

KW solid-phase carrier; IGF receptor; IGFBP-3; IGF-I.

XX Synthetic.

XX US6645775-B1.

XX 11-NOV-2003.

XX 28-NOV-2000; 2000US-00723931.

XX 04-APR-1997; 97US-00825852.

XX 31-MAR-1998; 98US-00052888.

XX (GETH) GENENTECH INC.

XX Clark RG, Lowman HB, Robinson ICAF;

XX WPI; 2004-050510/05.

DR Detection of insulin-like growth factor binding protein in biological
PT fluid, by contacting the fluid with antibody that binds epitopes and
PT peptide concentration to saturate insulin-like growth factor binding
PT sites.

PS Example 7; SEQ ID NO 69; 116pp; English.

XX The invention describes a method of determining an amount of insulin-like
CC growth factor binding protein (IGFBP) that binds a peptide in a
CC biological fluid. Measuring the amount of insulin-like growth factor
CC binding protein that binds a peptide in a biological fluid involves
CC contacting the fluid with a first antibody attached to a solid-phase
CC carrier and a concentration of the peptide for a time to saturate all IGF
CC binding sites on the IGFBP to form a saturated complex. The first
CC antibody binds epitopes on the IGFBP so that in the presence of the
CC antibody the IGF binding sites remain on the IGFBP for binding the
CC peptide thus forming a complex between the first antibody and the IGFBP.
CC The unbound peptide is removed and the saturated complex is contacted
CC with a labeled second antibody, which binds epitopes on the peptide that
CC are available for binding when the peptide is bound to the IGFBP. The
CC unbound second antibody is removed and the amount of labeled second bound
CC is analysed as a measure of the amount of IGFBP in the biological sample.
CC The method is useful for determining IGFBP that binds a peptide in a
CC biological fluid. The method provides antibody attached to a solid-phase
CC carrier and a peptide concentration that inhibits interaction of the IGF
CC with IGFBPs and does not bind to human IGF receptor. This is the amino
CC acid sequence of a peptide that binds IGFBP-3 blocking binding of IGFBP-3
CC to IGF-I.

XX Sequence 18 AA;

SQ

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12

DB 4 ECTIGP 9

RESULT 93

ADG39593

ID ADG39593 standard; peptide; 18 AA.

AC ADG39593;

DT 26-FEB-2004 (first entry)

DE IGFBP-3 binding peptide seq id 67.

XX Insulin-like growth factor binding protein; IGFBP;

KM Insulin-like growth factor; IGF binding site; IGFBP antibody;

KW solid-phase carrier; IGF receptor; IGFBP-3; IGF-I.

XX Synthetic.

XX US6645775-B1.

XX 11-NOV-2003.

XX 28-NOV-2000; 2000US-00723931.

XX 04-APR-1997; 97US-00825852.

XX 31-MAR-1998; 98US-00052888.

XX (GETH) GENENTECH INC.

XX Clark RG, Lowman HB, Robinson ICAF;

XX WPI; 2004-050510/05.

DR Detection of insulin-like growth factor binding protein in biological
PT fluid, by contacting the fluid with antibody that binds epitopes and
PT peptide concentration to saturate insulin-like growth factor binding
PT sites.

PS Example 7; SEQ ID NO 67; 116pp; English.

XX The invention describes a method of determining an amount of insulin-like
CC growth factor binding protein (IGFBP) that binds a peptide in a
CC biological fluid. Measuring the amount of insulin-like growth factor
CC binding protein that binds a peptide in a biological fluid involves
CC contacting the fluid with a first antibody attached to a solid-phase
CC carrier and a concentration of the peptide for a time to saturate all IGF
CC binding sites on the IGFBP to form a saturated complex. The first
CC antibody binds epitopes on the IGFBP so that in the presence of the
CC antibody the IGF binding sites remain on the IGFBP for binding the
CC peptide thus forming a complex between the first antibody and the IGFBP.
CC The unbound peptide is removed and the saturated complex is contacted
CC with a labeled second antibody, which binds epitopes on the peptide that
CC are available for binding when the peptide is bound to the IGFBP. The
CC unbound second antibody is removed and the amount of labeled second bound
CC is analysed as a measure of the amount of IGFBP in the biological sample.
CC The method is useful for determining IGFBP that binds a peptide in a
CC biological fluid. The method provides antibody attached to a solid-phase
CC carrier and a peptide concentration that inhibits interaction of the IGF
CC with IGFBPs and does not bind to human IGF receptor. This is the amino
CC acid sequence of a peptide that binds IGFBP-3 blocking binding of IGFBP-3
CC to IGF-I.

XX Sequence 18 AA;

SQ

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 66.7%; Pred. No. 1e+03;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12
||: ||
Db 4 ECVWGP 9

RESULT 94
AD162076
ID AD162076 standard; peptide; 18 AA.
XX
AC AD162076;
XX
DT 15-APR-2004 (first entry)
XX
DE IGFBP-3 binding peptide from g8 display #21.
XX
KW insulin-like growth factor; IGF; thiazolidinedione;
KW hyperglycaemic disorders; renal disorders; acute renal insufficiency;
KW chronic renal insufficiency; pyelonephritis; Turner's syndrome;
KW Laron's syndrome; congestive heart failure; neuromuscular disorders;
KW multiple sclerosis; trauma; infection; HIV; IGF-1; IGFBP-1;
KW protein co-ordinate data.
XX
OS Synthetic.
XX
PN US6677305-B1.
XX
PD 13-JAN-2004.
XX
PF 28-NOV-2000; 2000US-00723873.
XX
PR 04-APR-1997; 97US-00825852.
PR 31-MAR-1998; 98US-00052888.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark RG, Lowman HB, Robinson ICAF;
XX
DR WPI; 2004-153869/15.
XX
PT Sterile pharmaceutical composition comprising insulin-like growth factor
PT and thiazolidinedione, useful for treating hyperglycaemic disorders, renal
PT disorders, pyelonephritis, Turner's syndrome, Laron's syndrome.
XX
PS Example 7; SEQ ID NO 67; 116pp; English.
XX
SS The invention relates to a sterile pharmaceutical composition comprising
CC an insulin-like growth factor (IGF) and a thiazolidinedione. The
CC pharmaceutical composition is useful for treating hyperglycaemic
CC disorders, renal disorders such as acute and chronic renal insufficiency,
CC pyelonephritis, Turner's syndrome, Laron's syndrome, congestive heart
CC failure, neuromuscular disorders, multiple sclerosis, trauma, infections
CC such as HIV, etc. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 66.7%; Pred. No. 1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12
||: ||
Db 4 ECVWGP 9

RESULT 95
AD162078
ID AD162078 standard; peptide; 18 AA.
XX
AC AD162078;
XX
PN

DT 15-APR-2004 (first entry)
XX
DE IGFBP-3 binding peptide from g8 display #23.
XX
KW insulin-like growth factor; IGF; thiazolidinedione;
KW hyperglycaemic disorders; renal disorders; acute renal insufficiency;
KW chronic renal insufficiency; pyelonephritis; Turner's syndrome;
KW Laron's syndrome; congestive heart failure; neuromuscular disorders;
KW multiple sclerosis; trauma; infection; HIV; IGF-1; IGFBP-1;
KW protein co-ordinate data.
XX
OS Synthetic.
XX
PN US6677305-B1.
XX
PD 13-JAN-2004.
XX
PF 28-NOV-2000; 2000US-00723873.
XX
PR 04-APR-1997; 97US-00825852.
PR 31-MAR-1998; 98US-00052888.
XX
PA (GETH) GENENTECH INC.
XX
PI Clark RG, Lowman HB, Robinson ICAF;
XX
DR WPI; 2004-153869/15.
XX
PD Sterile pharmaceutical composition comprising insulin-like growth factor
PT and thiazolidinedione, useful for treating hyperglycaemic disorders, renal
PT disorders, pyelonephritis, Turner's syndrome, Laron's syndrome.
XX
PS Example 7; SEQ ID NO 69; 116pp; English.
XX
SS The invention relates to a sterile pharmaceutical composition comprising
CC an insulin-like growth factor (IGF) and a thiazolidinedione. The
CC pharmaceutical composition is useful for treating hyperglycaemic
CC disorders, renal disorders such as acute and chronic renal insufficiency,
CC pyelonephritis, Turner's syndrome, Laron's syndrome, congestive heart
CC failure, neuromuscular disorders, multiple sclerosis, trauma, infections
CC such as HIV, etc. The present sequence is used in the exemplification of
CC the present invention.
XX
SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12
||: ||
Db 4 ECLIGP 9

RESULT 96
AD157587
ID AD157587 standard; peptide; 18 AA.
XX
AC AD157587;
XX
DT 15-APR-2004 (first entry)
XX
DE Inhibitor of bonding of IGF-I to IGFBP-3, BP3-23B3.4.
XX
KW insulin-like growth factor-I; IGF-I; IGF binding protein; IGFBP3;
KW agonist; hyperglycaemia; obesity; neurological disorder;
KW cardiac disorder; congestive heart failure; renal disorder;
KW immunological disorder; anabolic disorder; protein co-ordinate data.
XX
OS Synthetic.
XX
PN US6683053-B1.
XX

[illegible]

PA	(GETH) GENENTECH INC.
XX	
PI	Clark RG, Lowman HB, Robinson ICAF;
XX	
DR	WPI; 2004-116578/12.
XX	
XX	
PT	New insulin-like growth factor binding protein, for preparing a
PT	composition for treating e.g. obesity-related, neurological, cardiac,
PT	renal or immunological disorders.
XX	
PS	Example 7; SEQ ID NO 69; 117pp; English.
XX	
CC	The invention relates to a peptide which inhibits the binding of insulin-
CC	like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not
CC	inhibit binding of IGF-1 to its receptor, comprising the peptides
CC	appearing as AD157608, AD157616-AD157620. Also included are a composition
CC	comprising the peptide in a carrier, a kit comprising a container
CC	containing the composition and instructions directing the user to utilize
CC	the composition. The composition is further comprises a growth hormone, a
CC	growth hormone releasing peptide, a growth hormone releasing hormone, a
CC	growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF
CC	in combination with an IGF binding protein, an IGF binding protein, a
CC	growth hormone in combination with growth hormone binding protein, a
CC	insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for
CC	preparing a composition for treating e.g. hyperglycaemic, obesity-
CC	related, neurological, cardiac (e.g. congestive heart failure), renal or
CC	immunological disorders. The present sequence inhibits binding of IGF-1
CC	to IGFBP-3.
XX	
SEQ	Sequence 18 AA;
Query Match	41.8%; Score 28; DB 8; Length 18;
Best Local Similarity	83.3%; Pred. No. 1e+03;
Matches	5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
DB	7 ECIIGP 12
	4 ECIIGP 9
RESULT 98	
AD157480	
ID	AD157480 standard; peptide; 18 AA.
AC	AD157480;
XX	
DT	22-APR-2004 (first entry)
XX	
DE	Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23B3.4.
XX	
KW	Insulin-like growth factor-I; IGF-I; IGF binding protein; IGFBP3;
KW	agonist; hypoglycaemia; obesity; neurological disorder;
KW	cardiac disorder; congestive heart failure; renal disorder;
KW	immunological disorder; anabolic disorder; protein co-ordinate data.
OS	Synthetic.
XX	
PN	US6680298-B1.
XX	
PD	20-JAN-2004.
XX	
PF	28-NOV-2000; 2000US-00724114.
XX	
PR	04-APR-1997; 97US-00825852.
PR	31-MAR-1998; 98US-00052888.
XX	
PA	(GETH) GENENTECH INC.
XX	
PI	Clark RG, Lowman HB, Robinson ICAF;
XX	
DR	WPI; 2004-141375/14.
PT	Increasing serum and tissue levels of insulin-like growth factor-I in

PT humans, useful for treating diabetes, comprises administering an amount
PT of a peptide that e.g. reduces plasma insulin secretion or blood glucose
XX levels.
XX
XX Example 7, SEQ ID NO 67, 121pp, English.
XX
CC The invention relates to a peptide which inhibits the binding of insulin-
CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not
CC inhibit binding of IGF-1 to its receptor, comprising the peptides
CC appearing as AD157501, AD157509-AD157513. Also included are a composition
CC comprising the peptide in a carrier, a kit comprising a container
CC containing the composition and instructions directing the user to utilize
CC the composition. The composition is further comprises a growth hormone, a
CC growth hormone releasing peptide, a growth hormone releasing hormone, a
CC in combination with an IGF binding protein, an IGF binding protein, a
CC growth hormone in combination with growth hormone binding protein,
CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for
CC preparing a composition for treating e.g. hyperglycaemic, obesity-
CC related, neurological, cardiac (e.g. congestive heart failure), renal or
CC immunological disorders. The present sequence inhibits binding of IGF-1
CC to IGFBP-3.
XX
XX Sequence 18 AA;
SQ
Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 66.7%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECTIGP 12
DB 4 ECTWGP 9
RESULT 99
AD157482
ID AD157482 standard; peptide; 18 AA.
XX
XX AD157482;
AC
XX 22-APR-2004 (first entry)
DT
XX
XX Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23B3.7.
DE
XX Insulin-like growth factor-I; IGF-1; IGF binding protein; IGFBP3;
KW agonist; hyperglycaemia; obesity; neurological disorder;
KW cardiac disorder; congestive heart failure; renal disorder;
KW immunological disorder; anabolic disorder; protein co-ordinate data.
XX
XX Synthetic.
OS
XX US6680298-B1.
PN
XX 20-JAN-2004.
PD
XX 28-NOV-2000; 2000US-00724114.
PF
XX 04-APR-1997; 97US-00825852.
PR
XX 31-MAR-1998; 98US-00052888.
XX
XX (GETH) GENENTECH INC.
PA
XX Clark RG, Lowman HB, Robinson ICAF,
PI
XX WPI; 2004-141375/14.
DR
XX
XX Increasing serum and tissue levels of insulin-like growth factor-I in
PT humans, useful for treating diabetes, comprises administering an amount
PT of a peptide that e.g. reduces plasma insulin secretion or blood glucose
PT levels.
XX
XX Example 7, SEQ ID NO 69, 121pp, English.
XX

CC The invention relates to a peptide which inhibits the binding of insulin-
CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not
CC inhibit binding of IGF-1 to its receptor, comprising the peptides
CC appearing as AD157501, AD157509-AD157513. Also included are a composition
CC comprising the peptide in a carrier, a kit comprising a container
CC containing the composition and instructions directing the user to utilize
CC the composition. The composition is further comprises a growth hormone, a
CC growth hormone releasing peptide, a growth hormone releasing hormone, a
CC in combination with an IGF binding protein, an IGF binding protein, a
CC growth hormone in combination with growth hormone binding protein, a
CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for
CC preparing a composition for treating e.g. hyperglycaemic, obesity-
CC related, neurological, cardiac (e.g. congestive heart failure), renal or
CC immunological disorders. The present sequence inhibits binding of IGF-1
CC to IGFBP-3.
XX
XX Sequence 18 AA;
SQ
Query Match 41.8%; Score 28; DB 8; Length 18;
Best Local Similarity 83.3%; Pred. No. 1e+03; 1; Indels 0; Gaps 0;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECTIGP 12
DB 4 ECTWGP 9
RESULT 100
ADJ56638
ID ADJ56638 standard; peptide; 18 AA.
XX
XX ADJ56638;
AC
XX 06-MAY-2004 (first entry)
DT
XX
XX Inhibitor of bonding of IGF-1 to IGFBP-3, BP3-23B3.7.
DE
XX Insulin-like growth factor-I; IGF-1; IGF binding protein; IGFBP3;
KW agonist; hyperglycaemia; obesity; neurological disorder;
KW cardiac disorder; congestive heart failure; renal disorder;
KW immunological disorder; anabolic disorder; protein co-ordinate data.
XX
XX Synthetic.
OS
XX US6693079-B1.
PN
XX 17-FEB-2004.
PD
XX 28-NOV-2000; 2000US-00724157.
PF
XX 04-APR-1997; 97US-00825852.
PR
XX 31-MAR-1998; 98US-00052888.
XX
XX (GETH) GENENTECH INC.
PA
XX Clark RG, Lowman HB, Robinson ICAF,
PI
XX WPI; 2004-223910/21.
DR
XX
XX New peptide that binds an IGF binding protein, useful for preparing a
PT composition for treating various diseases, e.g., cardiac or renal
PT disorders.
XX
XX Example 7, SEQ ID NO 69, 117pp, English.
PS
XX
XX The invention relates to a peptide which inhibits the binding of insulin-
CC like growth factor-1 (IGF-1) to IGF binding protein (IGFBP) but does not
CC inhibit binding of IGF-1 to its receptor, comprising the peptides
CC appearing as ADJ56652 and ADJ56586. Also included are a composition
CC comprising the peptide in a carrier, a kit comprising a container
CC containing the composition and instructions directing the user to utilize
CC the composition. The composition is further comprises a growth hormone, a

CC growth hormone releasing peptide, a growth hormone releasing hormone, a
 CC growth hormone secretagogue, an insulin-like growth factor (IGF), an IGF
 CC in combination with an IGF binding protein, an IGF binding protein, a
 CC growth hormone in combination with growth hormone binding protein, a
 CC insulin or hypoglycaemic agent. The peptide is useful as IGF agonist for
 CC preparing a composition for treating e.g. hyperglycaemic, obesity-
 CC related, neurological, cardiac (e.g. congestive heart failure), renal or
 CC immunological disorders. The present sequence inhibits binding of IGF-1
 to IGFBP-3.

XX
 SQ Sequence 18 AA;

Query Match 41.8%; Score 28; DB 8; Length 18;

Best Local Similarity 83.3%; Pred. No. 1e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECILGP 12

DB 4 ECIEGP 9

Search completed: January 20, 2006, 19:05:20
 Job time : 48.3462 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 ; Search time 12.5769 Seconds
(without alignments)
78.883 Million cell updates/sec

Title: US-09-662-293-5
Perfect score: 67
Sequence: 1 DENNSPECILGP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues
Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Issued Patents AA:*
1: /cgn2_6/prodata/1/1aa/5 COMB.rep:*
2: /cgn2_6/prodata/1/1aa/6 COMB.rep:*
3: /cgn2_6/prodata/1/1aa/7 COMB.rep:*
4: /cgn2_6/prodata/1/1aa/8 COMB.rep:*
5: /cgn2_6/prodata/1/1aa/9 COMB.rep:*
6: /cgn2_6/prodata/1/1aa/backfile1.rep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	100.0	12	2	US-09-292-225-5
2	34	50.7	20	1	US-08-484-635-187
3	34	50.7	20	1	US-08-484-631-187
4	34	50.7	20	1	US-08-827-570-187
5	32	47.8	15	1	US-08-179-481-17
6	32	47.8	15	1	US-08-484-635-135
7	32	47.8	19	1	US-08-484-631-135
8	32	47.8	19	1	US-08-827-570-135
9	31	46.3	9	6	5204326-137
10	30	44.8	16	1	US-08-092-817-6
11	30	44.8	16	1	US-08-485-128-6
12	30	44.8	16	2	US-09-824-637-6
13	30	44.8	20	1	US-08-484-135-43
14	30	44.8	20	1	US-08-484-635-27
15	30	44.8	20	1	US-08-484-631-27
16	30	44.8	20	1	US-08-827-570-27
17	30	44.8	20	2	US-09-449-064A-47
18	29	43.3	19	1	US-08-484-635-136
19	29	43.3	19	1	US-08-484-631-136
20	29	43.3	19	1	US-08-827-570-136
21	29	43.3	20	1	US-08-484-135-44
22	29	43.3	20	1	US-08-484-135-53
23	29	43.3	20	1	US-08-484-135-79
24	29	43.3	20	1	US-08-484-635-41
25	29	43.3	20	1	US-08-484-635-42
26	29	43.3	20	1	US-08-484-635-218
27	29	43.3	20	1	US-08-484-631-41

28	43.3	20	1	US-08-484-631-42	Sequence 42, Appl
29	43.3	20	1	US-08-827-570-41	Sequence 218, App
30	43.3	20	1	US-08-827-570-41	Sequence 41, Appl
31	43.3	20	1	US-08-827-570-42	Sequence 42, Appl
32	43.3	20	1	US-08-827-570-218	Sequence 218, App
33	43.3	20	2	US-09-449-064A-48	Sequence 48, Appl
34	43.3	20	2	US-09-449-064A-56	Sequence 56, Appl
35	43.3	20	2	US-09-449-064A-81	Sequence 81, Appl
36	43.3	20	2	US-08-598-873-18	Sequence 18, Appl
37	41.8	8	2	US-08-605-430-18	Sequence 18, Appl
38	41.8	8	2	US-09-717-054-18	Sequence 18, Appl
39	41.8	10	2	US-08-893-526A-20	Sequence 20, Appl
40	41.8	12	2	US-09-177-249-219	Sequence 219, App
41	41.8	12	2	US-09-812-283-219	Sequence 219, App
42	41.8	12	2	US-09-774-639-272	Sequence 11, Appl
43	41.8	15	1	US-08-049-783-11	Sequence 22, Appl
44	41.8	15	1	US-08-158-232-22	Sequence 22, Appl
45	41.8	15	1	US-08-304-626-22	Sequence 22, Appl
46	41.8	15	1	US-08-316-301A-23	Sequence 23, Appl
47	41.8	15	1	US-08-611-928-22	Sequence 23, Appl
48	41.8	15	2	US-09-224-024-5	Sequence 5, Appl1
49	41.8	15	2	US-09-173-891-22	Sequence 23, Appl
50	41.8	15	2	US-09-076-137-23	Sequence 23, Appl
51	41.8	15	2	US-09-738-363-23	Sequence 23, Appl
52	41.8	15	4	PCT-US92-03624-23	Sequence 23, Appl
53	41.8	15	4	PCT-US94-07902-5	Sequence 5, Appl1
54	41.8	16	1	US-08-474-696A-7	Sequence 157, App
55	41.8	18	1	US-08-484-635-157	Sequence 157, App
56	41.8	18	1	US-08-484-631-157	Sequence 157, App
57	41.8	18	1	US-08-827-570-157	Sequence 66, Appl
58	41.8	18	2	US-08-825-852-66	Sequence 66, Appl
59	41.8	18	2	US-08-825-852-68	Sequence 68, Appl
60	41.8	18	2	US-09-052-888-67	Sequence 67, Appl
61	41.8	18	2	US-09-052-888-69	Sequence 69, Appl
62	41.8	18	2	US-10-158-847-88	Sequence 88, Appl
63	41.8	18	2	US-09-723-890-67	Sequence 67, Appl
64	41.8	18	2	US-09-723-890-69	Sequence 69, Appl
65	41.8	18	2	US-09-723-901-67	Sequence 67, Appl
66	41.8	18	2	US-09-723-901-69	Sequence 69, Appl
67	41.8	18	2	US-09-723-931-67	Sequence 67, Appl
68	41.8	18	2	US-09-723-547-67	Sequence 67, Appl
69	41.8	18	2	US-09-724-127-67	Sequence 67, Appl
70	41.8	18	2	US-09-724-127-69	Sequence 69, Appl
71	41.8	18	2	US-09-723-913-67	Sequence 67, Appl
72	41.8	18	2	US-09-723-913-69	Sequence 69, Appl
73	41.8	18	2	US-09-723-873-67	Sequence 67, Appl
74	41.8	18	2	US-09-724-115-67	Sequence 67, Appl
75	41.8	18	2	US-09-724-115-69	Sequence 69, Appl
76	41.8	18	2	US-09-724-114-69	Sequence 69, Appl
77	41.8	18	2	US-09-723-913-67	Sequence 67, Appl
78	41.8	18	2	US-09-723-913-69	Sequence 69, Appl
79	41.8	18	2	US-09-723-912-67	Sequence 67, Appl
80	41.8	18	2	US-09-723-912-69	Sequence 69, Appl
81	41.8	18	2	US-09-724-095-67	Sequence 67, Appl
82	41.8	18	2	US-09-724-095-69	Sequence 69, Appl
83	41.8	18	2	US-09-724-157-67	Sequence 67, Appl
84	41.8	18	2	US-09-724-157-69	Sequence 69, Appl
85	41.8	18	2	US-09-724-062-67	Sequence 67, Appl
86	41.8	18	2	US-09-724-062-69	Sequence 69, Appl
87	41.8	18	2	US-09-724-065-67	Sequence 67, Appl
88	41.8	18	2	US-09-724-065-69	Sequence 69, Appl
89	41.8	18	2	US-10-158-825-88	Sequence 88, Appl
90	41.8	18	2	US-09-724-481-67	Sequence 67, Appl
91	41.8	18	2	US-09-724-481-69	Sequence 69, Appl
92	41.8	19	1	US-08-474-696A-1	Sequence 1, Appl1
93	41.8	19	1	US-08-474-696A-3	Sequence 3, Appl1
94	41.8	19	2	US-09-044-604-3	Sequence 3, Appl1
95	41.8	20	1	US-08-484-135-51	Sequence 51, Appl
96	41.8	20	1	US-08-484-135-75	Sequence 75, Appl
97	41.8	20	1	US-08-484-635-35	Sequence 35, Appl
98	41.8	20	1	US-08-484-635-167	Sequence 167, App
99	41.8	20	1	US-08-484-635-224	Sequence 224, App
100	41.8	20	1	US-08-484-631-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1
US-09-292-225-5
Sequence 5, Application US/09292225
Patent No. 6455666
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USES THEREOF
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 5
LENGTH: 12
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-09-292-225-5

Query Match
Best Local Similarity 100.0%; Score 67; DB 2; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEKNSPECILGP 12
Db 1 DEKNSPECILGP 12

RESULT 2
US-08-484-635-187
Sequence 187, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-187

Query Match
Best Local Similarity 50.7%; Score 34; DB 1; Length 20;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 3 KNSPECILGP 12
Db 2 KNNYRCQGRP 11

RESULT 3
US-08-484-631-187
Sequence 187, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids

TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-187

Query Match 50.7%; Score 34; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECILGP 12
DB 2 KNNVRCQFGP 11

RESULT 4
US-08-827-570-187
Sequence 187, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaehyad, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 187:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-187

Query Match 50.7%; Score 34; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 21;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 3 KNSPECILGP 12
DB 2 KNNVRCQFGP 11

DB 2 KNNVRCQFGP 11

RESULT 5
US-08-179-481-17
Sequence 17, Application US/08179481
Patent No. 5624816
GENERAL INFORMATION:
APPLICANT: CARAWAY, KENNETH L.
APPLICANT: CAROTHERS CARAWAY, CORALIE A.
APPLICANT: FREIGEN, NEVIS L.
TITLE OF INVENTION: ONCOGENE PRODUCT LIGAND
NUMBER OF SEQUENCES: 125
CORRESPONDENCE ADDRESS:
ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
STREET: 1100 NEW YORK AVENUE, N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A.
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/179,481
FILING DATE: 28-DEC-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/922,521
FILING DATE: 30-JUL-1992
ATTORNEY/AGENT INFORMATION:
NAME: KOKULIS, PAUL N.
REGISTRATION NUMBER: 16,773
REFERENCE/DOCKET NUMBER: 200702/UM92-08CIP
TELEPHONE: (202) 861-3000
TELEFAX: (202) 822-0944
TELLEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-179-481-17

Query Match 47.8%; Score 32; DB 1; Length 15;
Best Local Similarity 62.5%; Pred. No. 36;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 2 DDINSYEC 9

RESULT 6
US-08-484-635-135
Sequence 135, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaehyad, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-135

Query Match 47.8%; Score 32; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSFCTIGP 12
DB 2 KTKYKCYWGP 11

RESULT 7
US-08-484-631-135
Sequence 135, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631

FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-135

Query Match 47.8%; Score 32; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSFCTIGP 12
DB 2 KTKYKCYWGP 11

RESULT 8
US-08-827-570-135
Sequence 135, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 135:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-135

Query Match 47.8%; Score 32; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 45;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPFCILGP 12
DB 2 KTKYKCTMGP 11

RESULT 9
5204326-127
PATENT NO. 5204326
APPLICANT: FUJII, SETSURO; YAMAMOTO, YOSHIMITO; SHIMIZU, FUMIO
INAI, MASATOSHI; KINOSHITA, NAOSUMI; NAKAMURA, SHIZUO; HIROASHI,
MITSURU; SAKAMOTO, TAKASHI; TSUTSUMI, KAZUHIKO; SHIRASAKA, TETSUHIKO
TITLE OF INVENTION: POLYPEPTIDE DERIVATIVES AND CALCIUM
METABOLISM IMPROVING AGENT
NUMBER OF SEQUENCES: 147
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/493,359
FILING DATE: 14-MAR-1990
SEQ ID NO: 127;
LENGTH: 9
5204326-127

Query Match 46.3%; Score 31; DB 6; Length 9;
Best Local Similarity 62.5%; Pred. No. 4,6e+05;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPFCILG 11
DB 2 NSLTCVLG 9

RESULT 10
US-08-092-817-6
SEQUENCE 6, Application US/08092817
PATENT NO. 5496926
GENERAL INFORMATION:
APPLICANT: RUBINSTEIN, Menachem
APPLICANT: NOVICK, Daniela
APPLICANT: TAL, Nathan
TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,817
FILING DATE: 19-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 100696
FILING DATE: 19-JAN-1992

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/092,817
FILING DATE: 19-JUL-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 100696
FILING DATE: 19-JAN-1992

ADDRESSER: BROWDY AND NEIMARK
STREET: 419 Seventh Street, Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 102915
FILING DATE: 23-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: RUBINSTEIN-5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633

INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-092-817-6

Query Match 44.8%; Score 30; DB 1; Length 16;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPFC 8
DB 4 ERNEPFC 10

RESULT 11
US-08-485-128-6
SEQUENCE 6, Application US/08485128
PATENT NO. 6365713
GENERAL INFORMATION:
APPLICANT: RUBINSTEIN, Menachem
APPLICANT: NOVICK, Daniela
APPLICANT: TAL, Nathan
TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND
TITLE OF INVENTION: USE
NUMBER OF SEQUENCES: 6
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,128
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,817
FILING DATE: 19-JUL-1993
APPLICATION NUMBER: IL 100696
FILING DATE: 19-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 102915
FILING DATE: 23-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: RUBINSTEIN-5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,128
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/092,817
FILING DATE: 19-JUL-1993
APPLICATION NUMBER: IL 100696
FILING DATE: 19-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: IL 102915
FILING DATE: 23-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: TOWNSEND, G. Kevin
REGISTRATION NUMBER: 34,033
REFERENCE/DOCKET NUMBER: RUBINSTEIN-5A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
TELEX: 248633
INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-485-128-6

Query Match 44.8%; Score 30; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
Db 4 ERNRFQC 10

RESULT 12
US-09-824-637-6
Sequence 6, Application US/09824637
Patent No. 6703222
GENERAL INFORMATION:
APPLICANT: RUBINSTEIN, Menachem
APPLICANT: NOVICK, Daniela
APPLICANT: TAL, Nachan
APPLICANT: Fischer, Dina
TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND USE
FILE REFERENCE: RUBINSTEIN-5D
CURRENT APPLICATION NUMBER: US/09/824,637
CURRENT FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: US 08/485,128
PRIOR FILING DATE: 1995-06-07
PRIOR APPLICATION NUMBER: US 08/092,817
PRIOR FILING DATE: 1993-07-19
PRIOR APPLICATION NUMBER: IL 100696
PRIOR FILING DATE: 1992-01-19
PRIOR APPLICATION NUMBER: IL 102915
PRIOR FILING DATE: 1992-08-23
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
SEQ ID NO 6
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-09-824-637-6

Query Match 44.8%; Score 30; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 86;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
Db 4 ERNRFQC 10

RESULT 13
US-08-484-135-43
Sequence 43, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivlin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSES: Frank S. Digiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-43

Query Match 44.8%; Score 30; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 PECLTGP 12
Db 4 YKCLMGP 10

RESULT 14
US-08-484-635-27
Sequence 27, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSES: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-27

Query Match 44.8%; Score 30; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTIGP 12
DB 4 YKCLMGP 10

RESULT 15
US-08-484-631-27
Sequence 27, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaahya, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-27

Query Match 44.8%; Score 30; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;
QY 6 FECTIGP 12

DB 4 YKCLMGP 10

RESULT 16
US-08-827-570-27
Sequence 27, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaahya, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: linear
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-27

Query Match 44.8%; Score 30; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTIGP 12
DB 4 YKCLMGP 10

RESULT 17
US-09-449-064A-47
Sequence 47, Application US/09449064A
Patent No. 6703480
GENERAL INFORMATION:
APPLICANT: BALU, PALANI
TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN
TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND

;; TITLE OF INVENTION: USE
;; FILE REFERENCE: 0300-0005
;; CURRENT APPLICATION NUMBER: US/09/449,064A
;; CURRENT FILING DATE: 1999-11-24
;; NUMBER OF SEQ ID NOS: 93
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 47
;; LENGTH: 20
;; TYPE: PR1
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
;; NAME/KEY: MOD RES
;; LOCATION: (13)
;; OTHER INFORMATION: 1-Nal
US-09-449-064A-47

Query Match 44.8%; Score 30; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.1e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTICGP 12
DB 4 YKCLMGP 10

RESULT 18
US-08-484-635-136
;; Sequence 136, Application US/08484635
;; Patent No. 5773569
;; GENERAL INFORMATION:
;; APPLICANT: Wrighton, Nicholas C.
;; APPLICANT: Dower, William J.
;; APPLICANT: Chang, Ray S.
;; APPLICANT: Kashyap, Arun K.
;; APPLICANT: Jolliffe, Linda K.
;; APPLICANT: Johnson, Dana
;; APPLICANT: Mulcahy, Linda
;; TITLE OF INVENTION: Compounds and Peptides That Bind to the
;; TITLE OF INVENTION: Erythropoietin Receptor
;; NUMBER OF SEQUENCES: 259
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew
;; STREET: One Market Plaza, Stewart Street Tower
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105-1492
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,635
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/155,940
;; FILING DATE: 19-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Garrett-Wackowski, Eugenia
;; REGISTRATION NUMBER: 37,330
;; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-5043
;; TELEFAX: (415) 543-9600
;; INFORMATION FOR SEQ ID NO: 136:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:

;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-484-635-136

Query Match 43.3%; Score 29; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCTICGP 12
DB 2 KTKYRCWGP 11

RESULT 19
US-08-484-631-136
;; Sequence 136, Application US/08484631
;; Patent No. 5830851
;; GENERAL INFORMATION:
;; APPLICANT: Wrighton, Nicholas C.
;; APPLICANT: Dower, William J.
;; APPLICANT: Chang, Ray S.
;; APPLICANT: Kashyap, Arun K.
;; APPLICANT: Jolliffe, Linda K.
;; APPLICANT: Johnson, Dana
;; APPLICANT: Mulcahy, Linda
;; TITLE OF INVENTION: Compounds and Peptides That Bind to the
;; TITLE OF INVENTION: Erythropoietin Receptor
;; NUMBER OF SEQUENCES: 259
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Townsend and Townsend and Crew
;; STREET: One Market Plaza, Stewart Street Tower
;; CITY: San Francisco
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94105-1492
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/484,631
;; FILING DATE: 07-JUN-1995
;; CLASSIFICATION: 514
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/155,940
;; FILING DATE: 19-NOV-1993
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Garrett-Wackowski, Eugenia
;; REGISTRATION NUMBER: 37,330
;; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (415) 543-5043
;; TELEFAX: (415) 543-9600
;; INFORMATION FOR SEQ ID NO: 136:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 19 amino acids
;; TYPE: amino acid
;; STRANDEDNESS:
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
US-08-484-631-136

Query Match 43.3%; Score 29; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCTICGP 12
DB 2 KTKYRCWGP 11

RESULT 20

US-08-827-570-136
; Sequence 136, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/827,570
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,635
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Mackowski, Eugenia
; REGISTRATION NUMBER: 37,330
; REFERENCE/DOCKET NUMBER: 16528A-43-1-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-9600
; TELEFAX: (415) 543-5043
; INFORMATION FOR SEQ ID NO: 136:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 19 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-827-570-136

Query Match 43.3%; Score 29; DB 1; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.5e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCLGP 12
DB 2 KTKRCWCP 11

RESULT 21
US-08-484-135-44
; Sequence 44, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivlin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Frank S. DiGioglio
; STREET: 400 Garden City Plaza
; CITY: Garden City

STATE: New York
COUNTRY: U.S.A.
ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGioglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 44:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-135-44

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FPCILGP 12
DB 4 YSCIMGP 10

RESULT 22
US-08-484-135-53
; Sequence 53, Application US/08484135
; Patent No. 5767078
; GENERAL INFORMATION:
; APPLICANT: Johnson, Dana L
; APPLICANT: Zivlin, Robert A
; TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
; NUMBER OF SEQUENCES: 93
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Frank S. DiGioglio
; STREET: 400 Garden City Plaza
; CITY: Garden City
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 11530
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,135
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: DiGioglio, Frank S
; REGISTRATION NUMBER: 31,346
; REFERENCE/DOCKET NUMBER: 9594
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (516) 742-4343
; TELEFAX: (516) 742-4366
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-53

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12
: : : :
Db 4 YECRMGP 10

RESULT 23
US-08-484-135-79
Sequence 79, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivlin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. Digiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Digiglio, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 79:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-79

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12
: : : :
Db 4 YECRMGP 10

RESULT 24
US-08-484-635-41
Sequence 41, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.

APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowaki, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043

INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-41

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12
: : : :
Db 4 YECRMGP 10

RESULT 25
US-08-484-635-42
Sequence 42, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-42

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FRCILGP 12
Db 4 YSCILMP 10

RESULT 26
US-08-484-635-218
Sequence 218, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wighton, Nicholas C.
APPLICANT: Chang, Ray S.
APPLICANT: Dower, William J.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330

REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-218

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FRCILGP 12
Db 4 YSCILMP 10

RESULT 27
US-08-484-631-41
Sequence 41, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESSES:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-41

Query Match 43.3%; Score 29; DB 1; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTIGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 28

US-08-484-631-42
; Sequence 42, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94105-1492
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/484,631
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/155,940
; FILING DATE: 19-NOV-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Garrett-Wackowski, Eugenia
; REGISTRATION/DOCKET NUMBER: 37,330
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 543-5043
; TELEFAX: (415) 543-9600
; INFORMATION FOR SEQ ID NO: 42:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-484-631-42

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTIGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 29

US-08-484-631-218
; Sequence 218, Application US/08484631
; Patent No. 5830851
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.

APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION/DOCKET NUMBER: 37,330
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 218:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-218

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTIGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 30

US-08-827-570-41
; Sequence 41, Application US/08827570
; Patent No. 5986047
; GENERAL INFORMATION:
; APPLICANT: Wrighton, Nicholas C.
; APPLICANT: Dower, William J.
; APPLICANT: Chang, Ray S.
; APPLICANT: Kashyap, Arun K.
; APPLICANT: Jolliffe, Linda K.
; APPLICANT: Johnson, Dana
; APPLICANT: Mulcahy, Linda
; TITLE OF INVENTION: Compounds and Peptides That Bind to the
; TITLE OF INVENTION: Erythropoietin Receptor
; NUMBER OF SEQUENCES: 259
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Townsend and Townsend and Crew
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California

COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-41

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRCILGP 12
DB 4 YECRMGP 10

RESULT 31
US-08-827-570-42
Sequence 42, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Johnson, Dana
APPLICANT: Jolliffe, Linda K.
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-42

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 FRCILGP 12
DB 4 YSCIMGP 10

RESULT 32
US-08-827-570-218
Sequence 218, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Johnson, Dana
APPLICANT: Jolliffe, Linda K.
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 218:

SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-218

Query Match 43.3%; Score 29; DB 1; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FECTIGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 33
US-09-449-064A-48
Sequence 48, Application US/09449064A
Patent No. 6703480
GENERAL INFORMATION:
APPLICANT: BALU, PALANI
TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN
TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND
FILE REFERENCE: 0300-0005
CURRENT APPLICATION NUMBER: US/09/449,064A
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 48
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: MOD RES
LOCATION: (13)
OTHER INFORMATION: 1-Nal
US-09-449-064A-48

Query Match 43.3%; Score 29; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FECTIGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 34
US-09-449-064A-56
Sequence 56, Application US/09449064A
Patent No. 6703480
GENERAL INFORMATION:
APPLICANT: BALU, PALANI
TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN
TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND
FILE REFERENCE: 0300-0005
CURRENT APPLICATION NUMBER: US/09/449,064A
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 56
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
OTHER INFORMATION: peptide

NAME/KEY: MOD RES
LOCATION: (13)
OTHER INFORMATION: 1-Nal
US-09-449-064A-56

Query Match 43.3%; Score 29; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.6e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FECTIGP 12
: ||: ||
Db 4 YECRMGP 10

RESULT 35
US-09-449-064A-81
Sequence 81, Application US/09449064A
Patent No. 6703480
GENERAL INFORMATION:
APPLICANT: BALU, PALANI
TITLE OF INVENTION: NOVEL PEPTIDE DIMERS AS AGONISTS OF THE ERYTHROPOIETIN
TITLE OF INVENTION: (EPO) RECEPTOR, AND ASSOCIATED METHODS OF SYNTHESIS AND
FILE REFERENCE: 0300-0005
CURRENT APPLICATION NUMBER: US/09/449,064A
CURRENT FILING DATE: 1999-11-24
NUMBER OF SEQ ID NOS: 93
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 81
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
NAME/KEY: MOD RES
LOCATION: (13)
OTHER INFORMATION: 1-Nal
US-09-449-064A-81

Query Match 43.3%; Score 29; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.6e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FECTIGP 12
: ||: ||
Db 4 YSCLMGP 10

RESULT 36
US-08-598-873-18
Sequence 18, Application US/08598873
Patent No. 5928864
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
TITLE OF INVENTION: HEBNER, Kay
TITLE OF INVENTION: FHTT PROTEINS AND NUCLEIC ACIDS AND
NUMBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
ADDRESS: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/598,873

FILING DATE: 09-FEB-1996
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Friebe, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-598-873-18

Query Match 41.8%; Score 28; DB 1; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 1 DEBTAFSC 8

RESULT 37
US-08-605-430-18
Sequence 18, Application US/08605430
Patent No. 6242212
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/605,430
FILING DATE: 22-FEB-1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Friebe, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
US-08-605-430-18

Query Match 41.8%; Score 28; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 1 DEBTAFSC 8

RESULT 38
US-09-717-054-18
Sequence 18, Application US/09717054
Patent No. 6774217
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
Huebner, Kay
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
TITLE OF INVENTION: METHODS BASED THEREON
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/717,054
FILING DATE: 21-No. 6774217-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/605,430
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Friebe, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-717-054-18

Query Match 41.8%; Score 28; DB 2; Length 8;
Best Local Similarity 50.0%; Pred. No. 4.6e+05;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 1 DEBTAFSC 8

RESULT 39
US-08-893-526A-20
Sequence 20, Application US/08893526A
Patent No. 6096707
GENERAL INFORMATION:
APPLICANT: Heino, Jyrki
Ivaska, Johanna
APPLICANT: K pyl, Jarmo
TITLE OF INVENTION: Integrin Binding Peptide and Use Thereof
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSER: Sterne, Keesler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave., N.W.

CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/893,526A
FILING DATE: 11-JUL-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: KIM, JUDITH U.
REGISTRATION NUMBER: 40,679
REFERENCE/DOCKET NUMBER: 1708.0240000
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202/371-2600
TELEFAX: 202/371-2540
TELEX:
INFORMATION FOR SEQ ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: peptide
US-08-893-526A-20

Query Match 41.8%; Score 28; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 1.2e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 3 DESNSTYC 10

RESULT 40
US-09-177-249-219

/ Sequence 219, Application US/09177249
/ Patent No. 6229064
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Ohad, Nir
/ APPLICANT: Kiyosue, Tomohiro
/ APPLICANT: Yadegari, Ramlin
/ APPLICANT: Margosian, Linda
/ APPLICANT: Harada, John
/ APPLICANT: Goldberg, Robert B.
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
/ FILE REFERENCE: 023070-086120US
/ CURRENT APPLICATION NUMBER: US/09/177,249
/ CURRENT FILING DATE: 1998-10-22
/ EARLIER APPLICATION NUMBER: US 09/071,838
/ EARLIER FILING DATE: 1998-05-01
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 219
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Arabidopsis sp.
US-09-177-249-219

Query Match 41.8%; Score 28; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 9
DB 4 DLRRSPKCV 12

RESULT 41
US-09-812-283-219
/ Sequence 219, Application US/09812283
/ Patent No. 6828477
/ GENERAL INFORMATION:
/ APPLICANT: Fischer, Robert L.
/ APPLICANT: Ohad, Nir
/ APPLICANT: Kiyosue, Tomohiro
/ APPLICANT: Yadegari, Ramlin
/ APPLICANT: Margosian, Linda
/ APPLICANT: Harada, John
/ APPLICANT: Goldberg, Robert B.
/ APPLICANT: The Regents of the University of California
/ TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
/ FILE REFERENCE: 023070-086120US
/ CURRENT APPLICATION NUMBER: US/09/812,283
/ CURRENT FILING DATE: 2001-03-19
/ PRIOR APPLICATION NUMBER: 09/177,249
/ PRIOR FILING DATE: 1998-10-22
/ PRIOR APPLICATION NUMBER: US 09/071,838
/ PRIOR FILING DATE: 1998-05-01
/ NUMBER OF SEQ ID NOS: 324
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 219
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Arabidopsis sp.
US-09-812-283-219

Query Match 41.8%; Score 28; DB 2; Length 12;
Best Local Similarity 44.4%; Pred. No. 1.4e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 9
DB 4 DLRRSPKCV 12

RESULT 42
US-09-774-639-272
/ Sequence 272, Application US/09774639
/ Patent No. 6806351
/ GENERAL INFORMATION:
/ APPLICANT: Rosen et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P1
/ CURRENT APPLICATION NUMBER: US/09/774,639
/ CURRENT FILING DATE: 2001-07-09
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
/ SOFTWARE: Patentin Ver. 2.0
/ SEQ ID NO 272
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-774-639-272

Query Match 41.8%; Score 28; DB 2; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.7e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPECITG 11
DB 3 KGDLMCTIG 11

RESULT 43
US-08-049-783-11
/ Sequence 11, Application US/08049783

```
/ Patent No. 5439881
/ GENERAL INFORMATION:
/ APPLICANT: Narva, Kenneth E
/ APPLICANT: Schwab, George E
/ APPLICANT: Payne, Jewel M
/ TITLE OF INVENTION: Gene Encoding No. 5439881e1 Nematode-Active
/ TITLE OF INVENTION: Toxins Cloned from Bacillus thuringiensis Isolates
/ NUMBER OF SEQUENCES: 18
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Jeff Lloyd
/ STREET: 2421 N.W. 41st Street
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/049,783
/ FILING DATE: 19930419
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Lloyd, Jeff
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 11:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: AMINO ACID
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ US-08-049-783-11

Query Match 41.8%; Score 28; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
DB 6 DEKLSFOLI 14

RESULT 44
US-08-158-232-22
/ Sequence 22, Application US/08158232
/ Patent No. 5596071
/ GENERAL INFORMATION:
/ APPLICANT: Payne, Jewel
/ APPLICANT: Kennedy, M. Keith
/ APPLICANT: Randall, John Brooks
/ APPLICANT: Meier, Henry
/ APPLICANT: Ulick, Heidi Jane
/ APPLICANT: Foncerrada, Luis
/ APPLICANT: Schnepf, H. Ernest
/ APPLICANT: Schwab, George E.
/ APPLICANT: Fu, Jenny
/ TITLE OF INVENTION: No. 5596071e1 Bacillus thuringiensis Toxins Active
/ TITLE OF INVENTION: Against Hymenopteran Pests
/ NUMBER OF SEQUENCES: 51
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David R. Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
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/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/158,232
/ FILING DATE:
/ CLASSIFICATION: 435
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/887,980
/ FILING DATE: 22-MAY-1992
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/797,645
/ FILING DATE: 25-NOV-1991
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: US 07/703,977
/ FILING DATE: 22-MAY-1991
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Saliwanchik, David R.
/ REGISTRATION NUMBER: 31,794
/ REFERENCE/DOCKET NUMBER: M/SCU104.C1
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 904-375-8100
/ TELEFAX: 904-372-5800
/ INFORMATION FOR SEQ ID NO: 22:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 15 amino acids
/ TYPE: amino acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/ MOLECULE TYPE: peptide
/ US-08-158-232-22

Query Match 41.8%; Score 28; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
DB 6 DEKLSFOLI 14

RESULT 45
US-08-304-626-22
/ Sequence 22, Application US/08304626
/ Patent No. 5616495
/ GENERAL INFORMATION:
/ APPLICANT: Payne, Jewel M.
/ APPLICANT: Kennedy, M. Keith
/ APPLICANT: Randall, John Brooks
/ APPLICANT: Meier, Henry
/ APPLICANT: Ulick, Heidi Jane
/ APPLICANT: Foncerrada, Luis
/ APPLICANT: Schnepf, Harry B.
/ APPLICANT: Schwab, George E.
/ TITLE OF INVENTION: No. 5616495e1 Bacillus thuringiensis Isolates
/ TITLE OF INVENTION: Active Against Hymenopteran Pests and Genes Encoding
/ NUMBER OF SEQUENCES: 39
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: David R. Saliwanchik
/ STREET: 2421 N.W. 41st Street, Suite A-1
/ CITY: Gainesville
/ STATE: FL
/ COUNTRY: USA
/ ZIP: 32606
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: PatentIn Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/304,626
/ FILING DATE:
```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/887,980
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ 104
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-304-626-22

Query Match 41.8%; Score 28; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
DB 6 DEKLSFOLI 14

RESULT 46
US-08-316-301A-23
Sequence 23, Application US/08316301A

GENERAL INFORMATION:
APPLICANT: Schmepl, Harry E.
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Foncetrada, Luis
TITLE OF INVENTION: No. 5753492el Nematode-Active Toxins and Genes
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESSES:
ADDRESSER: Saliwanchik & Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/316,301A
FILING DATE: 30-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/871,510
FILING DATE: 23-APR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/693,018
FILING DATE: 03-MAY-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/565,544
FILING DATE: 10-AUG-1990
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/084,653
FILING DATE: 12-AUG-1987

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/830,050
FILING DATE: 31-JAN-1992
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Lloyd, Jeff
REGISTRATION NUMBER: 35,589
REFERENCE/DOCKET NUMBER: MA20CCCD1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-316-301A-23

Query Match 41.8%; Score 28; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
DB 6 DEKLSFOLI 14

RESULT 47
US-08-611-928-22
Sequence 22, Application US/08611928

GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Meyer, Henry
APPLICANT: Vick, Heidi Jane
APPLICANT: Foncetrada, Luis
APPLICANT: Schmepl, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 5824792el Bacillus thuringiensis Toxins Active
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSER: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/611,928
FILING DATE: 06-MAR-1996
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/158,232
FILING DATE: 24-NOV-1993
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
CLASSIFICATION: 530

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-611-928-22

Query Match 41.8%; Score 28; DB 1; Length 15;
Best local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
DB 6 DEKLSFOLI 14

RESULT 48
US-09-224-024-5
Sequence 5, Application US/09224024
Patent No. 6056953
GENERAL INFORMATION:
APPLICANT: Leslie Hickie
TITLE OF INVENTION: Materials and Methods for the Control of
NUMBER OF INVENTIONS: Calliphoridae Pests
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/224,024
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/856,226
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-224-024-5

Query Match 41.8%; Score 28; DB 2; Length 15;
Best local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
DB 6 DEKLSFOLI 14

RESULT 49
US-09-173-891-22
Sequence 22, Application US/09173891
Patent No. 6077937
GENERAL INFORMATION:
APPLICANT: Payne, Jewel
APPLICANT: Kennedy, M. Keith
APPLICANT: Randall, John Brooks
APPLICANT: Meier, Henry
APPLICANT: Vick, Heidi Jane
APPLICANT: Poncetrada, Luis
APPLICANT: Schaept, H. Ernest
APPLICANT: Schwab, George E.
APPLICANT: Fu, Jenny
TITLE OF INVENTION: No. 6077937el Bacillus thuringiensis Toxins Active
NUMBER OF INVENTIONS: Against Hymenopteran Pests
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/173,891
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/158,232
FILING DATE:
APPLICATION NUMBER: US 07/887,980
FILING DATE: 22-MAY-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/797,645
FILING DATE: 25-NOV-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/703,977
FILING DATE: 22-MAY-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M/SCJ104.C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-173-891-22

Query Match 41.8%; Score 28; DB 2; Length 15;
Best local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9
||| ||: |
Db 6 DEKLSFOLI 14

RESULT 50
US-09-076-137-23
Sequence 23, Application US/09076137B
Patent No. 6166195
GENERAL INFORMATION:
APPLICANT: Schepf, Harry E.
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Poncetrada, Luis
TITLE OF INVENTION: No. 6166195el Nematode-Active Toxins and Genes which Code
FILE REFERENCE: MA-20CCCD2
CURRENT APPLICATION NUMBER: US/09/076,137B
EARLIER FILING DATE: 1998-05-12
EARLIER APPLICATION NUMBER: 08/316,301
NUMBER OF SEQ ID NOS: 42
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 23
LENGTH: 15
TYPER: PRT
ORGANISM: Bacillus thuringiensis
US-09-076-137-23

Query Match 41.8%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9
||| ||: |
Db 6 DEKLSFOLI 14

RESULT 51
US-09-738-363-23
Sequence 23, Application US/09738363
Patent No. 6632792
GENERAL INFORMATION:
APPLICANT: Schepf, Harry E.
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Poncetrada, Luis
TITLE OF INVENTION: Nematocidal Proteins
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay

REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPER: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-738-363-23

Query Match 41.8%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9
||| ||: |
Db 6 DEKLSFOLI 14

RESULT 52
PCT-US92-03624-23
Sequence 23, Application PC/TUS9203624
GENERAL INFORMATION:
APPLICANT: Schepf, Harry E.
APPLICANT: Schwab, George E.
APPLICANT: Payne, Jewel M.
APPLICANT: Narva, Kenneth E.
APPLICANT: Poncetrada, Luis
TITLE OF INVENTION: Novel Nematode-Active Toxins and Genes
TITLE OF INVENTION: Which Code Therefor
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/03624
FILING DATE: 19920501
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: MA20CC2C1C1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPER: AMINO ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US92-03624-23

Query Match 41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPECT 9

Db 6 DEKLSFOLI 14

RESULT 53
PCT-US94-07902-5
Sequence 5, Application PC/TUS9407902
GENERAL INFORMATION:
APPLICANT:
APPLICANT: Street address: 4980 Carroll Canyon Road
APPLICANT: City: San Diego
APPLICANT: State/Province: California
APPLICANT: Country: US
APPLICANT: Postal code/Zip: 92121
APPLICANT: Phone number: (619) 453-8030 Fax number: (619) 453-6991
APPLICANT: Telex number:
TITLE OF INVENTION: Materials and Methods for the Control of
NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07902
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: M479
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-07902-5

Query Match 41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
Db 6 DEKLSFOLI 14

RESULT 54
US-08-474-696A-7
Sequence 7, Application US/08474696A
Patent No. 5843673
GENERAL INFORMATION:
APPLICANT: Sharpe-Timm, Kathy L.
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5843673thwestern Hwy.
CITY: Farmington Hills

STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,696A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-474-696A-7

Query Match 41.8%; Score 28; DB 1; Length 16;
Best Local Similarity 62.5%; Pred. No. 1.9e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECI 8
Db 7 DAKGSFPC 14

RESULT 55
US-08-484-635-157
Sequence 157, Application US/08484635
Patent No. 573569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaahyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia

REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-157

Query Match 41.8%; Score 28; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTILGP 12
| : : : | | |
DB 1 ERRFYKCRFGP 11

RESULT 56
US-08-484-631-157
Sequence 157, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-631-157

Query Match 41.8%; Score 28; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTILGP 12
| : : : | | |
DB 1 ERRFYKCRFGP 11

RESULT 57
US-08-827-570-157
Sequence 157, Application US/08827570
Patent No. 5986047
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/827,570
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,635
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 157:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-827-570-157

Query Match 41.8%; Score 28; DB 1; Length 18;
Best Local Similarity 36.4%; Pred. No. 2.2e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTILGP 12
| : : : | | |
DB 1 ERRFYKCRFGP 11

RESULT 58
US-08-825-852-66
Sequence 66, Application US/08825852

Patent No. 6121416
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,852
FILING DATE: 04-Apr-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-825-852-66

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECLIGP 12
Db 4 ECVWGP 9

RESULT 59
US-08-825-852-68
Sequence 68, Application US/08825852
Patent No. 6121416
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 79
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/825,852
FILING DATE: 04-Apr-1997
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 68:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-08-825-852-68

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECLIGP 12
Db 4 ECLIGP 9

RESULT 60
US-09-052-888-67
Sequence 67, Application US/09052888
Patent No. 6251865
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPacIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-052-888-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECLIGP 12
Db 4 ECVWGP 9

RESULT 61
US-09-052-888-69

Sequence 69, Application US/09052888
Patent No. 6251865
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
US-09-052-888-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECICLP 12
DB 4 ECICGP 9

RESULT 62
US-10-158-847-88
Sequence 88, Application US/10158847
Patent No. 6592865
GENERAL INFORMATION:
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF557
CURRENT APPLICATION NUMBER: US/10/158,847
PRIOR FILING DATE: 2002-06-03
CURRENT APPLICATION NUMBER: 60/295,004
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO 88
LENGTH: 18
TYPE: PRT
ORGANISM: homo sapiens
US-10-158-847-88

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 FECICLP 12
DB 4 ECICGP 9

DB 2 FECICGP 8

RESULT 63
US-09-723-890-67
Sequence 67, Application US/09723890
Patent No. 6608031
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,890
FILING DATE: 28-Mar-2000
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-723-890-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECICLP 12
DB 4 ECICGP 9

RESULT 64
US-09-723-890-69
Sequence 69, Application US/09723890
Patent No. 6608031
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
APPLICANT: Lowman, Henry B.
APPLICANT: Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,890
FILING DATE: 28-Mar-2000
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-723-890-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12
DB 4 ECTIGP 9

RESULT 65
US-09-723-901-67
Sequence 67, Application US/09723901
Patent No. 6620789
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,901
FILING DATE: 28-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-723-901-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12
DB 4 ECTIGP 9

RESULT 66
US-09-723-901-69
Sequence 69, Application US/09723901
Patent No. 6620789
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,901
FILING DATE: 28-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-723-901-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12
DB 4 ECTIGP 9

RESULT 67
US-09-723-547-67
Sequence 67, Application US/09723547
Patent No. 6632794

GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,547
FILING DATE: 28-No. 6632794-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-723-547-67
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECILGP 12
DB 4 ECVWGP 9
RESULT 68
US-09-723-547-69
Sequence 69, Application US/09723547
Patent No. 6632794
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,547

FILING DATE: 28-No. 6632794-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-723-547-69
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECILGP 12
DB 4 ECVWGP 9
RESULT 69
US-09-724-127-67
Sequence 67, Application US/09724127
Patent No. 6635619
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,127
FILING DATE: 28-No. 6635619-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-724-127-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIP 12
DB 4 ECVWGP 9

RESULT 70

US-09-724-127-69
Sequence 69, Application US/09724127
Patent No. 6635619
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpacin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,127
FILING DATE: 28-Mar-1998
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-724-127-69
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 63.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIP 12
DB 4 ECLIP 9

RESULT 71

US-09-723-931-67
Sequence 67, Application US/09723931
Patent No. 6645775
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Winpacin (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/723,931

FILING DATE: 28-Mar-1998

CLASSIFICATION: <Unknown>

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: 09/052,888

FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:

NAME: Haasek, Janet E.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/952-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-723-931-67
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIP 12
DB 4 ECVWGP 9

RESULT 72

US-09-723-931-69
Sequence 69, Application US/09723931
Patent No. 6645775
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpacin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,931
FILING DATE: 28-Mar-1998
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.

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/
/      REGISTRATION NUMBER: 28,616
/      REFERENCE/DOCKET NUMBER: P1071P1
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: 650/225-1896
/      TELEFAX: 650/952-9881
/      INFORMATION FOR SEQ ID NO: 69:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 18 amino acids
/      TYPE: Amino Acid
/      TOPOLOGY: Linear
/      US-09-723-931-69
/      SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Query Match      41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 ECIIGP 12
/      |||
/      4 ECIIGP 9

Db

RESULT 73
US-09-723-873-67
/ Sequence 67, Application US/09723873
/ Patent No. 6677305
/ GENERAL INFORMATION:
/ APPLICANT: Clark, Ross G1
/      Lowman, Henry B.
/      Robinson, Iain C.A.F.
/      TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
/      NUMBER OF SEQUENCES: 109
/      CORRESPONDENCE ADDRESS:
/      ADDRESSER: Genentech, Inc.
/      STREET: 1 DNA Way
/      CITY: South San Francisco
/      STATE: California
/      COUNTRY: USA
/      ZIP: 94080
/      COMPUTER READABLE FORM:
/      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/      COMPUTER: IBM PC compatible
/      OPERATING SYSTEM: PC-DOS/MS-DOS
/      SOFTWARE: WinPatIn (Genentech)
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/09/723,873
/      FILING DATE: 28-No. 6677305-2000
/      PRIOR APPLICATION NUMBER: US/09/052,888
/      FILING DATE: 31-Mar-1998
/      ATTORNEY/AGENT INFORMATION:
/      NAME: Hasak, Janet E.
/      REGISTRATION NUMBER: 28,616
/      REFERENCE/DOCKET NUMBER: P1071P1
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: 650/225-1896
/      TELEFAX: 650/952-9881
/      INFORMATION FOR SEQ ID NO: 67:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 18 amino acids
/      TYPE: Amino Acid
/      TOPOLOGY: Linear
/      US-09-723-873-67
/      SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Query Match      41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      7 ECIIGP 12
/      |||
/      4 ECIIGP 9

Db
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RESULT 74
US-09-723-873-69
/ Sequence 69, Application US/09723873
/ Patent No. 6677305
/ GENERAL INFORMATION:
/ APPLICANT: Clark, Ross G1
/      Lowman, Henry B.
/      Robinson, Iain C.A.F.
/      TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
/      NUMBER OF SEQUENCES: 109
/      CORRESPONDENCE ADDRESS:
/      ADDRESSER: Genentech, Inc.
/      STREET: 1 DNA Way
/      CITY: South San Francisco
/      STATE: California
/      COUNTRY: USA
/      ZIP: 94080
/      COMPUTER READABLE FORM:
/      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/      COMPUTER: IBM PC compatible
/      OPERATING SYSTEM: PC-DOS/MS-DOS
/      SOFTWARE: WinPatIn (Genentech)
/      CURRENT APPLICATION DATA:
/      APPLICATION NUMBER: US/09/723,873
/      FILING DATE: 28-No. 6677305-2000
/      PRIOR APPLICATION NUMBER: US/09/052,888
/      FILING DATE: 31-Mar-1998
/      ATTORNEY/AGENT INFORMATION:
/      NAME: Hasak, Janet E.
/      REGISTRATION NUMBER: 28,616
/      REFERENCE/DOCKET NUMBER: P1071P1
/      TELECOMMUNICATION INFORMATION:
/      TELEPHONE: 650/225-1896
/      TELEFAX: 650/952-9881
/      INFORMATION FOR SEQ ID NO: 69:
/      SEQUENCE CHARACTERISTICS:
/      LENGTH: 18 amino acids
/      TYPE: Amino Acid
/      TOPOLOGY: Linear
/      US-09-723-873-69
/      SEQUENCE DESCRIPTION: SEQ ID NO: 69:

Query Match      41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy      7 ECIIGP 12
/      |||
/      4 ECIIGP 9

Db

RESULT 75
US-09-724-114-67
/ Sequence 67, Application US/09724114
/ Patent No. 6680298
/ GENERAL INFORMATION:
/ APPLICANT: Clark, Ross G1
/      Lowman, Henry B.
/      Robinson, Iain C.A.F.
/      TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
/      NUMBER OF SEQUENCES: 109
/      CORRESPONDENCE ADDRESS:
/      ADDRESSER: Genentech, Inc.
/      STREET: 1 DNA Way
/      CITY: South San Francisco
/      STATE: California
/      COUNTRY: USA
/      ZIP: 94080
/      COMPUTER READABLE FORM:
/      MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
/      COMPUTER: IBM PC compatible
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,114
FILING DATE: 28-No. 6680298-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
US-09-724-114-67
SEQUENCE DESCRIPTION: SEQ ID NO: 67:

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
Db 4 ECVWGP 9

RESULT 76
US-09-724-114-69
Sequence 69, Application US/09724114
Patent No. 6680298
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,114
FILING DATE: 28-No. 6680298-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid

TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-724-114-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
Db 4 ECIIGP 9

RESULT 77
US-09-723-913-67
Sequence 67, Application US/09723913
Patent No. 6683053
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,913
FILING DATE: 28-No. 6683053-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-723-913-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
Db 4 ECVWGP 9

RESULT 78
US-09-723-913-69
Sequence 69, Application US/09723913
Patent No. 6683053
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.

Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,913
FILING DATE: 28-No. 6683053-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-723-913-69
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECIIGP 12
DB 4 ECIIGP 9
RESULT 79
US-09-723-912-67
Sequence 67, Application US/09723912
Patent No. 6689751
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,912
FILING DATE: 28-No. 6689751-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,888
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-723-912-67
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 ECIIGP 12
DB 4 ECIIGP 9
RESULT 80
US-09-723-912-69
Sequence 69, Application US/09723912
Patent No. 6689751
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/723,912
FILING DATE: 28-No. 6689751-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-723-912-69
Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12
|||
Db 4 ECIIGP 9

RESULT 81

US-09-724-095-67
Sequence 67, Application US/09724095
Patent No. 6693078

GENERAL INFORMATION:

APPLICANT: Clark, Ross G1

Lowman, Henry B.

Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules

NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,095

FILING DATE: 28-Mar-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,888

FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:

NAME: Haseak, Janet B.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 67:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-724-095-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12
|||
Db 4 ECIIGP 9

RESULT 82

US-09-724-095-69

Sequence 69, Application US/09724095

Patent No. 6693078

GENERAL INFORMATION:

APPLICANT: Clark, Ross G1

Lowman, Henry B.

Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules

NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,095

FILING DATE: 28-Mar-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052,888

FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:

NAME: Haseak, Janet B.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896

TELEFAX: 650/952-9881

INFORMATION FOR SEQ ID NO: 69:

SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids

TYPE: Amino Acid

TOPOLOGY: Linear

SEQUENCE DESCRIPTION: SEQ ID NO: 69:

US-09-724-095-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 ECIIGP 12
|||
Db 4 ECIIGP 9

RESULT 83

US-09-724-157-67

Sequence 67, Application US/09724157

Patent No. 6693079

GENERAL INFORMATION:

APPLICANT: Clark, Ross G1

Lowman, Henry B.

Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules

NUMBER OF SEQUENCES: 109

CORRESPONDENCE ADDRESS:

ADDRESSEE: Genentech, Inc.

STREET: 1 DNA Way

CITY: South San Francisco

STATE: California

COUNTRY: USA

ZIP: 94080

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/724,157

FILING DATE: 28-Mar-1998

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/052888

FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:

NAME: Haseak, Janet B.

REGISTRATION NUMBER: 28,616

REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-724-157-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
||: ||
DB 4 ECIWGP 9

RESULT 84
US-09-724-157-69
Sequence 69, Application US/09724157
Patent No. 6693079
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpactin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,157
FILING DATE: 28-Mar-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-724-157-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
||: ||
DB 4 ECIWGP 9

RESULT 85

US-09-724-062-67
Sequence 67, Application US/09724062
Patent No. 6713451
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpactin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,062
FILING DATE: 28-Mar-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998

ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-724-062-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
||: ||
DB 4 ECIWGP 9

RESULT 86
US-09-724-062-69
Sequence 69, Application US/09724062
Patent No. 6713451
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,062
FILING DATE: 28-No. 6719451-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-724-062-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12
DB 4 ECLIGP 9

RESULT 87
US-09-724-065-67
Sequence 67, Application US/09724065
Patent No. 6716586
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,065
FILING DATE: 28-No. 6716586-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:

US-09-724-065-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12
DB 4 ECLIGP 9

RESULT 88
US-09-724-065-69
Sequence 69, Application US/09724065
Patent No. 6716586
GENERAL INFORMATION:
APPLICANT: Clark, Rose G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
ADDRESSER: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatIn (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,065
FILING DATE: 28-No. 6716586-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasek, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/952-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-724-065-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIGP 12
DB 4 ECLIGP 9

RESULT 89
US-10-158-825-88
Sequence 88, Application US/10158825
Patent No. 6900033
GENERAL INFORMATION:
APPLICANT: Tom Parry et al.
TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
FILE REFERENCE: PF555
CURRENT APPLICATION NUMBER: US/10/158,825
CURRENT FILING DATE: 2002-06-03

PRIOR APPLICATION NUMBER: 60/294,976
PRIOR FILING DATE: 2001-06-04
NUMBER OF SEQ ID NOS: 158
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 88
LENGTH: 18
TYPE: PRT
ORGANISM: homo sapiens
US-10-158-825-88

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 71.4%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 6 ECICGP 12
DB 2 ECICWGP 8

RESULT 90
US-09-724-481-67
Sequence 67, Application US/09724481
Patent No. 6949349
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.
TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,481
FILING DATE: 28-Mar-2000
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 67:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 67:
US-09-724-481-67

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECICGP 12
DB 4 ECICWGP 9

RESULT 91

US-09-724-481-69
Sequence 69, Application US/09724481
Patent No. 6949349
GENERAL INFORMATION:
APPLICANT: Clark, Ross G1
Lowman, Henry B.
Robinson, Iain C.A.F.

TITLE OF INVENTION: Insulin-like Growth Factor Agonist Molecules
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Genentech, Inc.
STREET: 1 DNA Way
CITY: South San Francisco
STATE: California
COUNTRY: USA
ZIP: 94080

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Winpatin (Genentech)

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/724,481
FILING DATE: 28-Mar-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/052,888
FILING DATE: 31-Mar-1998
ATTORNEY/AGENT INFORMATION:
NAME: Haasak, Janet E.
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: P1071P1

TELECOMMUNICATION INFORMATION:
TELEPHONE: 650/225-1896
TELEFAX: 650/952-9881
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: Amino Acid
TOPOLOGY: Linear
SEQUENCE DESCRIPTION: SEQ ID NO: 69:
US-09-724-481-69

Query Match 41.8%; Score 28; DB 2; Length 18;
Best Local Similarity 83.3%; Pred. No. 2.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECICGP 12
DB 4 ECICWGP 9

RESULT 92
US-08-474-696A-1
Sequence 1, Application US/08474696A
Patent No. 5843673
GENERAL INFORMATION:
APPLICANT: Sharpe-Timm, Kathy L.
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5843673thwestern Hwy.
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,696A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-474-696A-1

Query Match 41.8%; Score 28; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 7 DAKGSFPC 14

RESULT 93
US-08-474-696A-3
Sequence 3, Application US/08474696A
Patent No. 5843673

GENERAL INFORMATION:
APPLICANT: Sharpe-Tilms, Kathy L.
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kohn & Associates
STREET: 30500 No. 5843673thwestern Hwy.
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,696A
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
TELECOMMUNICATION INFORMATION:
TELEPHONE: (810) 539-5050
TELEFAX: (810) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
FRAGMENT TYPE: N-terminal
US-08-474-696A-3

Query Match 41.8%; Score 28; DB 1; Length 19;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 7 DAKGSFPC 14

RESULT 94
US-09-044-604-3
Sequence 3, Application US/09044604
Patent No. 6531277

GENERAL INFORMATION:
APPLICANT: Tilms, Kathy L.
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 No. 6531277thwestern Hwy. Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,604
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 0994.00084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-044-604-3

Query Match 41.8%; Score 28; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 7 DAKGSFPC 14

RESULT 95
US-08-484-135-51
Sequence 51, Application US/08484135
Patent No. 5767078

GENERAL INFORMATION:
APPLICANT: Johnson, Dana L.
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. Digiglio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York

COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-51

Query Match 41.8%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIIGP 12
|:|:|
DB 3 SMDCRIGP 10

RESULT 96
US-08-484-135-75
Sequence 75, Application US/08484135
Patent No. 5767078
GENERAL INFORMATION:
APPLICANT: Johnson, Dana L
APPLICANT: Zivlin, Robert A
TITLE OF INVENTION: AGONIST PEPTIDE DIMERS
NUMBER OF SEQUENCES: 93
CORRESPONDENCE ADDRESS:
ADDRESSEE: Frank S. Digilio
STREET: 400 Garden City Plaza
CITY: Garden City
STATE: New York
COUNTRY: U.S.A..
ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,135
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: DIGILIO, Frank S
REGISTRATION NUMBER: 31,346
REFERENCE/DOCKET NUMBER: 9594
TELECOMMUNICATION INFORMATION:
TELEPHONE: (516) 742-4343
TELEFAX: (516) 742-4366
INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single

TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-135-75

Query Match 41.8%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIGP 12
|:|:|
DB 3 SMDCRIGP 10

RESULT 97
US-08-484-635-35
Sequence 35, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kashyap, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
APPLICANT: Mulcahy, Linda
TITLE OF INVENTION: Compounds and Peptides That Bind to the
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Stuart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Mackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-484-635-35

Query Match 41.8%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIGP 12
|:|:|
DB 3 SMDCRIGP 10

RESULT 98

US-08-484-635-167
Sequence 167, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaahyaad, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 167:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-484-635-167
Query Match 41.8%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 5 SPECIAGP 12
DB 4 SYSCARGP 11
RESULT 99
US-08-484-635-224
Sequence 224, Application US/08484635
Patent No. 5773569
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaahyaad, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259

CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,635
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/155,940
FILING DATE: 19-NOV-1993
ATTORNEY/AGENT INFORMATION:
NAME: Garrett-Wackowski, Eugenia
REGISTRATION NUMBER: 37,330
REFERENCE/DOCKET NUMBER: 16528A-43-1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 224:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
US-08-484-635-224

Query Match 41.8%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIAGP 12
DB 3 SYSCARGP 10

RESULT 100
US-08-484-631-35
Sequence 35, Application US/08484631
Patent No. 5830851
GENERAL INFORMATION:
APPLICANT: Wrighton, Nicholas C.
APPLICANT: Dower, William J.
APPLICANT: Chang, Ray S.
APPLICANT: Kaahyaad, Arun K.
APPLICANT: Jolliffe, Linda K.
APPLICANT: Johnson, Dana
TITLE OF INVENTION: Compounds and Peptides That Bind to the
TITLE OF INVENTION: Erythropoietin Receptor
NUMBER OF SEQUENCES: 259
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,631

; FILING DATE: 07-JUN-1995
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/155,940
 ; FILING DATE: 19-NOV-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Garrett-Wackowski, Eugenia
 ; REGISTRATION NUMBER: 37,330
 ; REFERENCE/DOCKET NUMBER: 16528A-43-1-2
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 543-9600
 ; TELEFAX: (415) 543-5043
 ; INFORMATION FOR SEQ ID NO: 35:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 20 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS:
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 ; US-08-484-631-35

Query Match 41.8%; Score 28; DB 1; Length 20;
 Best Local Similarity 50.0%; Pred. No. 2.4e+02;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIGP 12
 DB 3 SWDCRIGP 10

Search completed: January 20, 2006, 19:14:14
 Job time : 13.5769 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ; Search time 43.2692 Seconds
(without alignments)
115.878 Million cell updates/sec

Title: US-09-662-293-5
Perfect score: 67
Sequence: 1 DEKNSPEICILGP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	67	100.0	12	4	US-10-218-743-5
2	33	49.3	18	4	US-10-381-112-6
3	32	47.8	13	5	US-10-488-671-20
4	32	47.8	13	5	US-10-488-707-795
5	31	46.3	20	4	US-10-225-567A-1942
6	30	44.8	16	3	US-09-824-637-6
7	30	44.8	18	4	US-10-098-093-41
8	30	44.8	19	4	US-10-378-557-55
9	30	44.8	19	5	US-10-661-156-220
10	29	43.3	10	5	US-10-808-187-1834
11	29	43.3	10	5	US-10-807-807-1834
12	29	43.3	19	5	US-10-792-582-57
13	28	41.8	8	5	US-10-889-934-18
14	28	41.8	8	5	US-10-913-228-18
15	28	41.8	9	4	US-10-448-521-1
16	28	41.8	9	4	US-10-448-521-43
17	28	41.8	12	3	US-09-071-838-219
18	28	41.8	12	4	US-10-213-512-219
19	28	41.8	13	4	US-10-481-180-109
20	28	41.8	14	3	US-09-774-639-272
21	28	41.8	14	3	US-09-969-730-340
22	28	41.8	14	3	US-09-932-613-59
23	28	41.8	14	3	US-09-932-322-59
24	28	41.8	14	4	US-10-621-363-340
25	28	41.8	15	3	US-09-738-363-23
26	28	41.8	15	4	US-10-633-023-23
27	28	41.8	15	4	US-10-481-180-116

28	41.8	15	4	US-10-481-180-117	Sequence 117, App
29	41.8	16	4	US-10-481-180-120	Sequence 120, App
30	41.8	17	4	US-10-481-180-122	Sequence 122, App
31	41.8	18	3	US-09-864-761-43665	Sequence 43665, A
32	41.8	18	3	US-09-858-935B-107	Sequence 107, App
33	41.8	18	3	US-09-858-935B-110	Sequence 110, App
34	41.8	18	4	US-10-158-847-88	Sequence 88, App1
35	41.8	18	4	US-10-158-847-88	Sequence 88, App1
36	41.8	18	4	US-10-271-869-107	Sequence 107, App
37	41.8	18	4	US-10-271-869-110	Sequence 110, App
38	41.8	18	4	US-10-158-825-88	Sequence 88, App1
39	41.8	19	3	US-09-044-604-3	Sequence 3, App1
40	41.8	19	4	US-10-306-903-3	Sequence 3, App1
41	28	20	5	US-10-690-276-662	Sequence 662, App
42	41.0	20	4	US-10-196-394-65	Sequence 65, App1
43	40.3	9	4	US-10-357-175-89	Sequence 89, App1
44	40.3	9	4	US-10-357-175-115	Sequence 115, App
45	40.3	9	4	US-10-455-720-89	Sequence 89, App1
46	40.3	9	4	US-10-455-720-115	Sequence 115, App
47	40.3	9	4	US-10-350-508-55	Sequence 55, App
48	40.3	12	5	US-10-838-289-227	Sequence 227, App
49	40.3	12	5	US-10-607-595-435	Sequence 435, App
50	40.3	13	5	US-10-488-671-21	Sequence 21, App1
51	40.3	20	4	US-10-269-695-147	Sequence 147, App
52	27	20	4	US-10-410-998-147	Sequence 147, App
53	27	20	4	US-10-432-465-65	Sequence 65, App1
54	27	20	4	US-10-433-091-34	Sequence 34, App1
55	26	10	4	US-10-286-457-230	Sequence 230, App
56	38.8	10	4	US-10-352-786-455	Sequence 455, App
57	26	11	4	US-10-352-786-454	Sequence 454, App
58	38.8	11	4	US-10-352-786-541	Sequence 541, App
59	38.8	11	4	US-10-352-786-542	Sequence 542, App
60	26	11	5	US-10-471-346-19	Sequence 19, App1
61	38.8	12	4	US-10-352-786-627	Sequence 627, App
62	26	12	4	US-10-352-786-628	Sequence 628, App
63	26	12	3	US-09-880-713A-30	Sequence 30, App1
64	38.8	13	3	US-09-988-493-302	Sequence 302, App
65	26	13	4	US-10-352-786-717	Sequence 717, App
66	38.8	13	4	US-10-352-786-718	Sequence 718, App
67	26	13	4	US-10-412-964-40	Sequence 40, App1
68	38.8	13	5	US-10-352-786-813	Sequence 813, App
69	26	14	4	US-10-352-786-814	Sequence 814, App
70	26	14	4	US-10-615-659-45	Sequence 45, App1
71	26	14	4	US-10-615-659-45	Sequence 45, App1
72	26	14	4	US-10-473-287-39	Sequence 39, App1
73	26	14	5	US-10-473-287-39	Sequence 39, App1
74	26	15	4	US-10-352-786-914	Sequence 914, App
75	26	15	5	US-10-777-829-29	Sequence 29, App1
76	26	15	3	US-09-969-730-344	Sequence 344, App
77	26	16	3	US-10-114-500-15	Sequence 15, App1
78	38.8	16	4	US-10-352-786-1127	Sequence 1127, App
79	38.8	16	4	US-10-352-786-1128	Sequence 1128, App
80	38.8	16	4	US-10-352-786-121	Sequence 121, App
81	26	16	4	US-10-271-869-121	Sequence 121, App
82	26	16	4	US-10-352-786-1243	Sequence 1243, App
83	26	16	4	US-10-352-786-1244	Sequence 1244, App
84	26	16	4	US-10-754-437-25	Sequence 25, App1
85	26	16	4	US-10-754-437-29	Sequence 29, App1
86	26	16	4	US-10-754-437-31	Sequence 31, App1
87	26	16	4	US-09-864-761-43430	Sequence 43430, A
88	26	16	4	US-10-225-567A-1330	Sequence 1330, App
89	26	16	4	US-10-352-786-1365	Sequence 1365, App
90	26	16	4	US-10-352-786-1366	Sequence 1366, App

ALIGNMENTS

RESULT 1

US-10-218-743-5
; Sequence 5, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-5

Query Match

Best Local Similarity 100.0%; Score 67; DB 4; Length 12;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 DEKNSPECILGP 12
| | | | | | | | | | | | | |

Db 1 DEKNSPECILGP 12

RESULT 2

US-10-381-112-6
; Sequence 6, Application US/10381112
; Publication No. US20040086942A1
; GENERAL INFORMATION:
; APPLICANT: Lowman, Henry B.
; APPLICANT: Nakamura, Gerald R.
; APPLICANT: Reynolds, Mark E.
; APPLICANT: Starovaanik, Melissa A.
; TITLE OF INVENTION: IGR RECEPTOR ANTAGONISTS
; FILE REFERENCE: P1816R1
; CURRENT APPLICATION NUMBER: US/10/381,112
; CURRENT FILING DATE: 2003-10-27
; PRIOR APPLICATION NUMBER: US 60/278,540
; PRIOR FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: US 60/235,353
; PRIOR FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 595

SEQ ID NO 6

LENGTH: 18

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: clone g8b.22 shown in Table 2
US-10-381-112-6

Query Match

Best Local Similarity 49.3%; Score 33; DB 4; Length 18;
Matches 55.6%; Pred. No. 76;

Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 4 NSPFCILGP 12
| | | | | | | | | | | | | |

Db 1 NYEBCWGP 9

RESULT 3

US-10-488-671-20
; Sequence 20, Application US/10488671
; Publication No. US20040254106A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; TITLE OF INVENTION: Modified Factor IX
; FILE REFERENCE: MER-128
; CURRENT APPLICATION NUMBER: US/10/488,671
; CURRENT FILING DATE: 2004-03-04
; PRIOR APPLICATION NUMBER: PCT/EP02/09717
; PRIOR FILING DATE: 2002-08-30
; PRIOR APPLICATION NUMBER: EP 01121154.7
; PRIOR FILING DATE: 2001-09-04
; NUMBER OF SEQ ID NOS: 126
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-488-671-20

Query Match

Best Local Similarity 47.8%; Score 32; DB 5; Length 13;
Matches 62.5%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 8
| | | | | | | | | | | | | |

Db 1 DDINSYEC 8

RESULT 4

US-10-948-707-795
; Sequence 795, Application US/10948707
; Publication No. US20050187147A1
; GENERAL INFORMATION:
; APPLICANT: Ballatore, Carlo
; APPLICANT: Castellino, Angelo
; APPLICANT: Deshmala, Joel
; APPLICANT: Guo, Zijian
; APPLICANT: Li, Qing
; APPLICANT: Newman, Michael James
; APPLICANT: Sun, Chengzao
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
; FILE REFERENCE: 17967-003001
; CURRENT APPLICATION NUMBER: US/10/948,707
; CURRENT FILING DATE: 2004-09-22
; PRIOR APPLICATION NUMBER: 60/505,325
; PRIOR FILING DATE: 2003-09-22
; PRIOR APPLICATION NUMBER: 60/568,340
; PRIOR FILING DATE: 2004-05-04
; PRIOR APPLICATION NUMBER: 60/581,835
; PRIOR FILING DATE: 2004-06-22
; NUMBER OF SEQ ID NOS: 1422
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 795
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-948-707-795

Query Match

Best Local Similarity 47.8%; Score 32; DB 5; Length 13;
Matches 62.5%; Pred. No. 82;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
|:|:|:
Db 4 DDINSYEC 11

RESULT 5
US-10-225-567A-1942
; Sequence 1942, Application US/10225567A
; Publication No. US2003011798A1
; GENERAL INFORMATION:
; APPLICANT: Lifespan Biosciences
; APPLICANT: Brown, Joseph P.
; APPLICANT: Burner, Glenn C.
; APPLICANT: Roush, Christine L.
; TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTORS
; FILE REFERENCE: 1520-4-4
; CURRENT APPLICATION NUMBER: US/10/225,567A
; CURRENT FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 60/257,144
; PRIOR FILING DATE: 2000-12-19
; NUMBER OF SEQ ID NOS: 2292
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1942
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-225-567A-1942

Query Match 46.3%; Score 31; DB 4; Length 20;
Best Local Similarity 62.5%; Pred. No. 2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
|:|:|:
Db 13 DEKNTKC 20

RESULT 6
US-09-824-637-6
; Sequence 6, Application US/09824637
; Patent No. US2002004226A1
; GENERAL INFORMATION:
; APPLICANT: RUBINSTEIN, Menachem
; APPLICANT: NOVICK, Daniela
; APPLICANT: TAL, Nathan
; APPLICANT: Fleischer, Dina
; TITLE OF INVENTION: SOLUBLE LDL RECEPTOR, ITS PRODUCTION AND USE
; FILE REFERENCE: RUBINSTEIN-5D
; CURRENT APPLICATION NUMBER: US/09/824,637
; CURRENT FILING DATE: 2001-04-04
; PRIOR APPLICATION NUMBER: US 08/485,128
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: US 08/092,817
; PRIOR FILING DATE: 1993-07-19
; PRIOR APPLICATION NUMBER: IL 100696
; PRIOR FILING DATE: 1992-01-19
; PRIOR APPLICATION NUMBER: IL 102915
; PRIOR FILING DATE: 1992-08-23
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 16
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-824-637-6

Query Match 44.8%; Score 30; DB 3; Length 16;
Best Local Similarity 57.1%; Pred. No. 2.4e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
QY 2 EKNSPEC 8
|:|:|:

Db 4 ERNEFOC 10

RESULT 7
US-10-098-093-41
; Sequence 41, Application US/10098093
; Publication No. US20030092631A1
; GENERAL INFORMATION:
; APPLICANT: Deshayes, Kurt D.
; APPLICANT: Lowman, Henry B.
; APPLICANT: Schaffer, Michelle L.
; APPLICANT: Sidhu, Sachdev S.
; TITLE OF INVENTION: IGF ANTAGONIST PEPTIDES
; FILE REFERENCE: P1863R1
; CURRENT APPLICATION NUMBER: US/10/098,093
; CURRENT FILING DATE: 2002-03-13
; PRIOR APPLICATION NUMBER: US 60/275,904
; PRIOR FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 122
; SEQ ID NO 41
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-098-093-41

Query Match 44.8%; Score 30; DB 4; Length 18;
Best Local Similarity 33.3%; Pred. No. 2.7e+02;
Matches 3; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECILGP 12
::|:|:
Db 1 DAMDCVGP 9

RESULT 8
US-10-378-557-55
; Sequence 55, Application US/10378557
; Publication No. US20030186223A1
; GENERAL INFORMATION:
; APPLICANT: Ladner, Robert C.
; TITLE OF INVENTION: MODULAR RECOMBINANTIAL DISPLAY
; FILE REFERENCE: 3421.1013-001
; CURRENT APPLICATION NUMBER: US/10/378,557
; CURRENT FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: 60/361,121
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 65
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 55
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Selected library sequence
US-10-378-557-55

Query Match 44.8%; Score 30; DB 4; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8
|:|:|:
Db 12 NSPEC 16

RESULT 9
US-10-661-156-220
; Sequence 220, Application US/10661156
; Publication No. US20050100963A1
; GENERAL INFORMATION:

```
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussac, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibyllle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
/ TITLE OF INVENTION: Their use in Diagnosis and Therapy
/ FILE REFERENCE: D0617.70012US00
/ CURRENT APPLICATION NUMBER: US/10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 617
/ SOFTWARE: PaetSeq for Windows Version 4.0
/ SEQ ID NO 220
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-661-156-220
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Query Match          44.8%; Score 30; DB 5; Length 19;
Best Local Similarity 100.0%; Pred. No. 2.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Qy      4 NSPEC 8
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Db      12 NSPEC 16
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RESULT 10
/ Sequence 1834, Application US/10808187
/ Publication No. US2005009009A1
/ GENERAL INFORMATION:
/ APPLICANT: PEIRIS, JOSEPH S. M.
/ APPLICANT: YUEN, KWOK YUNG
/ APPLICANT: POON, LIT MAN
/ APPLICANT: GUAN, YI
/ APPLICANT: CHAN, KWOK HUNG
/ APPLICANT: NICHOLLS, JOHN
/ TITLE OF INVENTION: A DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS CAUSING SEVERE ACUTE
/ TITLE OF INVENTION: RESPIRATORY SYNDROME (SARS)
/ FILE REFERENCE: V9661.0078
/ CURRENT APPLICATION NUMBER: US/10/808,187
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,031
/ PRIOR FILING DATE: 2003-03-24
/ PRIOR APPLICATION NUMBER: 60/457,730
/ PRIOR FILING DATE: 2003-03-26
/ PRIOR APPLICATION NUMBER: 60/459,931
/ PRIOR FILING DATE: 2003-04-02
```

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/ PRIOR APPLICATION NUMBER: 60/460,357
/ PRIOR FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: 60/461,265
/ PRIOR FILING DATE: 2003-04-08
/ PRIOR APPLICATION NUMBER: 60/462,805
/ PRIOR FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: 60/468,139
/ PRIOR FILING DATE: 2003-05-05
/ PRIOR APPLICATION NUMBER: 60/464,886
/ PRIOR FILING DATE: 2003-04-23
/ PRIOR APPLICATION NUMBER: 60/471,200
/ PRIOR FILING DATE: 2003-05-16
/ NUMBER OF SEQ ID NOS: 2476
/ SOFTWARE: PatentIn ver. 3.2
/ SEQ ID NO 1834
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Human severe acute respiratory system virus
US-10-808-187-1834
```

```
Query Match          43.3%; Score 29; DB 5; Length 10;
Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECIL 10
        :|||:|:|
Db      2 KNSDHCVL 10
```

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RESULT 11
/ Sequence 1834, Application US/10807807
/ Publication No. US20050181357A1
/ GENERAL INFORMATION:
/ APPLICANT: LEUNG, FREDERICK C.
/ APPLICANT: PEIRIS, JOSEPH S. M.
/ APPLICANT: YUEN, KWOK YUNG
/ APPLICANT: POON, LIT MAN
/ APPLICANT: GUAN, YI
/ APPLICANT: CHAN, KWOK HUNG
/ APPLICANT: NICHOLLS, JOHN M.
/ TITLE OF INVENTION: A HIGH-THROUGHPUT DIAGNOSTIC ASSAY FOR THE HUMAN VIRUS
/ TITLE OF INVENTION: CAUSING SEVERE ACUTE RESPIRATORY SYNDROME (SARS)
/ FILE REFERENCE: V9661.0077
/ CURRENT APPLICATION NUMBER: US/10/807,807
/ PRIOR FILING DATE: 2004-03-24
/ PRIOR APPLICATION NUMBER: 60/457,031
/ PRIOR FILING DATE: 2003-03-24
/ PRIOR APPLICATION NUMBER: 60/457,730
/ PRIOR FILING DATE: 2003-03-26
/ PRIOR APPLICATION NUMBER: 60/459,931
/ PRIOR FILING DATE: 2003-04-02
/ PRIOR APPLICATION NUMBER: 60/460,357
/ PRIOR FILING DATE: 2003-04-03
/ PRIOR APPLICATION NUMBER: 60/461,265
/ PRIOR FILING DATE: 2003-04-08
/ PRIOR APPLICATION NUMBER: 60/462,805
/ PRIOR FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: 60/464,886
/ PRIOR FILING DATE: 2003-04-23
/ PRIOR APPLICATION NUMBER: 60/465,738
/ PRIOR FILING DATE: 2003-04-25
/ PRIOR APPLICATION NUMBER: 60/470,935
/ PRIOR FILING DATE: 2003-05-14
/ NUMBER OF SEQ ID NOS: 2487
/ SOFTWARE: PatentIn ver. 3.2
/ SEQ ID NO 1834
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Human severe acute respiratory system virus
US-10-807-807-1834
```

```
Query Match          43.3%; Score 29; DB 5; Length 10;
```

Best Local Similarity 55.6%; Pred. No. 2.2e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10
DB 2 KNSDHCVL 10

RESULT 12

US-10-792-582-57
Sequence 57, Application US/10792582
Publication No. US20050214859A1
GENERAL INFORMATION:
APPLICANT: Dransfield, Daniel T.
APPLICANT: Sato, Aaron K.
APPLICANT: Ladner, Robert C.
APPLICANT: Smitasava, Ajay
APPLICANT: Thomas, Regl
TITLE OF INVENTION: PEPTIDES THAT SPECIFICALLY BIND HGF
TITLE OF INVENTION: RECEPTOR (CMET) AND USES THEREOF
FILE REFERENCE: D0617,70013US01
CURRENT APPLICATION NUMBER: US/10/792,582
CURRENT FILING DATE: 2004-03-03
PRIOR APPLICATION NUMBER: US 60/451,588
PRIOR FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 619
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetically generated cMet-binding peptide
US-10-792-582-57

Query Match 43.3%; Score 29; DB 5; Length 19;
Best Local Similarity 83.3%; Pred. No. 4.3e+02;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPECIL 10
DB 11 TPECIL 16

RESULT 13

US-10-889-934-18
Sequence 18, Application US/10889934
Publication No. US20040265316A1
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
METHODS BASED THEREON
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/889,934
FILING DATE: 13-Jul-2004
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605,430

FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Friedel, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE

INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-889-934-18

Query Match 41.8%; Score 28; DB 5; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 1 DEBTAFSC 8

RESULT 14

US-10-913-228-18
Sequence 18, Application US/10913228
Publication No. US20050074797A1
GENERAL INFORMATION:
APPLICANT: Croce, Carlo M.
TITLE OF INVENTION: PHIT PROTEINS AND NUCLEIC ACIDS AND
METHODS BASED THEREON

NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSER: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/913,228
FILING DATE: 06-Aug-2004
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/605,430
FILING DATE: 22-FEB-1996
ATTORNEY/AGENT INFORMATION:
NAME: Friedel, Thomas E.
REGISTRATION NUMBER: 29,258
REFERENCE/DOCKET NUMBER: 8666-005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 8 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-10-913-228-18

Query Match 41.8%; Score 28; DB 5; Length 8;
Best Local Similarity 50.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 8
| : | : |
Db 1 DEKNSPEC 8

RESULT 15
US-10-448-521-1
; Sequence 1, Application US/10448521
; Publication No. US20040018205A1
; GENERAL INFORMATION:
; APPLICANT: FIRAT, HUSEYIN
; APPLICANT: LANGLADE-DEMOYAN, PIERRE
; APPLICANT: VILMER, ETIENNE
; APPLICANT: LEMONNIER, FRANCOIS
; APPLICANT: ROHRLICH, PIERRE
; APPLICANT: YOTUNDA, PATRICIA
; TITLE OF INVENTION: MUTATED IMMUNOGENIC PEPTIDES DERIVED FROM R9M,
; TITLE OF INVENTION: POLYNUCLEOTIDES CODING FOR SAME AND THERAPEUTIC USES
; FILE REFERENCE: 02356.0082
; CURRENT APPLICATION NUMBER: US/10/448,521
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: PCT/FR01/03779
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: CA 2,325,666
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-448-521-1

Query Match 41.8%; Score 28; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIIG 11
| : | : | : |
Db 4 ECIIG 8

RESULT 16
US-10-448-521-43
; Sequence 43, Application US/10448521
; Publication No. US20040018205A1
; GENERAL INFORMATION:
; APPLICANT: FIRAT, HUSEYIN
; APPLICANT: LANGLADE-DEMOYAN, PIERRE
; APPLICANT: VILMER, ETIENNE
; APPLICANT: LEMONNIER, FRANCOIS
; APPLICANT: ROHRLICH, PIERRE
; APPLICANT: YOTUNDA, PATRICIA
; TITLE OF INVENTION: MUTATED IMMUNOGENIC PEPTIDES DERIVED FROM R9M,
; TITLE OF INVENTION: POLYNUCLEOTIDES CODING FOR SAME AND THERAPEUTIC USES
; FILE REFERENCE: 02356.0082
; CURRENT APPLICATION NUMBER: US/10/448,521
; CURRENT FILING DATE: 2003-05-30
; PRIOR APPLICATION NUMBER: PCT/FR01/03779
; PRIOR FILING DATE: 2001-11-29
; PRIOR APPLICATION NUMBER: CA 2,325,666
; PRIOR FILING DATE: 2000-12-01
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 43
; LENGTH: 9
; TYPE: PRT

; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: peptide
US-10-448-521-43

Query Match 41.8%; Score 28; DB 4; Length 9;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIIG 11
| : | : | : |
Db 4 ECIIG 8

RESULT 17
US-09-071-838-219
; Sequence 219, Application US/09071838
; Patent No. US20020152501A1
; GENERAL INFORMATION:
; APPLICANT: Fischer, Robert L.
; APPLICANT: Chad, Nit
; APPLICANT: Kiyosue, Tomohiro
; APPLICANT: Yadegari, Ramin
; APPLICANT: Margosian, Linda
; APPLICANT: Harada, John
; TITLE OF INVENTION: Nucleic Acids That Control Seed and
; TITLE OF INVENTION: Fruit Development in Plants
; NUMBER OF SEQUENCES: 324
; CORRESPONDENCE ADDRESS:
; ADDRESS: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/071,838
; FILING DATE: 01-MAY-1998
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Bastian, Kevin L.
; REGISTRATION NUMBER: 34,774
; REFERENCE/DOCKET NUMBER: 023070-086100US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 219:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-071-838-219

Query Match 41.8%; Score 28; DB 3; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 9
| : | : | : |
Db 4 DRRSFKCV 12

RESULT 18
US-10-213-512-219
; Sequence 219, Application US/10213512

Publication No. US20030110536A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramlin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Combinations of Nucleic Acids That Control Seed and
FILE REFERENCE: 023070-086110US
CURRENT APPLICATION NUMBER: US/10/213,512
CURRENT FILING DATE: 2002-08-06
PRIOR APPLICATION NUMBER: US/09/177,206
PRIOR FILING DATE: 1998-10-22
PRIOR APPLICATION NUMBER: US 09/071,838
PRIOR FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 219
LENGTH: 12
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-10-213-512-219

Query Match 41.8%; Score 28; DB 4; Length 12;
Best Local Similarity 44.4%; Pred. No. 4.1e+02;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
| : ||| :
DB 4 DLRRSFKCV 12

RESULT 19
US-10-481-180-109
Sequence 109, Application US/10481180
Publication No. US2004017182A1
GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
APPLICANT: HUMAN SERVICES
APPLICANT: Valenzuela, Jesus G.
APPLICANT: Belkaid, Yasmine
APPLICANT: Kamhawi, Shaden
APPLICANT: Sacks, David
APPLICANT: Ribeiro, Jose M. C.
TITLE OF INVENTION: ANTI-ARTHRITIS VECTOR VACCINES, METHODS
TITLE OF INVENTION: OF SELECTING AND USES THEREOF
FILE REFERENCE: 4239-67347
CURRENT APPLICATION NUMBER: US/10/481,180
CURRENT FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: PCT/US02/19663
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,391
PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 884
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 109
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-109

Query Match 41.8%; Score 28; DB 4; Length 13;
Best Local Similarity 100.0%; Pred. No. 4.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECL 10
|||||
DB 5 FECL 9

RESULT 20
US-09-774-639-272
Sequence 272, Application US/09774639
Publication No. US2003003555A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P1
CURRENT APPLICATION NUMBER: US/09/774,639
CURRENT FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
NUMBER OF SEQ ID NOS: 371
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 272
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-774-639-272

Query Match 41.8%; Score 28; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFECIG 11
|||||
DB 3 KSDHCLIG 11

RESULT 21
US-09-969-730-340
Sequence 340, Application US/09969730
Publication No. US2003005443A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: P2013P2
CURRENT APPLICATION NUMBER: US/09/969,730
CURRENT FILING DATE: 2001-10-04
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,367
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,365
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,731
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,557
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,563
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/055,970

PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,986
PRIOR FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: 60/055,311
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,808
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,803
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,804
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,809
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,806
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,310
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,798
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,309
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,312
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/054,807
PRIOR FILING DATE: 1997-08-05
PRIOR APPLICATION NUMBER: 60/055,386
PRIOR FILING DATE: 1997-08-05
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 340
LENGTH: 14
TYPE: PRT
ORGANISM: Homo sapiens
US-09-969-730-340

Query Match 41.8%; Score 28; DB 3; Length 14;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFCTIG 11
| | | | |
Db 3 KGDLCITG 11

RESULT 22
US-09-932-613-59
Sequence 59, Application US/09932613
Publication No. US20030091565A1
GENERAL INFORMATION:
APPLICANT: Human Genome Sciences, Inc.
APPLICANT: Belzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Rosen, Craig A.
TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON
FILE REFERENCE: DYX-025.1 PCT; DYX-025.1 US
CURRENT APPLICATION NUMBER: US/09/932,613
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-613-59

Query Match 41.8%; Score 28; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12

Db 2 FDCILKP 8
| : | : |
| : | : |

RESULT 23
US-09-932-322-59
Sequence 59, Application US/09932322
Publication No. US20030194743A1
GENERAL INFORMATION:
APPLICANT: Dyax Corp.
APPLICANT: Belzer, James P.
APPLICANT: Potter, M. Daniel
APPLICANT: Fleming, Tony J.
APPLICANT: Ladner, Robert Charles
TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYS)
FILE REFERENCE: DYX-018.1 PCT; DYX-018.1 US
CURRENT APPLICATION NUMBER: US/09/932,322
CURRENT FILING DATE: 2001-08-17
NUMBER OF SEQ ID NOS: 458
SOFTWARE: PatentIn version 3.1
SEQ ID NO 59
LENGTH: 14
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Blys binding polypeptide
US-09-932-322-59

Query Match 41.8%; Score 28; DB 3; Length 14;
Best Local Similarity 57.1%; Pred. No. 4.8e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECTIGP 12
| : | : |
Db 2 FDCILKP 8

RESULT 24
US-10-621-363-340
Sequence 340, Application US/10621363
Publication No. US20040023283A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: 90 Human Secreted Proteins
FILE REFERENCE: PZ013P2C1
CURRENT APPLICATION NUMBER: US/10/621,363
CURRENT FILING DATE: 2003-07-18
PRIOR APPLICATION NUMBER: 09/969,730
PRIOR FILING DATE: 2001-10-06
PRIOR APPLICATION NUMBER: 09/774,639
PRIOR FILING DATE: 2001-02-01
PRIOR APPLICATION NUMBER: 60/238,291
PRIOR FILING DATE: 2000-10-06
PRIOR APPLICATION NUMBER: 09/244,112
PRIOR FILING DATE: 1999-02-04
PRIOR APPLICATION NUMBER: PCT/US98/16235
PRIOR FILING DATE: 1998-08-04
PRIOR APPLICATION NUMBER: 60/056,371
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,732
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,366
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,364
PRIOR FILING DATE: 1997-08-19
PRIOR APPLICATION NUMBER: 60/056,370
PRIOR FILING DATE: 1997-08-19
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 373
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 340
LENGTH: 14
TYPE: PRT

ORGANISM: Homo sapiens
US-10-621-363-340

Query Match 41.8%; Score 28; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 4.8e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSFECTIG 11
| | | | |
DB 3 KQDLHCILG 11

RESULT 25
US-09-738-363-23
Sequence 23, Application US/09738363
Patent No. US20010010932A1

GENERAL INFORMATION:
APPLICANT: Schepf, Harry E.
Schwab, George E.
Payne, Jewel M.
Narva, Kenneth E.
Poncetrada, Luis
TITLE OF INVENTION: Nematocidal Proteins
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Jay M. Sanders
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
STATE: FL
COUNTRY: USA
ZIP: 32606

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/738,363
FILING DATE: 15-Dec-2000
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/076,137
FILING DATE: 12-MAY-1998
ATTORNEY/AGENT INFORMATION:
NAME: Sanders, Jay
REGISTRATION NUMBER: 39,355
REFERENCE/DOCKET NUMBER: MA-20CCCD3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 352-375-8100
TELEFAX: 352-372-5800

INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 23:
US-09-738-363-23

Query Match 41.8%; Score 28; DB 3; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSFECTI 9
| | | | |
DB 6 DEKLSFQLI 14

RESULT 26
US-10-633-023-23
Sequence 23, Application US/10633023
Publication No. US20040018982A1

GENERAL INFORMATION:
APPLICANT: Schepf, H. Ernest
APPLICANT: Schwab, George
APPLICANT: Payne, Jewel
APPLICANT: Narva, Kenneth
APPLICANT: Poncetrada, Luis
TITLE OF INVENTION: Nematocidal Proteins
FILE REFERENCE: MA-20CCCD4
CURRENT APPLICATION NUMBER: US/10/633,023
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: US 09/738,363
PRIOR FILING DATE: 2000-12-15
PRIOR APPLICATION NUMBER: US 09/076,137
PRIOR FILING DATE: 1998-05-12
PRIOR APPLICATION NUMBER: US 08/316,301
PRIOR FILING DATE: 1994-09-30
PRIOR APPLICATION NUMBER: US 07/871,510
PRIOR FILING DATE: 1992-04-23
PRIOR APPLICATION NUMBER: US 07/830,050
PRIOR FILING DATE: 1992-01-31
PRIOR APPLICATION NUMBER: US 07/693,018
PRIOR FILING DATE: 1991-05-03
PRIOR APPLICATION NUMBER: US 07/675,772
PRIOR FILING DATE: 1991-03-27
PRIOR APPLICATION NUMBER: US 07/565,544
PRIOR FILING DATE: 1990-08-10
PRIOR APPLICATION NUMBER: US 07/557,246
PRIOR FILING DATE: 1990-07-24
PRIOR APPLICATION NUMBER: US 07/535,810
PRIOR FILING DATE: 1990-06-11
Remaining Prior Application data removed - See file wrapper or PALM.
NUMBER OF SEQ ID NOS: 40
SOFTWARE: Patentin version 3.2
SEQ ID NO 23
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: Internal amino acid sequence for 63B.
US-10-633-023-23

Query Match 41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 5.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSFECTI 9
| | | | |
DB 6 DEKLSFQLI 14

RESULT 27
US-10-481-180-116
Sequence 116, Application US/10481180
Publication No. US20040171821A1

GENERAL INFORMATION:
APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
HUMAN SERVICES
APPLICANT: Valenzuela, Jesus G.
APPLICANT: Belkaid, Yasmine
APPLICANT: Kanhaw, Shaden
APPLICANT: Sacks, David
TITLE OF INVENTION: ANTI-ARTHOPOD VECTOR VACCINES, METHODS
OF SELECTING AND USING THEREOF
FILE REFERENCE: 4239-67347
CURRENT APPLICATION NUMBER: US/10/481,180
CURRENT FILING DATE: 2003-12-17
PRIOR APPLICATION NUMBER: PCT/US02/19663
PRIOR FILING DATE: 2002-06-18
PRIOR APPLICATION NUMBER: US 60/299,391
PRIOR FILING DATE: 2001-06-19
NUMBER OF SEQ ID NOS: 884

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 116
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-116
```

```
Query Match      41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6  FECTIL 10
        |||||
Db      7  FECTIL 11
```

```
RESULT 28
US-10-481-180-117
/ Sequence 117, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamnawi, Shaden
/ APPLICANT: Sacks, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 117
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-117
```

```
Query Match      41.8%; Score 28; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 5.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6  FECTIL 10
        |||||
Db      5  FECTIL 9
```

```
RESULT 29
US-10-481-180-120
/ Sequence 120, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamnawi, Shaden
/ APPLICANT: Sacks, David
```

```
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 120
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-120
```

```
Query Match      41.8%; Score 28; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6  FECTIL 10
        |||||
Db      8  FECTIL 12
```

```
RESULT 30
US-10-481-180-122
/ Sequence 122, Application US/10481180
/ Publication No. US20040171821A1
/ GENERAL INFORMATION:
/ APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS
/ APPLICANT: REPRESENTED BY THE SECRETARY OF THE DEPARTMENT OF HEALTH AND
/ APPLICANT: HUMAN SERVICES
/ APPLICANT: Valenzuela, Jesus G.
/ APPLICANT: Belkaid, Yasmine
/ APPLICANT: Kamnawi, Shaden
/ APPLICANT: Sacks, David
/ APPLICANT: Ribeiro, Jose M. C.
/ TITLE OF INVENTION: ANTI-ARTHROPOD VECTOR VACCINES, METHODS
/ TITLE OF INVENTION: OF SELECTING AND USES THEREOF
/ FILE REFERENCE: 4239-67347
/ CURRENT APPLICATION NUMBER: US/10/481,180
/ PRIOR FILING DATE: 2003-12-17
/ PRIOR APPLICATION NUMBER: PCT/US02/19663
/ PRIOR FILING DATE: 2002-06-18
/ PRIOR APPLICATION NUMBER: US 60/299,391
/ NUMBER OF SEQ ID NOS: 884
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 122
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence; NOTE =
US-10-481-180-122
```

```
Query Match      41.8%; Score 28; DB 4; Length 17;
Best Local Similarity 100.0%; Pred. No. 5.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6  FECTIL 10
        |||||
Db      7  FECTIL 11
```

RESULT 31

```

US-09-864-761-43665
; Sequence 43665, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 43665
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC005104.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.88
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EST_HUMAN HIT: BR901608.1, EVALUATE 1.00e-03
US-09-864-761-43665

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 62.5%; Pred. No. 6.2e+02;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 32
US-09-858-935B-107
; Sequence 107, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubnagie, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 107
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-107

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 33
US-09-858-935B-110
; Sequence 110, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubnagie, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCE: P1794R1
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 110
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-110

Query Match      41.8%; Score 28; DB 3; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

```

```

RESULT 34
US-10-158-847-88
; Sequence 88, Application US/10158847

```

```
/ Publication No. US20030091557A1
/ GENERAL INFORMATION:
/ APPLICANT: Tom Parry et al.
/ TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
/ FILE REFERENCE: PF557
/ CURRENT APPLICATION NUMBER: US/10/158,847
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/295,004
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 158
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 88
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-158-847-88

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 ECICGP 12
      ||| |||
Db      2 ECICWGP 8

RESULT 35
US-10-158-825-88
/ Sequence 88, Application US/10158825
/ Publication No. US20030138894A1
/ GENERAL INFORMATION:
/ APPLICANT: Tom Parry et al.
/ TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
/ FILE REFERENCE: PF555
/ CURRENT APPLICATION NUMBER: US/10/158,825
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/294,976
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 158
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 88
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-158-825-88

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY      6 ECICGP 12
      ||| |||
Db      2 ECICWGP 8

RESULT 36
US-10-271-869-107
/ Sequence 107, Application US/10271869
/ Publication No. US20030211992A1
/ GENERAL INFORMATION:
/ APPLICANT: Dubaquié, Yves
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Lowman, Henry B.
/ TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
/ FILE REFERENCE: P1794R1
/ CURRENT APPLICATION NUMBER: US/10/271,869
/ PRIOR FILING DATE: 2002-10-16
/ PRIOR APPLICATION NUMBER: US/09/858,935
/ PRIOR FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/248,985
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/204,490
/ PRIOR FILING DATE: 2000-05-16
```

```
/ NUMBER OF SEQ ID NOS: 153
/ SEQ ID NO: 107
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-10-271-869-107

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 6.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      7 ECICGP 12
      ||| |||
Db      4 ECICWGP 9

RESULT 37
US-10-271-869-110
/ Sequence 110, Application US/10271869
/ Publication No. US20030211992A1
/ GENERAL INFORMATION:
/ APPLICANT: Dubaquié, Yves
/ APPLICANT: Filvaroff, Ellen
/ APPLICANT: Lowman, Henry B.
/ TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
/ FILE REFERENCE: P1794R1
/ CURRENT APPLICATION NUMBER: US/10/271,869
/ PRIOR FILING DATE: 2002-10-16
/ PRIOR APPLICATION NUMBER: US/09/858,935
/ PRIOR FILING DATE: 2002-07-02
/ PRIOR APPLICATION NUMBER: US 60/248,985
/ PRIOR FILING DATE: 2000-11-15
/ PRIOR APPLICATION NUMBER: US 60/204,490
/ PRIOR FILING DATE: 2000-05-16
/ NUMBER OF SEQ ID NOS: 153
/ SEQ ID NO: 110
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial sequence
/ FEATURE:
/ OTHER INFORMATION: Sequence is synthesized
US-10-271-869-110

Query Match          41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 83.3%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      7 ECICGP 12
      ||| |||
Db      4 ECICWGP 9

RESULT 38
US-10-158-825-88
/ Sequence 88, Application US/10158825
/ Publication No. US20040121429A9
/ GENERAL INFORMATION:
/ APPLICANT: Tom Parry et al.
/ TITLE OF INVENTION: Method and Compositions for Modulating ACE-2 Activity
/ FILE REFERENCE: PF555
/ CURRENT APPLICATION NUMBER: US/10/158,825
/ PRIOR FILING DATE: 2002-06-03
/ PRIOR APPLICATION NUMBER: 60/294,976
/ PRIOR FILING DATE: 2001-06-04
/ NUMBER OF SEQ ID NOS: 158
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO: 88
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-158-825-88
```

Query Match 41.8%; Score 28; DB 4; Length 18;
Best Local Similarity 71.4%; Pred. No. 6.2e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 6 FECTLGP 12
Db 2 FECTWGP 8

RESULT 39
US-09-044-604-3
Sequence 3, Application US/09044604
Patent No. US20020009718A1
GENERAL INFORMATION:
APPLICANT: Tims, Kathy L.
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: KOHN & ASSOCIATES
STREET: 30500 NO. US20020009718A1Western Hwy. Suite 410
CITY: Farmington Hills
STATE: Michigan
COUNTRY: US
ZIP: 48334
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/044,604
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Montgomery, Ilene N.
REGISTRATION NUMBER: 38,972
REFERENCE/DOCKET NUMBER: 0994.00084
TELECOMMUNICATION INFORMATION:
TELEPHONE: (248) 539-5050
TELEFAX: (248) 539-5055
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
US-09-044-604-3

Query Match 41.8%; Score 28; DB 3; Length 19;
Best Local Similarity 62.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 8
Db 7 DAKGSFPC 14

RESULT 40
US-10-306-903-3
Sequence 3, Application US/10306903
Publication No. US20030166014A1
GENERAL INFORMATION:
APPLICANT: Tims, Kathy
TITLE OF INVENTION: ENDOMETRIOSIS-SPECIFIC SECRETORY PROTEIN
FILE REFERENCE: 0994.00137
CURRENT APPLICATION NUMBER: US/10/306,903
CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 09/044,604
PRIOR FILING DATE: 1998-03-19
PRIOR APPLICATION NUMBER: 08/328,451
PRIOR FILING DATE: 1994-10-25
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patentin version 3.2
SEQ ID NO 3
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-306-903-3

Query Match 41.8%; Score 28; DB 4; Length 19;
Best Local Similarity 62.5%; Pred. No. 6.6e+02;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DEKNSPEC 8
Db 7 DAKGSFPC 14

RESULT 41
US-10-690-276-662
Sequence 662, Application US/10690276
Publication No. US20050112118A1
GENERAL INFORMATION:
APPLICANT: Myriad Genetics, Incorporated
APPLICANT: Climbora, Daniel
APPLICANT: Heichman, Karen
APPLICANT: Bartel, Paul
APPLICANT: Mauck, Kimberly
APPLICANT: Bush, Angie
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING INFLAMMATORY DISORDERS
FILE REFERENCE: 1834.01
CURRENT APPLICATION NUMBER: US/10/690,276
CURRENT FILING DATE: 2003-10-20
PRIOR APPLICATION NUMBER: 09/727,384
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: 60/168,377
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/168,379
PRIOR FILING DATE: 1999-12-02
PRIOR APPLICATION NUMBER: 60/185,056
PRIOR FILING DATE: 2000-02-25
PRIOR APPLICATION NUMBER: 10/035,344
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,571
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 10/035,343
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,572
PRIOR FILING DATE: 2001-01-04
PRIOR APPLICATION NUMBER: 10/099,924
PRIOR FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,179
PRIOR FILING DATE: 2001-03-15
Remaining Prior Application data removed - See File Wrapper or PAM.
NUMBER OF SEQ ID NOS: 728
SOFTWARE: Patentin version 3.2
SEQ ID NO 662
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-10-690-276-662

Query Match 41.8%; Score 28; DB 5; Length 20;
Best Local Similarity 80.0%; Pred. No. 6.9e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 8 CILGP 12
Db 6 CILGP 10

```
RESULT 42
US-10-196-394-65
; Sequence 65, Application US/10196394
; Publication No. US20030171278A1
; GENERAL INFORMATION:
; APPLICANT: Mark S. Dennis
; TITLE OF INVENTION: Compounds that Bind HER2
; FILE REFERENCE: P1713R1
; CURRENT APPLICATION NUMBER: US/10/196,394
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: US/09/609,721
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 60/142,232
; PRIOR FILING DATE: 1999-07-02
; NUMBER OF SEQ ID NOS: 162
; SEQ ID NO 65
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide sequence
US-10-196-394-65

Query Match          41.0%; Score 27.5; DB 4; Length 20;
Best Local Similarity 58.3%; Pred. No. 8.6e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;

QY      1 DENSPECTLGP 12
       |||:||||
Db      1 DEVESWGC1-GP 11

RESULT 43
US-10-357-175-89
; Sequence 89, Application US/10357175
; Publication No. US20030170707A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 81...89
; OTHER INFORMATION: TADG-12 peptide
US-10-357-175-89

Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPECTI 9
       ::||:|
Db      1 RSSFKCI 7

RESULT 44
US-10-357-175-115
; Sequence 115, Application US/10357175
; Publication No. US20030170707A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 89
```

```
; FILE REFERENCE: D6192CIP/D/CIP
; CURRENT APPLICATION NUMBER: US/10/357,175
; CURRENT FILING DATE: 2003-02-03
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 158
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 79...87
; OTHER INFORMATION: TADG-12 peptide
US-10-357-175-115

Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPECTI 9
       ::||:|
Db      3 RSSFKCI 9

RESULT 45
US-10-455-720-89
; Sequence 89, Application US/10455720
; Publication No. US20030207316A1
; GENERAL INFORMATION:
; APPLICANT: O'Brien, Timothy J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D2
; CURRENT APPLICATION NUMBER: US/10/455,720
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 89
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; LOCATION: 81...89
; OTHER INFORMATION: TADG-12 peptide
US-10-455-720-89

Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPECTI 9
       ::||:|
Db      1 RSSFKCI 7

RESULT 46
US-10-455-720-115
; Sequence 115, Application US/10455720
; Publication No. US20030207316A1
; GENERAL INFORMATION:
; APPLICANT: Underwood, Lowell J.
; TITLE OF INVENTION: Transmembrane Serine Protease Overexpressed
; FILE REFERENCE: D6192CIP/D2
; CURRENT APPLICATION NUMBER: US/10/455,720
; CURRENT FILING DATE: 2003-06-05
; PRIOR APPLICATION NUMBER: 09/650,371
; PRIOR FILING DATE: 2000-08-28
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 115
```



```
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ LOCATION: 79...87
/ OTHER INFORMATION: TADG-12 peptide
US-10-455-720-115
```

```
Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 57.1%; Pred. No. 1.7e+06;
Matches 4; Conservative 3; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy 3 KNSPECI 9
Db 3 RSPFKCI 9
```

```
RESULT 47
US-10-250-508-55
/ Sequence 55, Application US/10250508
/ Publication No. US20040121327A1
/ GENERAL INFORMATION:
/ APPLICANT: Manns, Michael
/ APPLICANT: Strassburg, Christian
/ TITLE OF INVENTION: Method for Predicting the Potential Risk of Carcinomas and
/ TITLE OF INVENTION: Inflammatory Bowel Diseases and Relevant Tests
/ FILE REFERENCE: 0310017848
/ CURRENT APPLICATION NUMBER: US/10/250,508
/ CURRENT FILING DATE: 2003-12-08
/ PRIOR APPLICATION NUMBER: PCT/DE02/00003
/ PRIOR FILING DATE: 2002-01-03
/ PRIOR APPLICATION NUMBER: DE 101 00 238.6
/ PRIOR FILING DATE: 2001-01-05
/ NUMBER OF SEQ ID NOS: 57
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 55
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ NAME/KEY: MISC_FEATURE
/ LOCATION: (1)..(9)
/ OTHER INFORMATION: amino acid residues 7-15 of UGT1A10 as shown in Figure 4
US-10-250-508-55
```

```
Query Match          40.3%; Score 27; DB 4; Length 9;
Best Local Similarity 44.4%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 1 DENSPECI 9
Db 1 DQPSFMCV 9
```

```
RESULT 48
US-10-838-289-227
/ Sequence 227, Application US/10838289
/ Publication No. US20050058603A1
/ GENERAL INFORMATION:
/ APPLICANT: Gao, Jinning
/ APPLICANT: Ai, Hua
/ TITLE OF INVENTION: DRUG DELIVERY SYSTEM BASED ON POLYMER
/ TITLE OF INVENTION: NANOSHELLS
/ FILE REFERENCE: CMRU-P01-040
/ CURRENT APPLICATION NUMBER: US/10/838,289
/ PRIOR FILING DATE: 2004-05-03
/ PRIOR APPLICATION NUMBER: US 60/502,429
/ PRIOR FILING DATE: 2003-09-12
/ PRIOR APPLICATION NUMBER: US 60/467,389
/ PRIOR FILING DATE: 2003-05-02
/ NUMBER OF SEQ ID NOS: 756
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 227
```

```
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Lung homing peptide
US-10-838-289-227
```

```
Query Match          40.3%; Score 27; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 5 SPECIIG 11
Db 5 NPDCTIG 11
```

```
RESULT 49
US-10-607-595-435
/ Sequence 435, Application US/10607595
/ Publication No. US20050074812A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruoslahti, Erkki
/ APPLICANT: Pasqualini, Renata
/ TITLE OF INVENTION: Molecules that Home to Various Selected Organs or
/ TITLE OF INVENTION: Tissues
/ FILE REFERENCE: P-LJ 4514
/ CURRENT APPLICATION NUMBER: US/10/607,595
/ CURRENT FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: US/09/722,250
/ PRIOR FILING DATE: 2000-11-22
/ PRIOR APPLICATION NUMBER: US 09/042,107
/ PRIOR FILING DATE: 1998-03-13
/ NUMBER OF SEQ ID NOS: 437
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 435
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-607-595-435
```

```
Query Match          40.3%; Score 27; DB 5; Length 12;
Best Local Similarity 57.1%; Pred. No. 6.2e+02;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy 5 SPECIIG 11
Db 5 NPDCTIG 11
```

```
RESULT 50
US-10-488-671-21
/ Sequence 21, Application US/10488671
/ Publication No. US20040254106A1
/ GENERAL INFORMATION:
/ APPLICANT: Carr, Francis J.
/ APPLICANT: Carter, Graham
/ TITLE OF INVENTION: Modified Factor IX
/ FILE REFERENCE: MER-128
/ CURRENT APPLICATION NUMBER: US/10/488,671
/ CURRENT FILING DATE: 2004-03-04
/ PRIOR APPLICATION NUMBER: PCT/EP02/09717
/ PRIOR FILING DATE: 2002-08-30
/ PRIOR APPLICATION NUMBER: EP 0112154.7
/ PRIOR FILING DATE: 2001-09-04
/ NUMBER OF SEQ ID NOS: 126
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 21
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-488-671-21
```

Query Match 40.3%; Score 27; DB 5; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.7e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 NSPEC 8
|:|:
DB 1 NSPEC 5

RESULT 51
US-10-269-695-147
Sequence 147, Application US/10269695
Publication No. US20030229023A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN DANIEL

APPLICANT: MIN, HOSUNG
TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
FILE REFERENCE: A-801A
CURRENT APPLICATION NUMBER: US/10/269,695
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/414,155
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/328,624
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 359
SOFTWARE: PatentIn version 3.1
SEQ ID NO 147
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-10-269-695-147
OTHER INFORMATION: Polypeptide capable of binding to Ang-2

Query Match 40.3%; Score 27; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
|:|:
DB 3 DKRPLECMFG 12

RESULT 52
US-10-410-998-147
Sequence 147, Application US/10410998
Publication No. US20030236193A1
GENERAL INFORMATION:
APPLICANT: OLINER, JONATHAN DANIEL
APPLICANT: MIN, HOSUNG
TITLE OF INVENTION: SPECIFIC BINDING AGENTS OF HUMAN ANGIOPOIETIN-2
FILE REFERENCE: A-801A
CURRENT APPLICATION NUMBER: US/10/410,998
CURRENT FILING DATE: 2003-04-09
PRIOR APPLICATION NUMBER: US/10/269,695
PRIOR FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/414,155
PRIOR FILING DATE: 2002-09-27
PRIOR APPLICATION NUMBER: US 60/328,624
PRIOR FILING DATE: 2001-10-11
NUMBER OF SEQ ID NOS: 359
SOFTWARE: PatentIn version 3.1
SEQ ID NO 147
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
US-10-410-998-147
OTHER INFORMATION: Polypeptide capable of binding to Ang-2

Query Match 40.3%; Score 27; DB 4; Length 20;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
|:|:
DB 3 DKRPLECMFG 12

RESULT 53
US-10-432-465-65
Sequence 65, Application US/10432465
Publication No. US20040091479A1
GENERAL INFORMATION:
APPLICANT: Nieland, John
APPLICANT: Kaufmann, Andreas
APPLICANT: Kather, Angela
APPLICANT: Schinz, Manuela
TITLE OF INVENTION: T-Cell Epitopes of the Papillomavirus L1
TITLE OF INVENTION: Protein and E7 Protein and Their Use in Diagnosis and
FILE REFERENCE: 50125/077001
CURRENT APPLICATION NUMBER: US/10/432,465
CURRENT FILING DATE: 2003-12-10
PRIOR APPLICATION NUMBER: PCT/EP01/14037
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: DE 10059631.2
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 116
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 65
LENGTH: 20
TYPE: PRT
ORGANISM: Human papillomavirus
US-10-432-465-65

Query Match 40.3%; Score 27; DB 4; Length 20;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSPECTIG 11
|:|:
DB 7 DYKOTOLCIG 17

RESULT 54
US-10-433-091-34
Sequence 34, Application US/10433091
Publication No. US20040101533A1
GENERAL INFORMATION:
APPLICANT: MÜLLER, RAINER
APPLICANT: NIELAND, JOHN
APPLICANT: GABELSBERGER, JOSEF
APPLICANT: HERBST, RUTH
TITLE OF INVENTION: MEDICAMENT FOR PREVENTING OR TREATING TUMORS CAUSED BY
FILE REFERENCE: 037067/0115
CURRENT APPLICATION NUMBER: US/10/433,091
CURRENT FILING DATE: 2003-11-25
PRIOR APPLICATION NUMBER: PCT/EP01/14038
PRIOR FILING DATE: 2001-11-30
PRIOR APPLICATION NUMBER: DE 100 59 630.4
PRIOR FILING DATE: 2000-12-01
NUMBER OF SEQ ID NOS: 72
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 34
LENGTH: 20
TYPE: PRT
ORGANISM: Human papillomavirus type 18
US-10-433-091-34

Query Match 40.3%; Score 27; DB 4; Length 20;
Best Local Similarity 54.5%; Pred. No. 1.1e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSPECTIG 11
| | | | |
DB 7 DYKOTOLCTIG 17

RESULT 55
US-10-286-457-230
; Sequence 230, Application US/10286457
; Publication No. US20030166004A1
; GENERAL INFORMATION:
; APPLICANT: JENO GYURIS et al.
; TITLE OF INVENTION: ENDOTHELIAL-CELL BINDING PEPTIDES FOR DIAGNOSIS AND THERAPY
; FILE REFERENCE: GPCI-PO1-178
; CURRENT APPLICATION NUMBER: US/10/286,457
; PRIOR FILING DATE: 2002-11-01
; PRIOR APPLICATION NUMBER: 60/334822
; NUMBER OF SEQ ID NOS: 684
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 230
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: artificial sequence isolated from random peptide libraries, based
US-10-286-457-230

Query Match 38.8%; Score 26; DB 4; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSPEC 8
| | | | |
DB 4 KNOFHC 9

RESULT 56
US-10-352-786-454
; Sequence 454, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 454
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-454

Query Match 38.8%; Score 26; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
| | | | |
DB 1 EVNTLRCLG 10

RESULT 57
US-10-352-786-455
; Sequence 455, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US

; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 455
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-455

Query Match 38.8%; Score 26; DB 4; Length 10;
Best Local Similarity 50.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
| | | | |
DB 1 EVNTLRCLG 10

RESULT 58
US-10-114-500-19
; Sequence 19, Application US/10114500
; Publication No. US20030100746A1
; GENERAL INFORMATION:
; APPLICANT: Godbole, Shubhada
; APPLICANT: Boyle, Bryan J
; APPLICANT: Arterburn, Matthew C
; APPLICANT: Liu, Chenghua
; APPLICANT: Tang, Y Tom
; APPLICANT: Dmanac, Radote T
; TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
; FILE REFERENCE: HYS-40CON
; CURRENT APPLICATION NUMBER: US/10/114,500
; PRIOR FILING DATE: 2002-04-01
; PRIOR APPLICATION NUMBER: US 09/802,704
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: US 09/560,875
; PRIOR FILING DATE: 2000-04-27
; PRIOR APPLICATION NUMBER: US 09/496,914
; PRIOR FILING DATE: 2000-02-03
; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 19
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-114-500-19

Query Match 38.8%; Score 26; DB 4; Length 11;
Best Local Similarity 44.4%; Pred. No. 8.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 NSPECTIG 12
| | | | |
DB 1 NOYRCICPP 9

RESULT 59
US-10-352-786-541
; Sequence 541, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US

```
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 541
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-541
```

```
Query Match          38.8%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECILG 11
      ||: |||
Db      1 EVNTRLRCQLG 10
```

```
RESULT 60
US-10-352-786-542
/ Sequence 542, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 542
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-542
```

```
Query Match          38.8%; Score 26; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECILG 11
      ||: |||
Db      1 EVNTRLRCPLG 10
```

```
RESULT 61
US-10-471-346-19
/ Sequence 19, Application US/10471346
/ Publication No. US20040236050A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ FILE REFERENCE: Godbole, Shubhada D
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 541
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-471-346-19
```

```
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 19
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-471-346-19
```

```
Query Match          38.8%; Score 26; DB 5; Length 11;
Best Local Similarity 44.4%; Pred. No. 8.6e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      4 NSFCILCP 12
      ||: |||
Db      1 NQYRCICPP 9
```

```
RESULT 62
US-10-352-786-627
/ Sequence 627, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 627
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-627
```

```
Query Match          38.8%; Score 26; DB 4; Length 12;
Best Local Similarity 50.0%; Pred. No. 9.4e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
Qy      2 EKNSPECILG 11
      ||: |||
Db      1 EVNTRLRCQLG 10
```

```
RESULT 63
US-10-352-786-628
/ Sequence 628, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 628
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-628
```

Query Match 38.8%; Score 26; DB 4; Length 12;
 Best Local Similarity 50.0%; Pred. No. 9,4e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
 DB 1 EVNTLRCPG 10

RESULT 64
 US-09-880-713A-30
 ; Sequence 30, Application US/09880713A
 ; Patent No. US20020049307A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Aebersold, Ruedi
 ; APPLICANT: Zhou, Huijin
 ; TITLE OF INVENTION: Selective Labeling and Isolation of Phosphopeptides and
 ; FILE REFERENCE: 39-00
 ; CURRENT APPLICATION NUMBER: US/09/880,713A
 ; PRIOR FILING DATE: 2001-06-12
 ; PRIOR APPLICATION NUMBER: US 60/210,972
 ; PRIOR FILING DATE: 2000-06-12
 ; NUMBER OF SEQ ID NOS: 34
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 30
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-880-713A-30

Query Match 38.8%; Score 26; DB 3; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIIGP 12
 DB 5 APELLISP 12

RESULT 65
 US-09-988-493-302
 ; Sequence 302, Application US/09988493
 ; Publication No. US2003006449A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Herath, Herath Mudiyanselage Achula Chandrasiri
 ; APPLICANT: O'Hare, Michael John
 ; APPLICANT: Page, Martin John
 ; APPLICANT: Parekh, Rajesh Bhikhu
 ; APPLICANT: Waterfield, Michael Derek
 ; TITLE OF INVENTION: Proteins, Genes, and Their Use for
 ; FILE REFERENCE: 2543-1-024
 ; CURRENT APPLICATION NUMBER: US/09/988,493
 ; PRIOR FILING DATE: 2002-05-21
 ; PRIOR APPLICATION NUMBER: PCT/GB01/01219
 ; PRIOR FILING DATE: 2001-03-20
 ; PRIOR APPLICATION NUMBER: GB 0006695.1
 ; PRIOR FILING DATE: 2000-03-20
 ; PRIOR APPLICATION NUMBER: GB 0007265.2
 ; PRIOR FILING DATE: 2000-02-24
 ; NUMBER OF SEQ ID NOS: 308
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 302
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: homo sapien
 US-09-988-493-302

Query Match 38.8%; Score 26; DB 3; Length 13;
 Best Local Similarity 62.5%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIIGP 12
 DB 5 APELLISP 12

RESULT 66
 US-10-352-786-717
 ; Sequence 717, Application US/10352786
 ; Publication No. US20030228353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowart, Donald R.
 ; TITLE OF INVENTION: Bioactive Keratin Peptides
 ; FILE REFERENCE: KER020/4-024US
 ; CURRENT APPLICATION NUMBER: US/10/352,786
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 630/352,396
 ; PRIOR FILING DATE: 2002-01-28
 ; NUMBER OF SEQ ID NOS: 4468
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 717
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Consensus Peptide
 US-10-352-786-717

Query Match 38.8%; Score 26; DB 4; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
 DB 1 EVNTLRCPG 10

RESULT 67
 US-10-352-786-718
 ; Sequence 718, Application US/10352786
 ; Publication No. US20030228353A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cowart, Donald R.
 ; TITLE OF INVENTION: Bioactive Keratin Peptides
 ; FILE REFERENCE: KER020/4-024US
 ; CURRENT APPLICATION NUMBER: US/10/352,786
 ; PRIOR FILING DATE: 2003-06-06
 ; PRIOR APPLICATION NUMBER: 630/352,396
 ; PRIOR FILING DATE: 2002-01-28
 ; NUMBER OF SEQ ID NOS: 4468
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 718
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Artificial
 ; FEATURE:
 ; OTHER INFORMATION: Consensus Peptide
 US-10-352-786-718

Query Match 38.8%; Score 26; DB 4; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
 DB 1 EVNTLRCPG 10

RESULT 68
 US-10-412-964-40
 ; Sequence 40, Application US/10412964
 ; Publication No. US20040106150A1
 ; GENERAL INFORMATION:

```

/ APPLICANT: Wang, Yinqi Karen
/ TITLE OF INVENTION: Inverse Labeling Method for the Rapid
/ FILE REFERENCE: 4-31692B
/ CURRENT APPLICATION NUMBER: US/10/412,964
/ PRIOR FILING DATE: 2003-04-14
/ PRIOR APPLICATION NUMBER: 60/257,559
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: 60/332,965
/ PRIOR FILING DATE: 2001-11-19
/ PRIOR APPLICATION NUMBER: 10/016,627
/ PRIOR FILING DATE: 2001-12-10
/ NUMBER OF SEQ ID NOS: 83
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 40
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Peptide obtained from Oncoprotein 18
/ NAME/KEY: PHOSPHORYLATION
/ LOCATION: 11
/ OTHER INFORMATION: The serine is phosphorylated
US-10-412-964-40

```

```

Query Match          38.8%; Score 26; DB 4; Length 13;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      5 SPECTILGP 12
DB      5 APELILSP 12

```

```

RESULT 69
US-10-948-707-1280
/ Sequence 1280, Application US/10948707
/ Publication No. US20050187147A1
/ GENERAL INFORMATION:
/ APPLICANT: Ballatore, Carlo
/ APPLICANT: Castellino, Angelo
/ APPLICANT: Desharnais, Joel
/ APPLICANT: Guo, Zijian
/ APPLICANT: Li, Qing
/ APPLICANT: Newman, Michael James
/ APPLICANT: Sun, Chengzao
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INCREASING
/ FILE REFERENCE: 17967-003001
/ CURRENT APPLICATION NUMBER: US/10/948,707
/ CURRENT FILING DATE: 2004-09-22
/ PRIOR APPLICATION NUMBER: 60/505,325
/ PRIOR FILING DATE: 2003-09-22
/ PRIOR APPLICATION NUMBER: 60/568,340
/ PRIOR FILING DATE: 2004-05-04
/ PRIOR APPLICATION NUMBER: 60/581,835
/ PRIOR FILING DATE: 2004-06-22
/ NUMBER OF SEQ ID NOS: 1422
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1280
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo Sapiens
US-10-948-707-1280

```

```

Query Match          38.8%; Score 26; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 1e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY      5 SPECTILGP 12
DB      2 APELILSP 9

```

```

RESULT 70
US-10-352-786-813
/ Sequence 813, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowbar, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 60/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 813
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-813

```

```

Query Match          38.8%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY      2 EKNSPECTILG 11
DB      1 EYNTLRCPQLG 10

```

```

RESULT 71
US-10-352-786-814
/ Sequence 814, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowbar, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 60/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 814
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-814

```

```

Query Match          38.8%; Score 26; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY      2 EKNSPECTILG 11
DB      1 EYNTLRCPQLG 10

```

```

RESULT 72
US-10-615-659-45
/ Sequence 45, Application US/10615659
/ Publication No. US20040157234A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
/ FILE REFERENCE: D0283 NP

```

/ CURRENT APPLICATION NUMBER: US/10/615,659
/ CURRENT FILING DATE: 2003-07-09
/ PRIOR APPLICATION NUMBER: U.S. 60/394,725
/ PRIOR FILING DATE: 2002-07-09
/ NUMBER OF SEQ ID NOS: 102
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 45
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-615-659-45

Query Match 38.8%; Score 26; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7
|||
Db 7 KNSFE 11

RESULT 73
US-10-635-977-45
/ Sequence 45, Application US/10635977
/ Publication No. US20040171131A1
/ GENERAL INFORMATION:
/ APPLICANT: Bristol-Myers Squibb Company
/ TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING A NOVEL TESTIS-SPECIFIC TUBULIN
/ FILE REFERENCE: D0283A CIP
/ CURRENT APPLICATION NUMBER: US/10/635,977
/ CURRENT FILING DATE: 2003-08-07
/ PRIOR APPLICATION NUMBER: U.S. 60/394,725
/ PRIOR FILING DATE: 2002-07-09
/ PRIOR APPLICATION NUMBER: U.S. 10/615,659
/ PRIOR FILING DATE: 2003-07-09
/ NUMBER OF SEQ ID NOS: 103
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 45
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-635-977-45

Query Match 38.8%; Score 26; DB 4; Length 14;
Best Local Similarity 100.0%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7
|||
Db 7 KNSFE 11

RESULT 74
US-10-473-287-39
/ Sequence 39, Application US/10473287
/ Publication No. US20040221327A1
/ GENERAL INFORMATION:
/ APPLICANT: GERSHWIN, M. ERIC
/ TITLE OF INVENTION: ANTIBODIES AGAINST AUTOANTIGENS OF PRIMARY BILIARY
/ TITLE OF INVENTION: CIRRHOSIS AND METHODS OF MAKING AND USING THEM
/ FILE REFERENCE: ABX-UCD PCT
/ CURRENT APPLICATION NUMBER: US/10/473,287
/ CURRENT FILING DATE: 2003-09-26
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 39
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Human mab
US-10-473-287-39

Query Match 38.8%; Score 26; DB 5; Length 14;
Best Local Similarity 45.5%; Pred. No. 1.1e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 2 EKNSPECILGP 12
: |||
Db 3 QANSFPPTFGP 13

RESULT 75
US-10-473-287-43
/ Sequence 43, Application US/10473287
/ Publication No. US20040221327A1
/ GENERAL INFORMATION:
/ APPLICANT: GERSHWIN, M. ERIC
/ TITLE OF INVENTION: ANTIBODIES AGAINST AUTOANTIGENS OF PRIMARY BILIARY
/ TITLE OF INVENTION: CIRRHOSIS AND METHODS OF MAKING AND USING THEM
/ FILE REFERENCE: ABX-UCD PCT
/ CURRENT APPLICATION NUMBER: US/10/473,287
/ CURRENT FILING DATE: 2003-09-26
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 43
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Human mab
US-10-473-287-43

Query Match 38.8%; Score 26; DB 5; Length 14;
Best Local Similarity 40.0%; Pred. No. 1.1e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECILG 11
: |||
Db 3 QHNSYPCSRG 12

RESULT 76
US-09-767-460-29
/ Sequence 29, Application US/09767460
/ Patent No. US2002009756A1
/ GENERAL INFORMATION:
/ APPLICANT: Mandell, Arnold
/ APPLICANT: Selz, Karen
/ APPLICANT: Shlesinger, Michael
/ TITLE OF INVENTION: Algorithmic Design of Peptides for Binding and/or Modulation of
/ TITLE OF INVENTION: Functions of Receptors and/or Other Proteins
/ FILE REFERENCE: 01561-0002-CPUS01
/ CURRENT APPLICATION NUMBER: US/09/767,460
/ CURRENT FILING DATE: 2001-01-23
/ NUMBER OF SEQ ID NOS: 96
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 29
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-09-767-460-29

Query Match 38.8%; Score 26; DB 3; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
: |||
Db 6 DRNHDFC 12

RESULT 77

US-10-352-786-913
; Sequence 913, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 913
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-913

Query Match 38.8%; Score 26; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSFCTIG 11
| : | : | : |
DB 1 EYNTLRCLG 10

RESULT 78
US-10-352-786-914
; Sequence 914, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowart, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCE: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; CURRENT FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 914
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-914

Query Match 38.8%; Score 26; DB 4; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSFCTIG 11
| : | : | : |
DB 1 EYNTLRCLG 10

RESULT 79
US-10-777-829-29
; Sequence 29, Application US/10777829
; Publication No. US20050027457A1
; GENERAL INFORMATION:
; APPLICANT: MANDELL, ARNOLD J.
; APPLICANT: SELZ, KAREN A.
; APPLICANT: SHLESINGER, MICHAEL F.
; TITLE OF INVENTION: ALGORITHMIC DESIGN OF PEPTIDES FOR BINDING AND/OR MODULATION OF
; FILE REFERENCE: 31010-701.301
; CURRENT APPLICATION NUMBER: US/10/777,829

; CURRENT FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 09/767,460
; PRIOR FILING DATE: 2001-01-23
; PRIOR APPLICATION NUMBER: 09/490,701
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-777-829-29

Query Match 38.8%; Score 26; DB 5; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFEC 8
| : | : | : |
DB 6 DRNHFDG 12

RESULT 80
US-10-818-067-29
; Sequence 29, Application US/10818067
; Publication No. US20050119454A1
; GENERAL INFORMATION:
; APPLICANT: MANDELL, ARNOLD J.
; APPLICANT: SELZ, KAREN A.
; APPLICANT: SHLESINGER, MICHAEL F.
; TITLE OF INVENTION: ALGORITHMIC DESIGN OF PEPTIDES FOR BINDING AND/OR MODULATION OF
; FILE REFERENCE: 31010-701.502
; CURRENT APPLICATION NUMBER: US/10/818,067
; CURRENT FILING DATE: 2004-04-02
; PRIOR APPLICATION NUMBER: 10/777,829
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 09/767,460
; PRIOR FILING DATE: 2000-01-23
; PRIOR APPLICATION NUMBER: 09/490,701
; PRIOR FILING DATE: 2000-01-24
; NUMBER OF SEQ ID NOS: 107
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 29
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Synthetic peptide
US-10-818-067-29

Query Match 38.8%; Score 26; DB 5; Length 15;
Best Local Similarity 42.9%; Pred. No. 1.2e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFEC 8
| : | : | : |
DB 6 DRNHFDG 12

RESULT 81
US-09-774-639-245
; Sequence 245, Application US/09774639
; Publication No. US2003003555A1
; GENERAL INFORMATION:
; APPLICANT: ROSEN et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; CURRENT FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112


```
/ PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
/ NUMBER OF SEQ ID NOS: 371
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 245
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-774-639-245

Query Match          38.8%; Score 26; DB 3; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSFECTILGP 12
         | | | | |
Db       4 KTRPACILLYP 13

RESULT 82
US-09-969-730-344
/ Sequence 344, Application US/09969730
/ Publication No. US20030054443A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2
/ CURRENT APPLICATION NUMBER: US/09/969,730
/ PRIOR FILING DATE: 2001-10-04
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,370
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,367
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,365
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,731
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,557
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,563
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/055,970
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,986
/ PRIOR FILING DATE: 1997-08-18
/ PRIOR APPLICATION NUMBER: 60/055,311
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,808
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,803
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,804
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,809
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,806
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,310
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/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,798
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,309
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,312
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/054,807
/ PRIOR FILING DATE: 1997-08-05
/ PRIOR APPLICATION NUMBER: 60/055,386
/ PRIOR FILING DATE: 1997-08-05
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 344
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-09-969-730-344

Query Match          38.8%; Score 26; DB 3; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSFECTILGP 12
         | | | | |
Db       4 KTRPACILLYP 13

RESULT 83
US-10-114-500-15
/ Sequence 15, Application US/10114500
/ Publication No. US20030100746A1
/ GENERAL INFORMATION:
/ APPLICANT: Godbole, Shubhada
/ APPLICANT: Boyle, Bryan J
/ APPLICANT: Atterburn, Matthew C
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Tang, Y Tom
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
/ FILE REFERENCE: HYS-40CON
/ CURRENT APPLICATION NUMBER: US/10/114,500
/ PRIOR FILING DATE: 2002-04-01
/ PRIOR APPLICATION NUMBER: US 09/802,704
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 15
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-114-500-15

Query Match          38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      4 NSFECTILGP 12
         | | | | |
Db       6 NGYRCICPP 14

RESULT 84
US-10-352-786-1017
/ Sequence 1017, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
```

```
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 6J0/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1017
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1017

Query Match      38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSFCTIG 11
| | | | |
Db      1 EVNTRCQLG 10

RESULT 85
US-10-352-786-1018
/ Sequence 1018, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowbat, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 6J0/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1018
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1018

Query Match      38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSFCTIG 11
| | | | |
Db      1 EVNTRCPLG 10

RESULT 86
US-10-621-363-344
/ Sequence 344, Application US/10621363
/ Publication No. US20040023283A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2C1
/ CURRENT APPLICATION NUMBER: US/10/621,363
/ CURRENT FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
```

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/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,370
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 344
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-621-363-344

Query Match      38.8%; Score 26; DB 4; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      3 KNSFCTIGP 12
| | | | |
Db      4 KTPAECLTYP 13

RESULT 87
US-10-471-346-15
/ Sequence 15, Application US/10471346
/ Publication No. US20040236090A1
/ GENERAL INFORMATION:
/ APPLICANT: Hyseq, Inc
/ APPLICANT: Godbole, Shubhada D
/ APPLICANT: Boyle, Bryan J
/ APPLICANT: Arterburn, Matthew C
/ APPLICANT: Liu, Chenghua
/ APPLICANT: Tang, Y Tom
/ APPLICANT: Drmanac, Radoje T
/ TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO FIBULIN-LIKE POLYPEPTIDES AND
/ FILE REFERENCE: 24059-040-061
/ CURRENT APPLICATION NUMBER: US/10/471,346
/ CURRENT FILING DATE: 2003-09-08
/ PRIOR APPLICATION NUMBER: US 09/802,704
/ PRIOR FILING DATE: 2001-03-08
/ PRIOR APPLICATION NUMBER: US 09/560,875
/ PRIOR FILING DATE: 2000-04-27
/ PRIOR APPLICATION NUMBER: US 09/496,914
/ PRIOR FILING DATE: 2000-02-03
/ NUMBER OF SEQ ID NOS: 22
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 15
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-471-346-15

Query Match      38.8%; Score 26; DB 5; Length 16;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      4 NSFCTIGP 12
| | | | |
Db      6 NQYRCTCP 14

RESULT 88
US-10-352-786-1127
```

```

; Sequence 1127, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCES: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1127
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-1127

```

```

Query Match      38.8%; Score 26; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      2 EKNSPCTIG 11
      |||
Db      1 EVNLTLCQIG 10

```

```

RESULT 89
US-10-352-786-1128
; Sequence 1128, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCES: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1128
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Consensus Peptide
US-10-352-786-1128

```

```

Query Match      38.8%; Score 26; DB 4; Length 17;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

```

```

Qy      2 EKNSPCTIG 11
      |||
Db      1 EVNLTLCQIG 10

```

```

RESULT 90
US-09-858-935B-121
; Sequence 121, Application US/09858935B
; Publication No. US20030069177A1
; GENERAL INFORMATION:
; APPLICANT: Dubagule, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCES: P1794R1
; CURRENT APPLICATION NUMBER: US/09/858,935B
; CURRENT FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985

```

```

; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 121
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-09-858-935B-121

```

```

Query Match      38.8%; Score 26; DB 3; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      7 ECIIGP 12
      |||
Db      4 ECIWGP 9

```

```

RESULT 91
US-10-271-869-121
; Sequence 121, Application US/10271869
; Publication No. US20030211992A1
; GENERAL INFORMATION:
; APPLICANT: Dubagule, Yves
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Lowman, Henry B.
; TITLE OF INVENTION: METHOD FOR TREATING CARTILAGE DISORDERS
; FILE REFERENCES: P1794R1
; CURRENT APPLICATION NUMBER: US/10/271,869
; PRIOR FILING DATE: 2002-10-16
; PRIOR APPLICATION NUMBER: US/09/858,935
; PRIOR FILING DATE: 2002-07-02
; PRIOR APPLICATION NUMBER: US 60/248,985
; PRIOR FILING DATE: 2000-11-15
; PRIOR APPLICATION NUMBER: US 60/204,490
; PRIOR FILING DATE: 2000-05-16
; NUMBER OF SEQ ID NOS: 153
; SEQ ID NO 121
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Artificial
; FEATURE:
; OTHER INFORMATION: Sequence is synthesized
US-10-271-869-121

```

```

Query Match      38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

Qy      7 ECIIGP 12
      |||
Db      4 ECIWGP 9

```

```

RESULT 92
US-10-352-786-1243
; Sequence 1243, Application US/10352786
; Publication No. US20030228353A1
; GENERAL INFORMATION:
; APPLICANT: Cowser, Donald R.
; TITLE OF INVENTION: Bioactive Keratin Peptides
; FILE REFERENCES: KER020/4-024US
; CURRENT APPLICATION NUMBER: US/10/352,786
; PRIOR FILING DATE: 2003-06-06
; PRIOR APPLICATION NUMBER: 630/352,396
; PRIOR FILING DATE: 2002-01-28
; NUMBER OF SEQ ID NOS: 4468
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 1243
; LENGTH: 18

```

/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1243

Query Match 38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0;

Qy 2 EKNSECTIG 11
| : | : | :
Db 1 EVNTRCQIG 10

RESULT 93
US-10-352-786-1244
/ Sequence 1244, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowart, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ PRIOR FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 630/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1244
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1244

Query Match 38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0;

Qy 2 EKNSECTIG 11
| : | : | :
Db 1 EVNTRCQIG 10

RESULT 94
US-10-754-437-25
/ Sequence 25, Application US/10754437
/ Publication No. US20040146915A1
/ GENERAL INFORMATION:
/ APPLICANT: METAMORPHIX, INC.
/ APPLICANT: Ferrite, Bonita J.M.
/ APPLICANT: Johnston, Eric V.
/ APPLICANT: Denise, Sue
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING CANINE GENDER
/ FILE REFERENCE: MM1130-1
/ CURRENT APPLICATION NUMBER: US/10/754,437
/ PRIOR FILING DATE: 2004-01-09
/ PRIOR APPLICATION NUMBER: US 60/439,188
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 25
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Homo sapiens X
US-10-754-437-25

Query Match 38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

Qy 6 FECTIG 11
| : | : | :
Db 7 FACILIG 12

RESULT 95
US-10-754-437-29
/ Sequence 29, Application US/10754437
/ Publication No. US20040146915A1
/ GENERAL INFORMATION:
/ APPLICANT: METAMORPHIX, INC.
/ APPLICANT: Ferrite, Bonita J.M.
/ APPLICANT: Johnston, Eric V.
/ APPLICANT: Denise, Sue
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING CANINE GENDER
/ FILE REFERENCE: MM1130-1
/ CURRENT APPLICATION NUMBER: US/10/754,437
/ PRIOR FILING DATE: 2004-01-09
/ PRIOR APPLICATION NUMBER: US 60/439,188
/ PRIOR FILING DATE: 2003-01-10
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 29
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Canis familiaris X
US-10-754-437-29

Query Match 38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

Qy 6 FECTIG 11
| : | : | :
Db 7 FACILIG 12

RESULT 96
US-10-754-437-31
/ Sequence 31, Application US/10754437
/ Publication No. US20040146915A1
/ GENERAL INFORMATION:
/ APPLICANT: METAMORPHIX, INC.
/ APPLICANT: Ferrite, Bonita J.M.
/ APPLICANT: Johnston, Eric V.
/ APPLICANT: Denise, Sue
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING CANINE GENDER
/ FILE REFERENCE: MM1130-1
/ CURRENT APPLICATION NUMBER: US/10/754,437
/ PRIOR FILING DATE: 2004-01-09
/ PRIOR APPLICATION NUMBER: US 60/439,188
/ PRIOR FILING DATE: 2003-01-10
/ NUMBER OF SEQ ID NOS: 99
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 31
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Canis familiaris X
US-10-754-437-31

Query Match 38.8%; Score 26; DB 4; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.4e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0;

Qy 6 FECTIG 11
| : | : | :
Db 7 FACILIG 12

RESULT 97
US-09-864-761-43430
/ Sequence 43430, Application US/09864761
/ Patent No. US20020048763A1

```
/ GENERAL INFORMATION:
/ APPLICANT: Penn, Sharon G.
/ APPLICANT: Rank, David R.
/ APPLICANT: Hanzel, David K.
/ APPLICANT: Chen, Wensheng
/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
/ FILE REFERENCE: Aecmca-X-1
/ CURRENT APPLICATION NUMBER: US/09/664,761
/ PRIOR FILING DATE: 2001-05-23
/ PRIOR APPLICATION NUMBER: US 60/180,312
/ PRIOR FILING DATE: 2000-02-04
/ PRIOR APPLICATION NUMBER: US 60/207,456
/ PRIOR FILING DATE: 2000-05-26
/ PRIOR APPLICATION NUMBER: US 09/632,366
/ PRIOR FILING DATE: 2000-08-03
/ PRIOR APPLICATION NUMBER: GB 24263,6
/ PRIOR FILING DATE: 2000-10-04
/ PRIOR APPLICATION NUMBER: US 60/236,359
/ PRIOR FILING DATE: 2000-09-27
/ PRIOR APPLICATION NUMBER: PCT/US01/00666
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00667
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00664
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00669
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00665
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00668
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00663
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00662
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00661
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: PCT/US01/00670
/ PRIOR FILING DATE: 2001-01-30
/ PRIOR APPLICATION NUMBER: US 60/234,687
/ PRIOR FILING DATE: 2000-09-21
/ PRIOR APPLICATION NUMBER: US 09/608,408
/ PRIOR FILING DATE: 2000-06-30
/ PRIOR APPLICATION NUMBER: US 09/774,203
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 49117
/ SOFTWARE: Annomax Sequence Listering Engine vers. 1.1
/ SEQ ID NO 43430
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: MAP TO AC008009.4
/ OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.6
/ OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.4
/ OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.7
/ OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
/ OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 2.1
/ OTHER INFORMATION: EST_HUMAN HIT: AV706204.1, EVALUE 3.70e-02
US-09-664-761-43430
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Query Match      38.8%; Score 26; DB 3; Length 19;
Best Local Similarity 100.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      2 EKNSP 6
      |||||
Db      1 EKNSP 5

RESULT 98
US-10-225-567A-1330
```

```
/ Sequence 1330, Application US/10225567A
/ Publication No. US20030113798A1
/ GENERAL INFORMATION:
/ APPLICANT: Lifespan Biosciences
/ APPLICANT: Brown, Joseph P.
/ APPLICANT: Burner, Glenn C.
/ APPLICANT: Roush, Christine L.
/ TITLE OF INVENTION: ANTIGENIC PEPTIDES AND ANTIBODIES FOR G PROTEIN-COUPLED RECEPTOR
/ FILE REFERENCE: 1920-4-4
/ CURRENT APPLICATION NUMBER: US/10/225,567A
/ CURRENT FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 60/257,144
/ PRIOR FILING DATE: 2000-12-19
/ NUMBER OF SEQ ID NOS: 2292
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1330
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-225-567A-1330
```

```
Query Match      38.8%; Score 26; DB 4; Length 19;
Best Local Similarity 40.0%; Pred. No. 1.5e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 DEKNSPFCIL 10
      ||:|:|
Db      4 DEQGRRCVIL 13
```

```
RESULT 99
US-10-352-786-1365
/ Sequence 1365, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 6J0/352,396
/ PRIOR FILING DATE: 2002-01-28
/ NUMBER OF SEQ ID NOS: 4468
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1365
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Consensus Peptide
US-10-352-786-1365
```

```
Query Match      38.8%; Score 26; DB 4; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 EKNSPFCILG 11
      ||:|:|
Db      1 EYNTLRQCLG 10
```

```
RESULT 100
US-10-352-786-1366
/ Sequence 1366, Application US/10352786
/ Publication No. US20030228353A1
/ GENERAL INFORMATION:
/ APPLICANT: Cowser, Donald R.
/ TITLE OF INVENTION: Bioactive Keratin Peptides
/ FILE REFERENCE: KER020/4-024US
/ CURRENT APPLICATION NUMBER: US/10/352,786
/ CURRENT FILING DATE: 2003-06-06
/ PRIOR APPLICATION NUMBER: 6J0/352,396
/ PRIOR FILING DATE: 2002-01-28
```

NUMBER OF SEQ ID NOS: 4468
SOFTWARE: Patencin version 3.2
SEQ ID NO: 1366
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Consensus Peptide
US-10-352-786-1366

Query Match 38.8%; Score 26; DB 4; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIG 11
| | | | |
| | | | |
Db 1 EYVTLRCQLG 10

Search completed: January 20, 2006, 19:45:41
Job time : 44.2692 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2006 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 : Search time 4.84615 Seconds
(without alignments)
25.093 Million cell updates/sec

Title: US-09-662-293-5

Perfect score: 67

Sequence: 1 DEKNSPFCILGP 12

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

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2: /cnr2_6/prodata/1/pubppa/US07_NEW_PUB.pep:*
3: /cnr2_6/prodata/1/pubppa/US09_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	44.8	19	6	US-10-939-890-220
2	28	41.8	9	6	US-10-517-784-11
3	28	41.8	14	6	US-10-986-501-340
4	27	40.3	19	6	US-10-503-575-200
5	26	38.8	16	7	US-10-986-501-344
6	26	38.8	18	7	US-11-033-039-1313
7	26	38.8	13	6	US-10-503-575-163
8	24	35.8	13	6	US-10-511-559-965
9	24	35.8	13	6	US-10-511-559-966
10	24	35.8	13	6	US-10-511-559-967
11	24	35.8	13	6	US-10-511-559-968
12	24	35.8	16	7	US-10-467-657-8750
13	23	35.1	17	7	US-11-090-497-22
14	23	34.3	9	6	US-10-517-784-37
15	23	34.3	9	7	US-11-208-541-1
16	23	34.3	10	6	US-10-859-643-533
17	23	34.3	10	7	US-10-859-643-533
18	23	34.3	10	7	US-11-097-864-533
19	23	34.3	10	7	US-11-097-864-533
20	23	34.3	10	7	US-11-097-864-533
21	23	34.3	10	7	US-11-097-864-533
22	23	34.3	13	6	US-10-511-559-883
23	23	34.3	13	6	US-10-511-559-884
24	23	34.3	14	6	US-10-939-890-79
25	23	34.3	15	7	US-11-054-515-2765

26	23	34.3	16	6	US-10-939-890-349	Sequence 349, App
27	23	34.3	16	6	US-10-939-890-825	Sequence 825, App
28	23	34.3	17	6	US-10-834-397-207	Sequence 207, App
29	23	34.3	19	6	US-10-939-890-218	Sequence 218, App
30	23	34.3	19	6	US-10-939-890-221	Sequence 221, App
31	23	34.3	19	6	US-10-939-890-348	Sequence 348, App
32	23	34.3	19	6	US-10-939-890-824	Sequence 824, App
33	23	34.3	20	7	US-11-022-562-188	Sequence 188, App
34	23	34.3	20	7	US-11-022-562-189	Sequence 189, App
35	22	32.8	9	6	US-10-982-145-38	Sequence 38, App1
36	22	32.8	9	6	US-10-982-145-57	Sequence 57, App1
37	22	32.8	9	6	US-10-982-145-58	Sequence 58, App1
38	22	32.8	9	6	US-10-982-145-63	Sequence 63, App1
39	22	32.8	9	6	US-10-982-145-64	Sequence 64, App1
40	22	32.8	11	6	US-10-873-427A-24	Sequence 24, App1
41	22	32.8	12	6	US-10-873-427A-23	Sequence 23, App1
42	22	32.8	13	6	US-10-511-559-892	Sequence 892, App1
43	22	32.8	13	6	US-10-873-427A-20	Sequence 20, App1
44	22	32.8	13	6	US-10-970-847-21	Sequence 21, App1
45	22	32.8	14	6	US-10-939-890-66	Sequence 66, App1
46	22	32.8	14	6	US-10-873-427A-19	Sequence 19, App1
47	22	32.8	14	7	US-11-198-847-278	Sequence 278, App1
48	22	32.8	14	7	US-11-112-784-79	Sequence 79, App1
49	22	32.8	15	6	US-10-939-890-199	Sequence 199, App
50	22	32.8	15	6	US-10-467-657-8630	Sequence 8630, App
51	22	32.8	15	6	US-10-467-657-8789	Sequence 8789, App
52	22	32.8	15	6	US-10-873-427A-14	Sequence 14, App1
53	22	32.8	16	6	US-10-873-427A-13	Sequence 13, App1
54	22	32.8	16	6	US-10-962-145C-9	Sequence 9, App1
55	22	32.8	17	6	US-10-969-314-28	Sequence 28, App1
56	22	32.8	17	6	US-10-873-427A-12	Sequence 12, App1
57	22	32.8	18	7	US-11-106-415-221	Sequence 221, App1
58	22	32.8	18	7	US-11-106-415-238	Sequence 238, App1
59	22	32.8	20	7	US-11-106-415-188	Sequence 188, App1
60	22	32.8	20	7	US-11-106-415-214	Sequence 214, App
61	22	32.8	20	7	US-11-106-415-286	Sequence 286, App
62	22	32.8	20	7	US-10-467-657-8643	Sequence 8643, App
63	22	32.8	21	31.3	US-10-859-643-570	Sequence 570, App1
64	21	31.3	9	7	US-11-097-912-570	Sequence 570, App1
65	21	31.3	9	7	US-11-097-912-570	Sequence 570, App1
66	21	31.3	10	6	US-10-859-643-167	Sequence 167, App
67	21	31.3	10	7	US-11-097-912-167	Sequence 167, App
68	21	31.3	10	7	US-11-119-098-38	Sequence 38, App1
69	21	31.3	12	7	US-11-016-706-45	Sequence 45, App1
70	21	31.3	13	6	US-10-511-559-272	Sequence 272, App
71	21	31.3	13	6	US-10-511-559-272	Sequence 272, App
72	21	31.3	13	6	US-10-511-559-274	Sequence 274, App
73	21	31.3	13	6	US-10-511-559-274	Sequence 274, App
74	21	31.3	13	6	US-10-511-559-849	Sequence 849, App
75	21	31.3	13	7	US-11-016-706-7	Sequence 7, App1
76	21	31.3	14	6	US-10-929-988-451	Sequence 451, App1
77	21	31.3	15	7	US-11-106-903-234	Sequence 234, App
78	21	31.3	15	7	US-11-145-702-45	Sequence 45, App1
79	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
80	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
81	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
82	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
83	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
84	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
85	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
86	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
87	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
88	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
89	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
90	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
91	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
92	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
93	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
94	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
95	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
96	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
97	21	31.3	15	7	US-11-041-893-275	Sequence 275, App
98	21	31.3	15	7	US-11-041-893-275	Sequence 275, App

99 20 29.9 9 7 US-11-045-024-2802
100 20 29.9 9 7 US-11-045-024-6167

Sequence 2802, Ap
Sequence 6167, Ap

ALIGNMENTS

RESULT 1
US-10-939-890-220

/ Sequence 220, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:

/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappa, Palanappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddi
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 220
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-220

Query Match 44.8%; Score 30; DB 6; Length 19;
Best Local Similarity 100.0%; Pred. No. 7.9;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NSPEC 8
| | | | |

Db 12 NSPEC 16

RESULT 2
US-10-517-784-11

/ Sequence 11, Application US/10517784
/ Publication No. US20060003315A1
/ GENERAL INFORMATION:

/ APPLICANT: GROSS, Gideon
/ APPLICANT: MARGALIT, Alon
/ TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
/ TITLE OF INVENTION: PEPTIDE EPITOPES

/ FILE REFERENCE: GAVISH-004 US
/ CURRENT APPLICATION NUMBER: US/10/517,784
/ CURRENT FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: US 60/388,273
/ PRIOR FILING DATE: 2002-06-12
/ PRIOR APPLICATION NUMBER: PCT/IL03/00501
/ PRIOR FILING DATE: 2003-06-12
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 11
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic
US-10-517-784-11

Query Match 41.8%; Score 28; DB 6; Length 9;
Best Local Similarity 100.0%; Pred. No. 5.5e+04;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIIG 11
| | | | |

Db 4 ECIIG 8

RESULT 3
US-10-986-501-340

/ Sequence 340, Application US/10986501
/ Publication No. US20050244845A1
/ GENERAL INFORMATION:

/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2C1
/ CURRENT APPLICATION NUMBER: US/10/986,501
/ CURRENT FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: US/10/621,363
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 340
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-340

Query Match 41.8%; Score 28; DB 6; Length 14;
Best Local Similarity 55.6%; Pred. No. 14;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 3 KNSFECIG 11
| | | | |

Db 3 KQDLHCIG 11


```
RESULT 4
US-10-503-575-200
/ Sequence 200, Application US/10503575
/ Publication No. US20050244823A1
/ GENERAL INFORMATION:
/ APPLICANT: Drifffhout, Jan Wouter
/ APPLICANT: van Veele, Petrus Antonius
/ APPLICANT: Koning, Frits
/ TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
/ FILE REFERENCE: 2799/72843-PCT-US
/ CURRENT APPLICATION NUMBER: US/10/503,575
/ PRIOR FILING DATE: 2004-08-04
/ PRIOR APPLICATION NUMBER: PCT/NL03/00077
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: EP 02075456.0
/ PRIOR FILING DATE: 2002-02-04
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 200
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-503-575-200

Query Match      40.3%; Score 27; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 29;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECIFIC 12
DB 12 SYCLCKP 19

RESULT 5
US-10-986-501-344
/ Sequence 344, Application US/10986501
/ Publication No. US20050244845A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: 90 Human Secreted Proteins
/ FILE REFERENCE: P2013P2C1
/ CURRENT APPLICATION NUMBER: US/10/986,501
/ PRIOR FILING DATE: 2004-11-12
/ PRIOR APPLICATION NUMBER: US/10/621,363
/ PRIOR FILING DATE: 2003-07-18
/ PRIOR APPLICATION NUMBER: 09/969,730
/ PRIOR FILING DATE: 2001-10-06
/ PRIOR APPLICATION NUMBER: 09/774,639
/ PRIOR FILING DATE: 2001-02-01
/ PRIOR APPLICATION NUMBER: 60/238,291
/ PRIOR FILING DATE: 2000-10-06
/ PRIOR APPLICATION NUMBER: 09/244,112
/ PRIOR FILING DATE: 1999-02-04
/ PRIOR APPLICATION NUMBER: PCT/US98/16235
/ PRIOR FILING DATE: 1998-08-04
/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See file Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 373
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 344
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-344
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Query Match      38.8%; Score 26; DB 6; Length 16;
Best Local Similarity 50.0%; Pred. No. 38;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPECI 12
DB 4 KTRPACILVP 13

RESULT 6
US-11-033-039-1313
/ Sequence 1313, Application US/11033039
/ Publication No. US20060002947A1
/ GENERAL INFORMATION:
/ APPLICANT: HUMPHREYS, ROBERT
/ APPLICANT: XU, MINZHEN
/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
/ FILE REFERENCE: RH-2017US01
/ CURRENT APPLICATION NUMBER: US/11/033,039
/ PRIOR FILING DATE: 2005-01-11
/ PRIOR APPLICATION NUMBER: 10/245,871
/ PRIOR FILING DATE: 2002-09-17
/ PRIOR APPLICATION NUMBER: 10/197,000
/ PRIOR FILING DATE: 2002-07-17
/ PRIOR APPLICATION NUMBER: 09/396,813
/ PRIOR FILING DATE: 1999-09-14
/ NUMBER OF SEQ ID NOS: 1452
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 1313
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ NAME/KEY: MOD_RES
/ LOCATION: (5)..(5)
/ OTHER INFORMATION: Ava
US-11-033-039-1313

Query Match      38.8%; Score 26; DB 7; Length 18;
Best Local Similarity 33.3%; Pred. No. 43;
Matches 4; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSPECI 12
DB 6 DIARTPKVIVIP 17

RESULT 7
US-10-503-575-163
/ Sequence 163, Application US/10503575
/ Publication No. US20050244823A1
/ GENERAL INFORMATION:
/ APPLICANT: Drifffhout, Jan Wouter
/ APPLICANT: van Veele, Petrus Antonius
/ APPLICANT: Koning, Frits
/ TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
/ FILE REFERENCE: 2799/72843-PCT-US
/ CURRENT APPLICATION NUMBER: US/10/503,575
/ PRIOR FILING DATE: 2004-08-04
/ PRIOR APPLICATION NUMBER: PCT/NL03/00077
/ PRIOR FILING DATE: 2003-02-04
/ PRIOR APPLICATION NUMBER: EP 02075456.0
/ PRIOR FILING DATE: 2002-02-04
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 163
/ LENGTH: 19
/ TYPE: PRT
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/ ORGANISM: Homo sapiens
US-10-503-575-163

Query Match 38.8%; Score 26; DB 6; Length 19;
Best Local Similarity 33.3%; Pred. No. 45;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 1 DEKNSPECILGP 12
| : : : :
Db 4 DDINGQSLXGP 15

RESULT 8
US-10-511-559-965

/ Sequence 965, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 965

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Potential Epitope of human Factor VIII

US-10-511-559-965

Query Match 35.8%; Score 24; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECLIG 11
| : : : :
Db 7 ECLIG 11

RESULT 9
US-10-511-559-966

/ Sequence 966, Application US/10511559

/ Publication No. US20050256304A1

/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 966

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-966

Query Match 35.8%; Score 24; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECLIG 11
| : : : :
Db 6 ECLIG 10

RESULT 10
US-10-511-559-967

/ Sequence 967, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 967

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Potential Epitope of human Factor VIII

US-10-511-559-967

Query Match 35.8%; Score 24; DB 6; Length 13;
Best Local Similarity 60.0%; Pred. No. 74;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECLIG 11
| : : : :
Db 4 ECLIG 8

RESULT 11
US-10-511-559-968

/ Sequence 968, Application US/10511559

/ Publication No. US20050256304A1

/ GENERAL INFORMATION:

/ APPLICANT: JONES, Tim

/ APPLICANT: BAKER, Matthew

/ APPLICANT: CARR, Francis, J.

/ TITLE OF INVENTION: MODIFIED FACTOR VIII

/ FILE REFERENCE: MER-133

/ CURRENT APPLICATION NUMBER: US/10/511,559

/ CURRENT FILING DATE: 2004-10-15

/ PRIOR APPLICATION NUMBER: PCT/EP03/04063

/ PRIOR FILING DATE: 2003-04-17

/ PRIOR APPLICATION NUMBER: EP 02008712.8

/ PRIOR FILING DATE: 2002-04-18

/ PRIOR APPLICATION NUMBER: EP 03006554.4

/ PRIOR FILING DATE: 2003-03-24

/ NUMBER OF SEQ ID NOS: 1147

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 968

/ LENGTH: 13

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Potential Epitope of human Factor VIII
 US-10-511-559-968

Query Match 35.8%; Score 24; DB 6; Length 13;
 Best Local Similarity 60.0%; Pred. No. 74;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECLIG 11
 DB 1 ECLIG 5

RESULT 12
 US-10-467-657-8750
 Sequence 8750, Application US/10467657
 Publication No. US20050260581A1
 GENERAL INFORMATION:
 APPLICANT: CHIRON SPA
 APPLICANT: FONTANA Maria Rita
 APPLICANT: PIZZA Mariagrazia
 APPLICANT: MASIGNANI Vega
 APPLICANT: MONACI Elisabetta
 TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
 FILE REFERENCE:
 CURRENT APPLICATION NUMBER: US/10/467,657
 CURRENT FILING DATE: 2003-08-11
 PRIOR APPLICATION NUMBER: GB-0103424.8
 PRIOR FILING DATE: 2001-02-12
 NUMBER OF SEQ ID NOS: 9218
 SOFTWARE: SeqMn99, version 1.04
 SEQ ID NO 8750
 LENGTH: 16
 TYPE: PRT
 ORGANISM: Neisseria gonorrhoeae
 US-10-467-657-8750

Query Match 35.8%; Score 24; DB 6; Length 16;
 Best Local Similarity 42.9%; Pred. No. 91;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIL 10
 DB 1 NDFACLI 7

RESULT 13
 US-11-090-497-22
 Sequence 22, Application US/11090497
 Publication No. US2005028263A1
 GENERAL INFORMATION:
 APPLICANT: Large Scale Biology Corporation
 TITLE OF INVENTION: FLEXIBLE VACCINE ASSEMBLY AND VACCINE DELIVERY PLATFORM
 FILE REFERENCE: N8630
 CURRENT APPLICATION NUMBER: US/11/090,497
 CURRENT FILING DATE: 2005-03-25
 PRIOR APPLICATION NUMBER: 60/386,921
 PRIOR FILING DATE: 2002-06-07
 PRIOR APPLICATION NUMBER: 60/407,795
 PRIOR FILING DATE: 2002-09-03
 NUMBER OF SEQ ID NOS: 22
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 22
 LENGTH: 17
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Created from Seq ID No: 10 inserted into TMV
 US-11-090-497-22

Query Match 35.1%; Score 23.5; DB 7; Length 17;
 Best Local Similarity 46.2%; Pred. No. 1.2e+02;

Matches 6; Conservative 2; Mismatches 4; Indels 1; Gaps 1;

QY 1 DERNS-FECLIGP 12
 DB 3 DERNSPFTTLGAP 15

RESULT 14
 US-10-517-784-37
 Sequence 37, Application US/10517784
 Publication No. US20060003315A1
 GENERAL INFORMATION:
 APPLICANT: GROSS, Gladeon
 APPLICANT: MARGALIT, Alon
 TITLE OF INVENTION: MEMBRANE-ANCHORED BETA-2 MICROGLOBULIN COVALENTLY LINKED TO MHC
 FILE REFERENCE: GAVISH-004 US
 CURRENT APPLICATION NUMBER: US/10/517,784
 CURRENT FILING DATE: 2004-12-13
 PRIOR APPLICATION NUMBER: US 60/388,273
 PRIOR FILING DATE: 2002-06-12
 PRIOR APPLICATION NUMBER: PCT/IL03/00501
 PRIOR FILING DATE: 2003-06-12
 NUMBER OF SEQ ID NOS: 64
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 37
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Synthetic
 US-10-517-784-37

Query Match 34.3%; Score 23; DB 6; Length 9;
 Best Local Similarity 80.0%; Pred. No. 5.5e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSPE 7
 DB 4 RNSPE 8

RESULT 15
 US-11-208-541-1
 Sequence 1, Application US/11208541
 Publication No. US20050287160A1
 GENERAL INFORMATION:
 APPLICANT: ITOH, Kyogo
 APPLICANT: HARADA, Mamoru
 TITLE OF INVENTION: HLA-A24 Binding Peptides of Enhancer of Zeste Homolog 2
 FILE REFERENCE: 541818
 CURRENT APPLICATION NUMBER: US/11/208,541
 CURRENT FILING DATE: 2005-08-23
 NUMBER OF SEQ ID NOS: 18
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 1
 LENGTH: 9
 TYPE: PRT
 ORGANISM: Artificial
 FEATURE:
 OTHER INFORMATION: EZH2 291-299
 US-11-208-541-1

Query Match 34.3%; Score 23; DB 7; Length 9;
 Best Local Similarity 42.9%; Pred. No. 5.5e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 FECLIGP 12
 DB 2 YDCFLHP 8

RESULT 16

```
US-10-859-643-533
; Sequence 533, Application US/10859643
; Publication No. US2006000293A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 533
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-533
```

```
Query Match      34.3% Score 23; DB 6; Length 10;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 EKNSPECIL 10
      :|||:|
      2 QKNVDHCLL 10

Db

RESULT 17
US-10-859-643-635
; Sequence 635, Application US/10859643
; Publication No. US2006000293A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; PRIOR FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-635
```

```
Query Match      34.3% Score 23; DB 6; Length 10;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 EKNSPECIL 10
      :|||:|
      2 QKNVDHCLL 10

Db

RESULT 18
US-11-097-864-533
```

```
; Sequence 533, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 533
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-533
```

```
Query Match      34.3% Score 23; DB 7; Length 10;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 EKNSPECIL 10
      :|||:|
      2 QKNVDHCLL 10

Db

RESULT 19
US-11-097-864-635
; Sequence 635, Application US/11097864
; Publication No. US20050265924A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Eld, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
; TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
; FILE REFERENCE: 511582006205
; CURRENT APPLICATION NUMBER: US/11/097,864
; PRIOR FILING DATE: 2005-04-01
; PRIOR APPLICATION NUMBER: US 10/062,109
; PRIOR FILING DATE: 2002-01-31
; PRIOR APPLICATION NUMBER: US 10/005,480
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 635
; LENGTH: 10
; TYPE: PRT
; ORGANISM: Homo Sapien
US-11-097-864-635
```

```
Query Match      34.3% Score 23; DB 7; Length 10;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      2 EKNSPECIL 10
      :|||:|
      2 QKNVDHCLL 10

Db

RESULT 20
```

US-11-097-912-533
/ Sequence 533, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bld, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P108
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ PRIOR FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 533
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-533

Query Match 34.3%; Score 23; DB 7; Length 10;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKNSPECIL 10
Db 2 QKNVDHCLL 10

RESULT 21
US-11-097-912-635
/ Sequence 635, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Challita-Bld, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P108
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ PRIOR FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 635
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-635

Query Match 34.3%; Score 23; DB 7; Length 10;
Best Local Similarity 44.4%; Pred. No. 88;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy 2 EKNSPECIL 10
Db 2 QKNVDHCLL 10

RESULT 22
US-10-511-559-883
/ Sequence 883, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CAR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ PRIOR FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 883
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-883

Query Match 34.3%; Score 23; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 11e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KNSFEC 8
Db 7 KDBFDC 12

RESULT 23
US-10-511-559-884
/ Sequence 884, Application US/10511559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CAR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ PRIOR FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 884
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-884

Query Match 34.3%; Score 23; DB 6; Length 13;
Best Local Similarity 50.0%; Pred. No. 11e+02;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 KNSFEC 8
Db 7 KDBFDC 12

```
RESULT 24
US-10-939-890-79
; Sequence 79, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappa, Palanappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylla
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 79
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
; US-10-939-890-79

Query Match      34.3% Score 23; DB 6; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.2e+02;
Matches 3; Conservative 4; Mismatches 0; Indels 0; Gaps 0;

QY      4 NSPECIL 10
       ::|||:
Db      7 DAMECIM 13

RESULT 25
US-11-054-515-2765
; Sequence 2765, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
```

```
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2765
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-11-054-515-2765

Query Match      34.3% Score 23; DB 7; Length 15;
Best Local Similarity 80.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      3 KNSPE 7
       |||:
Db      10 KNAPE 14

RESULT 26
US-10-939-890-349
; Sequence 349, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappa, Palanappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylla
; APPLICANT: Ramalingam, Kondareddiar
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; CURRENT FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 349
```

LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURES:
OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-349

Query Match 34.3%; Score 23; DB 6; Length 16;

Best Local Similarity 30.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFCLIG 11
Db 4 EEDWYCMIG 13

RESULT 27
US-10-939-890-825

Sequence 825, Application US/10939890
Publication No. US20050250700A1

GENERAL INFORMATION:

APPLICANT: Sato, Aaron K.

APPLICANT: Sexton, Daniel J.

APPLICANT: Dransfield, Daniel T.

APPLICANT: Ladner, Robert C.

APPLICANT: Arbogast, Christophe

APPLICANT: Bussac, Philippe

APPLICANT: Fan, Hong

APPLICANT: Khurana, Sudha

APPLICANT: Kinder, Karen E.

APPLICANT: Marinelli, Edmund R.

APPLICANT: Nanjappa, Palanappa

APPLICANT: Nunn, Adrian D.

APPLICANT: Pillai, Radhakrishna

APPLICANT: Pochon, Sibylle

APPLICANT: Ramalingam, Kondaredtalar

APPLICANT: Shrivastava, Ajay

APPLICANT: Song, Bo

APPLICANT: Swenson, Rolf E.

APPLICANT: Von Wronski, Mathew A.

TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES

FILE REFERENCE: D0617.70014US00

CURRENT APPLICATION NUMBER: US/10/939,890

PRIOR FILING DATE: 2004-09-13

PRIOR APPLICATION NUMBER: US 10/661,156

PRIOR FILING DATE: 2003-09-11

PRIOR APPLICATION NUMBER: US 10/382,082

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: PCT/US03/06731

PRIOR FILING DATE: 2003-03-03

PRIOR APPLICATION NUMBER: US 60/440,411

PRIOR FILING DATE: 2003-01-15

PRIOR APPLICATION NUMBER: US 60/360,851

PRIOR FILING DATE: 2002-03-01

NUMBER OF SEQ ID NOS: 883

SOFTWARE: PseBseq for Windows Version 4.0

SEQ ID NO 825

LENGTH: 16

TYPE: PRT

ORGANISM: Artificial sequence

FEATURE:

OTHER INFORMATION: Synthetic peptide

NAME/KEY: MOD_RES

LOCATION: (1)-(1)

OTHER INFORMATION: ACETYLATION

FEATURE:

NAME/KEY: MOD_RES

LOCATION: (16)-(16)

OTHER INFORMATION: Lys residue modified with biotin JJ spacer linker

US-10-939-890-825

Query Match 34.3%; Score 23; DB 6; Length 16;

Best Local Similarity 30.0%; Pred. No. 1.4e+02; Indels 0; Gaps 0;

Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFCLIG 11
Db 4 EEDWYCMIG 13

RESULT 28
US-10-834-397-207

Sequence 207, Application US/10834397
Publication No. US20060003334A1

GENERAL INFORMATION:

APPLICANT: Knappik, Achim

APPLICANT: Pack, Peter

APPLICANT: Lag, V1C

APPLICANT: Ge, Laming

APPLICANT: Moroney, Simon

APPLICANT: Plueckhuhn, Andreas

TITLE OF INVENTION: Protein/(poly)peptide libraries

NUMBER OF SEQUENCES: 373

CORRESPONDENCE ADDRESS:

ADDRESS: James F. Haley, Jr., Esq. c/o Fish & Neave

STREET: 1251 Avenue of the Americas

CITY: New York

STATE: New York

COUNTRY: USA

ZIP: 10021

COMPUTER READABLE FORM:

MEDIUM TYPE: floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/834,397

FILING DATE: 29-Apr-2004

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/490,324

FILING DATE: 24-Jan-2000

APPLICATION NUMBER: US/09/025,769

FILING DATE: 18-Feb-1998

APPLICATION NUMBER: EP 95 11 3021.0

FILING DATE: 18-AUG-1995

ATTORNEY/AGENT INFORMATION:

NAME: James F. Haley, Jr., Esq.

REGISTRATION NUMBER: 27,794

REFERENCE/DOCKET NUMBER: MORPHO/5

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)596-9000

TELEFAX: (212)596-9090

INFORMATION FOR SEQ ID NO: 207:

SEQUENCE CHARACTERISTICS:

LENGTH: 17 amino acids

TYPE: amino acid

STRANDEDNESS: <Unknown>

TOPOLOGY: linear

MOLECULE TYPE: protein

FRAGMENT TYPE: internal

SEQUENCE DESCRIPTION: SEQ ID NO: 207:

US-10-834-397-207

Query Match 34.3%; Score 23; DB 6; Length 17;

Best Local Similarity 80.0%; Pred. No. 1.5e+02;

Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7

Db 11 KNSFD 15

RESULT 29
US-10-939-890-218

Sequence 218, Application US/10939890

```
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladhner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buseat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palanippa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 218
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-221

Query Match          34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 221
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-221

Query Match          34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```



```
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 348
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: KDR or KDR/VEGF Complex Binding Polypeptide
US-10-939-890-348

Query Match          34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 30.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 EKNSPCTIG 11
Db      7 EBDWYCMIG 16

RESULT 32
US-10-939-890-824
/ Sequence 824, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Buesat, Philippe
/ APPLICANT: Ren, Hong
/ APPLICANT: Knutane, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappa, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Poehon, Sibylle
/ APPLICANT: Ramalingam, Kondaredtlar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Matthew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 824
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: ACETYLTATION
/ FEATURE:
```

```
/ NAME/KEY: MOD_RES
/ LOCATION: (19)..(19)
/ OTHER INFORMATION: Lys residue modified with Biotin JJ spacer linker
US-10-939-890-824

Query Match          34.3%; Score 23; DB 6; Length 19;
Best Local Similarity 30.0%; Pred. No. 1.7e+02;
Matches 3; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY      2 EKNSPCTIG 11
Db      7 EBDWYCMIG 16

RESULT 33
US-11-022-562-188
/ Sequence 188, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ FILE REFERENCE: DEN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 188
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-188

Query Match          34.3%; Score 23; DB 7; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      2 EKNSPCT 7
Db      13 EKNNYR 18

RESULT 34
US-11-022-562-189
/ Sequence 189, Application US/11022562
/ Publication No. US20050249742A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruprecht, Ruth M.
/ APPLICANT: Shisong, Jiang
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
/ FILE REFERENCE: DEN-043CN
/ CURRENT APPLICATION NUMBER: US/11/022,562
/ CURRENT FILING DATE: 2004-12-22
/ PRIOR APPLICATION NUMBER: PCT/US03/20322
/ PRIOR FILING DATE: 2003-06-27
/ PRIOR APPLICATION NUMBER: 60/392718
/ PRIOR FILING DATE: 2002-06-27
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 189
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Simian Immunodeficiency Virus
US-11-022-562-189

Query Match          34.3%; Score 23; DB 7; Length 20;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
```

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKSPFE 7
|||:
Db 3 EKSMYR 8

RESULT 35
US-10-982-145-38
Sequence 38, Application US/10982145
Publication No. US20050272645A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Maring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins: Antiviral and
FILE REFERENCE: UCLA-001CIP2
CURRENT APPLICATION NUMBER: US/10/982,145
PRIOR FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US03/14106
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 10/141,645
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US02/12353
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/284,855
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 38
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: generated by replacement of variants in consensus
US-10-982-145-38

Query Match 32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11
|:|:
Db 4 CVLG 7

RESULT 36
US-10-982-145-50
Sequence 50, Application US/10982145
Publication No. US20050272645A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Maring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins: Antiviral and
FILE REFERENCE: UCLA-001CIP2
CURRENT APPLICATION NUMBER: US/10/982,145
PRIOR FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US03/14106
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 10/141,645
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US02/12353
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/284,855
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 50
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: generated by replacement of variants in consensus
US-10-982-145-50

Query Match 32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11
|:|:
Db 4 CVLG 7

RESULT 37
US-10-982-145-57
Sequence 57, Application US/10982145
Publication No. US20050272645A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Maring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins: Antiviral and
FILE REFERENCE: UCLA-001CIP2
CURRENT APPLICATION NUMBER: US/10/982,145
PRIOR FILING DATE: 2004-11-05
PRIOR APPLICATION NUMBER: US03/14106
PRIOR FILING DATE: 2003-05-06
PRIOR APPLICATION NUMBER: 10/141,645
PRIOR FILING DATE: 2002-05-06
PRIOR APPLICATION NUMBER: US02/12353
PRIOR FILING DATE: 2002-04-18
PRIOR APPLICATION NUMBER: 60/284,855
NUMBER OF SEQ ID NOS: 135
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 57
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: generated by replacement of variants in consensus
US-10-982-145-57

Query Match 32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11
|:|:
Db 4 CVLG 7

RESULT 38
US-10-982-145-58
Sequence 58, Application US/10982145
Publication No. US20050272645A1
GENERAL INFORMATION:
APPLICANT: Robert Lehrer
APPLICANT: Alan Maring
APPLICANT: Alexander Cole
APPLICANT: Teresa Hong
TITLE OF INVENTION: Retrocyclins: Antiviral and
FILE REFERENCE: UCLA-001CIP2
CURRENT APPLICATION NUMBER: US/10/982,145

```
/ CURRENT FILING DATE: 2004-11-05
/ PRIOR APPLICATION NUMBER: US03/14106
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: 10/141,645
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US02/12353
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: 60/284,855
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 58
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: generated by replacement of variants in consensus
/ US-10-982-145-58
```

```
Query Match      32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CILG 11
      |||
Db      4 CVLG 7
```

```
RESULT 39
US-10-982-145-63
/ Sequence 63, Application US/10982145
/ Publication No. US20050272645A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert Lehrer
/ APPLICANT: Alan Waring
/ APPLICANT: Alexander Cole
/ APPLICANT: Teresa Hong
/ TITLE OF INVENTION: Retrocyclins: Antiviral and
/ TITLE OF INVENTION: Antimicrobial Peptides
/ FILE REFERENCE: UCLA-001CIP2
/ CURRENT APPLICATION NUMBER: US/10/982,145
/ PRIOR APPLICATION NUMBER: US03/14106
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: 10/141,645
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US02/12353
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: 60/284,855
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 63
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: generated by replacement of variants in consensus
/ US-10-982-145-63
```

```
Query Match      32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CILG 11
      |||
Db      4 CVLG 7
```

```
RESULT 40
US-10-982-145-64
```

```
/ Sequence 64, Application US/10982145
/ Publication No. US20050272645A1
/ GENERAL INFORMATION:
/ APPLICANT: Robert Lehrer
/ APPLICANT: Alan Waring
/ APPLICANT: Alexander Cole
/ APPLICANT: Teresa Hong
/ TITLE OF INVENTION: Retrocyclins: Antiviral and
/ TITLE OF INVENTION: Antimicrobial Peptides
/ FILE REFERENCE: UCLA-001CIP2
/ CURRENT APPLICATION NUMBER: US/10/982,145
/ PRIOR APPLICATION NUMBER: US03/14106
/ PRIOR FILING DATE: 2003-05-06
/ PRIOR APPLICATION NUMBER: 10/141,645
/ PRIOR FILING DATE: 2002-05-06
/ PRIOR APPLICATION NUMBER: US02/12353
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: 60/284,855
/ PRIOR FILING DATE: 2001-04-18
/ NUMBER OF SEQ ID NOS: 135
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 64
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: generated by replacement of variants in consensus
/ US-10-982-145-64
```

```
Query Match      32.8%; Score 22; DB 6; Length 9;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      8 CILG 11
      |||
Db      4 CVLG 7
```

```
RESULT 41
US-10-873-427A-24
/ Sequence 24, Application US/10873427A
/ Publication No. US20050281914A1
/ GENERAL INFORMATION:
/ APPLICANT: STEELE, JAMES L.
/ APPLICANT: BRODBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
/ TITLE OF INVENTION: AND PEPO3
/ FILE REFERENCE: WARP:009US
/ CURRENT APPLICATION NUMBER: US/10/873,427A
/ PRIOR FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: 60/452,257
/ PRIOR FILING DATE: 2003-06-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: Patencin Ver. 2.1
/ SEQ ID NO 24
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ US-10-873-427A-24
```

```
Query Match      32.8%; Score 22; DB 6; Length 11;
Best Local Similarity 66.7%; Pred. No. 1.5e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      7 ECVLGP 12
      |||
Db      2 ECVLGP 7
```

RESULT 42
US-10-873-427A-23
; Sequence 23, Application US/10873427A
; Publication No. US20050281914A1
; GENERAL INFORMATION:
; APPLICANT: STEELE, JAMES L.
; APPLICANT: BROADBENT, JEFFREY R.
; APPLICANT: SRIDHAR, VIDYA R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
; TITLE OF INVENTION: AND PEPO3
; FILE REFERENCE: WARP:009US
; CURRENT APPLICATION NUMBER: US/10/873,427A
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/452,257
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 23
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-23

Query Match 32.8%; Score 22; DB 6; Length 12;
Best Local Similarity 66.7%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
| : |||
DB 3 EPIVIGP 8

RESULT 43
US-10-511-559-892
; Sequence 892, Application US/10511559
; Publication No. US20050256304A1
; GENERAL INFORMATION:
; APPLICANT: JONES, Tim
; APPLICANT: BAKER, Matthew
; APPLICANT: CARR, Francis, J.
; TITLE OF INVENTION: MODIFIED FACTOR VIII
; FILE REFERENCE: MER-133
; CURRENT APPLICATION NUMBER: US/10/511,559
; CURRENT FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: PCT/EP03/04063
; PRIOR FILING DATE: 2003-04-17
; PRIOR APPLICATION NUMBER: EP 02008712.8
; PRIOR FILING DATE: 2002-04-18
; PRIOR APPLICATION NUMBER: EP 03006554.4
; PRIOR FILING DATE: 2003-03-24
; NUMBER OF SEQ ID NOS: 1147
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 892
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-892

Query Match 32.8%; Score 22; DB 6; Length 13;
Best Local Similarity 36.4%; Pred. No. 1.8e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 2 EKNSPECTIGP 12
| : |||
DB 2 EKDVHSGIIGP 12

RESULT 44
US-10-873-427A-20
; Sequence 20, Application US/10873427A
; Publication No. US20050281914A1
; GENERAL INFORMATION:
; APPLICANT: STEELE, JAMES L.
; APPLICANT: BROADBENT, JEFFREY R.
; APPLICANT: SRIDHAR, VIDYA R.
; TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
; TITLE OF INVENTION: AND PEPO3
; FILE REFERENCE: WARP:009US
; CURRENT APPLICATION NUMBER: US/10/873,427A
; CURRENT FILING DATE: 2004-06-21
; PRIOR APPLICATION NUMBER: 60/452,257
; PRIOR FILING DATE: 2003-06-20
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-20

Query Match 32.8%; Score 22; DB 6; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.8e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
| : |||
DB 2 EPIVIGP 7

RESULT 45
US-10-970-847-21
; Sequence 21, Application US/10970847
; Publication No. US2006002854A1
; GENERAL INFORMATION:
; APPLICANT: Hanahan, Douglas
; APPLICANT: Rucslawski, Erkki
; TITLE OF INVENTION: MOLECULES THAT SELECTIVELY HOME TO
; TITLE OF INVENTION: VASCULATURE OF PRE-MALIGNANT DYSPLASTIC LESIONS OR
; FILE REFERENCE: 66821-311
; CURRENT APPLICATION NUMBER: US/10/970,847
; CURRENT FILING DATE: 2004-10-20
; PRIOR APPLICATION NUMBER: 60/513,407
; PRIOR FILING DATE: 2003-10-21
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 21
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic construct
US-10-970-847-21

Query Match 32.8%; Score 22; DB 6; Length 13;
Best Local Similarity 75.0%; Pred. No. 1.8e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CIIIG 11
| : |||
DB 5 CIIIG 8

RESULT 46
US-10-939-890-66
; Sequence 66, Application US/10939890

```

/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Kourana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappa, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylla
/ APPLICANT: Ramalingam, Kondareddi
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Matthew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 66
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
/ US-10-939-890-66

```

```

Query Match      32.8%; Score 22; DB 6; Length 14;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

```

```

QY      7 ECIIG 11
       :|||
Db      10 KCIIG 14

```

```

RESULT 47
US-10-873-427A-19
/ Sequence 19, Application US/10873427A
/ Publication No. US20050281914A1
/ GENERAL INFORMATION:
/ APPLICANT: STEEL, JAMES L.
/ APPLICANT: BROEDBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEPO2
/ TITLE OF INVENTION: AND PEPO3
/ FILE REFERENCE: WARF.009US
/ CURRENT APPLICATION NUMBER: US/10/873,427A
/ PRIOR FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: 60/452,257
/ PRIOR FILING DATE: 2003-06-20
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 19
/ LENGTH: 14

```

```

/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
/ OTHER INFORMATION: Peptide
/ US-10-873-427A-19

```

```

Query Match      32.8%; Score 22; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 1.9e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      7 ECIIGP 12
       :|||
Db      3 EPIIGP 8

```

```

RESULT 48
US-11-198-847-278
/ Sequence 278, Application US/11198847
/ Publication No. US20050271589A1
/ GENERAL INFORMATION:
/ APPLICANT: University of Utah Research Foundation
/ APPLICANT: Cognetix, Inc.
/ APPLICANT: Jones, Robert M.
/ APPLICANT: Garrett, James E.
/ APPLICANT: Watkins, Maren
/ APPLICANT: Olivera, Baldomero M.
/ TITLE OF INVENTION: B-Superfamily Conotoxins
/ FILE REFERENCE: 2314-296
/ CURRENT APPLICATION NUMBER: US/11/198,847
/ PRIOR FILING DATE: 2005-08-08
/ PRIOR APPLICATION NUMBER: US 10/838,226
/ PRIOR FILING DATE: 2004-05-05
/ PRIOR APPLICATION NUMBER: US 10/058,053
/ PRIOR FILING DATE: 2000-01-29
/ PRIOR APPLICATION NUMBER: US 60/264323
/ PRIOR FILING DATE: 2001-01-29
/ NUMBER OF SEQ ID NOS: 340
/ SOFTWARE: PatentIn version 3.0
/ SEQ ID NO 278
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Conus vexillum
/ US-11-198-847-278

```

```

Query Match      32.8%; Score 22; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.9e+02;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

```

```

QY      6 EECIIGP 12
       :|||
Db      1 FCCIFAP 7

```

```

RESULT 49
US-11-112-784-79
/ Sequence 79, Application US/11112784
/ Publication No. US20050287554A1
/ GENERAL INFORMATION:
/ APPLICANT: Archambault, Jacques
/ TITLE OF INVENTION: Regions of Papilloma Virus E1 Helicase Involved in E1
/ TITLE OF INVENTION: Oligomerization
/ FILE REFERENCE: 13/069-1-D1
/ CURRENT APPLICATION NUMBER: US/11/112,784
/ PRIOR FILING DATE: 2005-04-22
/ PRIOR APPLICATION NUMBER: US/10/339,268
/ PRIOR FILING DATE: 2003-01-09
/ PRIOR APPLICATION NUMBER: US 60/093,626
/ PRIOR FILING DATE: 1998-07-21
/ NUMBER OF SEQ ID NOS: 79
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 79
/ LENGTH: 14

```

```
/ TYPE: PRT
/ ORGANISM: C-terminal B1
US-11-112-784-79

Query Match          32.8%; Score 22; DB 7; Length 14;
Best Local Similarity 42.9%; Pred. No. 1.9e+02;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 SPECIFIC 11
      :|:|:|
Db      2 AFRCPV 8

RESULT 50
US-10-939-890-199
/ Sequence 199, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen E.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddiar
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0617.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ CURRENT FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 199
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-199

Query Match          32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY      2 KNSPEC 8
      :|:|:|
Db      6 BKDHWC 12

RESULT 51
US-10-467-657-8690
/ Sequence 8690, Application US/10467657

/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: PONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 8690
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8690

Query Match          32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 44.4%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      3 KNSPEC 11
      :|:|:|
Db      1 KNRACFP 9

RESULT 52
US-10-467-657-8789
/ Sequence 8789, Application US/10467657
/ Publication No. US20050260581A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ APPLICANT: FONTANA Maria Rita
/ APPLICANT: PIZZA Mariagrazia
/ APPLICANT: MASIGNANI Vega
/ APPLICANT: MONACI Elisabetta
/ TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
/ FILE REFERENCE:
/ CURRENT APPLICATION NUMBER: US/10/467,657
/ CURRENT FILING DATE: 2003-08-11
/ PRIOR APPLICATION NUMBER: GB-0103424.8
/ PRIOR FILING DATE: 2001-02-12
/ NUMBER OF SEQ ID NOS: 9218
/ SOFTWARE: SeqWin99, version 1.04
/ SEQ ID NO 8789
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8789

Query Match          32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY      3 KNSPEC 8
      :|:|:|
Db      1 KNSGRC 6

RESULT 53
US-10-873-427A-14
/ Sequence 14, Application US/10873427A
/ Publication No. US20050281914A1
/ GENERAL INFORMATION:
/ APPLICANT: STERILE, JAMES L.
/ APPLICANT: BROADBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
/ TITLE OF INVENTION: AND PEP03
```

FILE REFERENCE: WARP:009US
CURRENT APPLICATION NUMBER: US/10/873,427A
CURRENT FILING DATE: 2004-06-21
PRIOR APPLICATION NUMBER: 60/452,257
PRIOR FILING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 14
LENGTH: 15
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-14

Query Match 32.8%; Score 22; DB 6; Length 15;
Best Local Similarity 66.7%; Pred. No. 2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
|:|
Db 1 EPVLGP 6

RESULT 54
US-10-873-427A-13
Sequence 13, Application US/10873427A
Publication No. US20050281914A1
GENERAL INFORMATION:
APPLICANT: STEELE, JAMES L.
APPLICANT: BROADBENT, JEFFREY R.
APPLICANT: SRIDHAR, VIDYA R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
FILE REFERENCE: WARP:009US
CURRENT APPLICATION NUMBER: US/10/873,427A
CURRENT FILING DATE: 2004-06-21
PRIOR FILING DATE: 2003-06-20
PRIOR APPLICATION NUMBER: 60/452,257
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 13
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-13

Query Match 32.8%; Score 22; DB 6; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
|:|
Db 2 EPVLGP 7

RESULT 55
US-10-873-427A-18
Sequence 18, Application US/10873427A
Publication No. US20050281914A1
GENERAL INFORMATION:
APPLICANT: STEELE, JAMES L.
APPLICANT: BROADBENT, JEFFREY R.
APPLICANT: SRIDHAR, VIDYA R.
TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
FILE REFERENCE: WARP:009US
CURRENT APPLICATION NUMBER: US/10/873,427A
CURRENT FILING DATE: 2004-06-21

PRIOR APPLICATION NUMBER: 60/452,257
PRIOR FILING DATE: 2003-06-20
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 18
LENGTH: 16
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-18

Query Match 32.8%; Score 22; DB 6; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.2e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
|:|
Db 3 EPVLGP 8

RESULT 56
US-10-969-314-28
Sequence 28, Application US/10969314
Publication No. US20050249719A1
GENERAL INFORMATION:
APPLICANT: SHAN, LU
APPLICANT: BETHUNE, MICHAEL
APPLICANT: KHOSLA, CHAITAN
APPLICANT: GASS, JONATHAN
APPLICANT: FYLE, GAIL G.
APPLICANT: GRAY, GARY
APPLICANT: STROMBERGER, GREGG
TITLE OF INVENTION: ENZYME TREATMENT OF FOODSTUFFS FOR
FILE REFERENCE: STAN-361
CURRENT APPLICATION NUMBER: US/10/969,314
CURRENT FILING DATE: 2004-10-19
PRIOR APPLICATION NUMBER: 60/565,668
PRIOR FILING DATE: 2004-04-26
PRIOR APPLICATION NUMBER: 10/367,405
PRIOR FILING DATE: 2003-02-14
PRIOR APPLICATION NUMBER: 60/357,238
PRIOR FILING DATE: 2002-02-14
PRIOR APPLICATION NUMBER: 60/380,761
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 60/392,782
PRIOR FILING DATE: 2002-06-28
PRIOR APPLICATION NUMBER: 60/422,933
PRIOR FILING DATE: 2002-10-31
NUMBER OF SEQ ID NOS: 46
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 17
TYPE: PRT
ORGANISM: Trifolium aestivum
US-10-969-314-28

Query Match 32.8%; Score 22; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECIIGP 12
|:|
Db 3 EPVLGP 8

RESULT 57
US-10-873-427A-12
Sequence 12, Application US/10873427A
Publication No. US20050281914A1

```
/ GENERAL INFORMATION:
/ APPLICANT: STEELE, JAMES L.
/ APPLICANT: BROADBENT, JEFFREY R.
/ APPLICANT: SRIDHAR, VIDYA R.
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS INVOLVING ENDOPEPTIDASES PEP02
/ FILE REFERENCE: AND PEP03
/ CURRENT APPLICATION NUMBER: US/10/873,427A
/ PRIOR FILING DATE: 2004-06-21
/ PRIOR APPLICATION NUMBER: 60/452,257
/ NUMBER OF SEQ ID NOS: 33
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 17
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-873-427A-12

Query Match          32.8%; Score 22; DB 6; Length 17;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      7 ECILGP 12
Db      3 EYVLGP 8

RESULT 58
US-11-106-415-221
/ Sequence 221, Application US/11106415
/ Publication No. US20050287153A1
/ GENERAL INFORMATION:
/ APPLICANT: MARK S. DENNIS
/ TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 221
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-221

Query Match          32.8%; Score 22; DB 7; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CILGP 12
Db      13 CLWGP 17

RESULT 59
US-11-106-415-238
/ Sequence 238, Application US/11106415
/ Publication No. US20050287153A1
/ GENERAL INFORMATION:
/ APPLICANT: MARK S. DENNIS
/ TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
```

```
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 238
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-238

Query Match          32.8%; Score 22; DB 7; Length 18;
Best Local Similarity 60.0%; Pred. No. 2.5e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy      8 CILGP 12
Db      13 CLWGP 17

RESULT 60
US-10-962-145C-9
/ Sequence 9, Application US/10962145C
/ Publication No. US20050249754A1
/ GENERAL INFORMATION:
/ APPLICANT: DIEMOLDER, HELMUT
/ APPLICANT: JUNG, MARIA-CHRISTINA
/ TITLE OF INVENTION: CD4+ T-LYMPHOCYTE-SPECIFIC HEPATITIS C VIRUS EPITOPES
/ FILE REFERENCE: 085449-0167
/ CURRENT APPLICATION NUMBER: US/10/962,145C
/ CURRENT FILING DATE: 2004-10-07
/ PRIOR APPLICATION NUMBER: PCT/EP03/03732
/ PRIOR FILING DATE: 2003-04-10
/ PRIOR APPLICATION NUMBER: EP 02008033.9
/ PRIOR FILING DATE: 2002-04-10
/ NUMBER OF SEQ ID NOS: 17
/ SOFTWARE: PatentIn Ver. 3.3
/ SEQ ID NO 9
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Hepatitis C virus
US-10-962-145C-9

Query Match          32.8%; Score 22; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy      3 KNSPECTLGP 12
Db      9 KNGSMRIYGP 18

RESULT 61
US-11-106-415-188
/ Sequence 188, Application US/11106415
/ Publication No. US20050287153A1
/ GENERAL INFORMATION:
/ APPLICANT: MARK S. DENNIS
/ TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
/ FILE REFERENCE: P1774R1P2
/ CURRENT APPLICATION NUMBER: US/11/106,415
/ CURRENT FILING DATE: 2005-04-13
/ PRIOR APPLICATION NUMBER: US 10/186,229
/ PRIOR FILING DATE: 2002-06-28
/ NUMBER OF SEQ ID NOS: 425
/ SEQ ID NO 188
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: sequence is synthesized
US-11-106-415-188

Query Match          32.8%; Score 22; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
```


Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
|:|
DB 14 CLWGP 18

RESULT 62
US-11-106-415-214
Sequence 214, Application US/11106415
Publication No. US20050287153A1
GENERAL INFORMATION:
APPLICANT: MARK S. DENNIS
TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
FILE REFERENCE: P1774R12
CURRENT APPLICATION NUMBER: US/11/106,415
CURRENT FILING DATE: 2005-04-13
PRIOR APPLICATION NUMBER: US 10/186,229
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 425
SEQ ID NO 214
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-106-415-214

Query Match 32.8%; Score 22; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
|:|
DB 14 CLWGP 18

RESULT 63
US-11-106-415-288
Sequence 288, Application US/11106415
Publication No. US20050287153A1
GENERAL INFORMATION:
APPLICANT: MARK S. DENNIS
TITLE OF INVENTION: Serum Albumin Binding Peptides for Tumor Targeting
FILE REFERENCE: P1774R12
CURRENT APPLICATION NUMBER: US/11/106,415
CURRENT FILING DATE: 2005-04-13
PRIOR APPLICATION NUMBER: US 10/186,229
PRIOR FILING DATE: 2002-06-28
NUMBER OF SEQ ID NOS: 425
SEQ ID NO 288
LENGTH: 20
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: sequence is synthesized
US-11-106-415-288

Query Match 32.8%; Score 22; DB 7; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
|:|
DB 14 CLWGP 18

RESULT 64
US-10-467-657-8643
Sequence 8643, Application US/10467657
Publication No. US20050260581A1
GENERAL INFORMATION:
APPLICANT: CHIRON SpA

APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12
NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 8643
LENGTH: 7
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae
US-10-467-657-8643

Query Match 31.3%; Score 21; DB 6; Length 7;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FNCIL 10
|:|
DB 3 FNCIL 7

RESULT 65
US-10-859-643-50
Sequence 50, Application US/10859643
Publication No. US20060002993A1
GENERAL INFORMATION:
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fais, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
FILE REFERENCE: 511582006203
CURRENT APPLICATION NUMBER: US/10/859,643
CURRENT FILING DATE: 2004-06-02
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FaastSeq for Windows Version 4.0
SEQ ID NO 50
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-10-859-643-50

Query Match 31.3%; Score 21; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECIL 10
|:|
DB 1 KNSPECIL 8

RESULT 66
US-10-859-643-570
Sequence 570, Application US/10859643
Publication No. US20060002993A1
GENERAL INFORMATION:
APPLICANT: Chailita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Fais, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick

```
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ TITLE OF INVENTION: Cancer
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 570
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-570
```

```
Query Match          31.3%; Score 21; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
        |||
        1 KNVDRCLL 8
```

```
RESULT 67
US-11-097-864-50
/ Sequence 50, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 50
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-50
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
        |||
        1 KNVDRCLL 8
```

```
RESULT 68
US-11-097-864-570
/ Sequence 570, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
```

```
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 570
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-570
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
        |||
        1 KNVDRCLL 8
```

```
RESULT 69
US-11-097-912-50
/ Sequence 50, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 50
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-50
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 KNSPECIL 10
        |||
        1 KNVDRCLL 8
```

```
RESULT 70
US-11-097-912-570
/ Sequence 570, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
```

```
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ PRIOR FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR FILING DATE: 2001-11-07
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 570
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-912-570
```

```
Query Match          31.3%; Score 21; DB 7; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      3 NSPEC 8
      |||||
      1 KQVYDHCLL 8
DB
```

```
RESULT 71
US-10-859-643-167
/ Sequence 167, Application US/10859643
/ Publication No. US20060002993A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Fairle, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2P10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006203
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 167
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-10-859-643-167
```

```
Query Match          31.3%; Score 21; DB 6; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSPEC 8
      |||||
      6 NKFRFC 10
DB
```

```
RESULT 72
US-11-097-864-167
/ Sequence 167, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Fairle, Mary
/ APPLICANT: Hubert, Rene S.
```

```
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ PRIOR FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 167
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-11-097-864-167
```

```
Query Match          31.3%; Score 21; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSPEC 8
      |||||
      6 NKFRFC 10
DB
```

```
RESULT 73
US-11-097-912-167
/ Sequence 167, Application US/11097912
/ Publication No. US20050265921A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Fairle, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2P10B
/ TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006204
/ CURRENT APPLICATION NUMBER: US/11/097,912
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 167
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Saplen
US-11-097-912-167
```

```
Query Match          31.3%; Score 21; DB 7; Length 10;
Best Local Similarity 60.0%; Pred. No. 2.1e+02;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      4 NSPEC 8
      |||||
      6 NKFRFC 10
DB
```

```
RESULT 74
US-11-119-098-38
/ Sequence 38, Application US/11119098
/ Publication No. US20050267030A1
/ GENERAL INFORMATION:
/ APPLICANT: Tsao, Philip S.
/ APPLICANT: Mochly-Rosen, Daria
/ TITLE OF INVENTION: Use of deltaPKC Peptides for Modulation of Reactive Oxygen Specie
```

```
/ FILE REFERENCE: 58600-8213.US00
/ CURRENT APPLICATION NUMBER: US/11/119,098
/ CURRENT FILING DATE: 2005-04-29
/ PRIOR APPLICATION NUMBER: US 60/567,315
/ PRIOR FILING DATE: 2004-04-30
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 38
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: modified delta VL-1 peptide
US-11-119-098-38

Query Match
Best Local Similarity 31.3%; Score 21; DB 7; Length 10;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 4 NSFE 7
    |||
Db 3 NSFE 6

RESULT 75
US-11-016-706-45
/ Sequence 45, Application US/11/016,706
/ Publication No. US2005024434A1
/ GENERAL INFORMATION:
/ APPLICANT: CASTILLO, GERARDO
/ APPLICANT: LAKE, THOMAS P.
/ APPLICANT: NGUYEN, BETH P.
/ APPLICANT: SANDERS, VIRGINIA J.
/ APPLICANT: SNOW, ALAN D.
/ TITLE OF INVENTION: SMALL PEPTIDES FOR THE TREATMENT OF ALZHEIMER'S DISEASE AND
/ TITLE OF INVENTION: OTHER BETA-AMYLOID PROTEIN FIBRILLOGENESIS DISORDERS
/ FILE REFERENCE: PROTEO.P03C13
/ CURRENT APPLICATION NUMBER: US/11/016,706
/ CURRENT FILING DATE: 2004-12-16
/ PRIOR APPLICATION NUMBER: 09/962,955
/ PRIOR FILING DATE: 2001-09-24
/ PRIOR APPLICATION NUMBER: 09/938,275
/ PRIOR FILING DATE: 2001-08-22
/ PRIOR APPLICATION NUMBER: 08/947,057
/ PRIOR FILING DATE: 1997-10-08
/ NUMBER OF SEQ ID NOS: 89
/ SOFTWARE: PatentIn Ver. 3.2
/ SEQ ID NO 45
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-016-706-45

Query Match
Best Local Similarity 31.3%; Score 21; DB 7; Length 12;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 3 KNSF 6
    |||
Db 1 KNSF 4

RESULT 76
US-10-511-559-271
/ Sequence 271, Application US/10/511,559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
```

```
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 271
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-271

Query Match
Best Local Similarity 31.3%; Score 21; DB 6; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ILGP 12
    |||
Db 9 ILGP 12

RESULT 77
US-10-511-559-272
/ Sequence 272, Application US/10/511,559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
/ CURRENT APPLICATION NUMBER: US/10/511,559
/ CURRENT FILING DATE: 2004-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP03/04063
/ PRIOR FILING DATE: 2003-04-17
/ PRIOR APPLICATION NUMBER: EP 02008712.8
/ PRIOR FILING DATE: 2002-04-18
/ PRIOR APPLICATION NUMBER: EP 03006554.4
/ PRIOR FILING DATE: 2003-03-24
/ NUMBER OF SEQ ID NOS: 1147
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 272
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-272

Query Match
Best Local Similarity 31.3%; Score 21; DB 6; Length 13;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 9 ILGP 12
    |||
Db 6 ILGP 9

RESULT 78
US-10-511-559-273
/ Sequence 273, Application US/10/511,559
/ Publication No. US20050256304A1
/ GENERAL INFORMATION:
/ APPLICANT: JONES, Tim
/ APPLICANT: BAKER, Matthew
/ APPLICANT: CARR, Francis, J.
/ TITLE OF INVENTION: MODIFIED FACTOR VIII
/ FILE REFERENCE: MER-133
```

RESULT 80
 US-10-511-559-849
 / Sequence 849, Application US/10511559
 / Publication No. US20050256304A1
 / GENERAL INFORMATION:
 / APPLICANT: JONES, Tim
 / APPLICANT: BAKER, Matthew
 / APPLICANT: CARR, Francis, J.
 / TITLE OF INVENTION: MODIFIED FACTOR VIII

RESULT 32
US-10-929-988-451
; Sequence 451, Application US/10929988
; Publication No. US20050277568A1
; GENERAL INFORMATION:
; APPLICANT: CWTILA, STEVEN E.
; APPLICANT: BALU, PALANI

```
/ APPLICANT: DUFFIN, DAVID J.
/ APPLICANT: EPIPLANT, SUNILA
/ APPLICANT: MERRILL, BARBARA MCEOWEN
/ APPLICANT: SCHATZ, PETER JOSEPH
/ TITLE OF INVENTION: COMPOUNDS HAVING AFFINITY FOR THE GRANULOCYTE-COLONY
/ TITLE OF INVENTION: STIMULATING FACTOR RECEPTOR (G-CSFR) AND ASSOCIATED
/ FILE REFERENCE: 0300-0014
/ CURRENT APPLICATION NUMBER: US/10/929,988
/ CURRENT FILING DATE: 2004-08-30
/ PRIOR APPLICATION NUMBER: US/09/620,091
/ PRIOR FILING DATE: 2000-07-20
/ NUMBER OF SEQ ID NOS: 491
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 451
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-929-988-451
```

```
Query Match      31.3%; Score 21; DB 6; Length 14;
Best Local Similarity 40.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
```

```
QY      2 EKNSPFCILG 11
DB      5 KKKKECCAG 14
```

```
RESULT 83
US-11-106-932-45
/ Sequence 45, Application US/11106932
/ Publication No. US20050260697A1
/ GENERAL INFORMATION:
/ APPLICANT: WANG, KA-WANG KEVIN
/ APPLICANT: HAYES, RONALD
/ APPLICANT: LIU, MING CHEN
/ APPLICANT: OLI, MONIKA
/ TITLE OF INVENTION: PROTEOLYTIC MARKERS AS DIAGNOSTIC BIOMARKERS FOR CANCER, ORGAN
/ TITLE OF INVENTION: INJURY AND MUSCLE REHABILITATION/EXERCISE OVERTRAINING
/ FILE REFERENCE: 5853-549-1
/ CURRENT APPLICATION NUMBER: US/11/106,932
/ CURRENT FILING DATE: 2005-04-15
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 45
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Bos taurus
US-11-106-932-45
```

```
Query Match      31.3%; Score 21; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 3e+02;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      1 DEKNS 5
DB      4 DEKKS 8
```

```
RESULT 84
US-11-145-703-234
/ Sequence 234, Application US/11145703
/ Publication No. US2005026067A1
/ GENERAL INFORMATION:
/ APPLICANT: Cohen, Daniel
/ APPLICANT: Blumenfeld, Marta
/ APPLICANT: Chumakov, Ilya
/ APPLICANT: Bouguetelerc, Lydie
/ APPLICANT: Bihain, Bernard
```

```
/ APPLICANT: Essioux, Laurent
/ TITLE OF INVENTION: SCHIZOPHRENIA ASSOCIATED GENES, PROTEINS AND BIALLELIC MARKERS
/ FILE REFERENCE: 53 US16 DIV
/ CURRENT APPLICATION NUMBER: US/11/145,703
/ CURRENT FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US/10/147,603
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: 09/539,333
/ PRIOR FILING DATE: 2000-03-30
/ PRIOR APPLICATION NUMBER: US 60/126,903
/ PRIOR FILING DATE: 1999-03-30
/ PRIOR APPLICATION NUMBER: US 60/131,971
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: US 60/132,065
/ PRIOR FILING DATE: 1999-04-30
/ PRIOR APPLICATION NUMBER: US 60/143,928
/ PRIOR FILING DATE: 1999-07-14
/ PRIOR APPLICATION NUMBER: US 60/145,915
/ PRIOR FILING DATE: 1999-07-27
/ PRIOR APPLICATION NUMBER: US 60/146,453
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: US 60/146,452
/ PRIOR FILING DATE: 1999-07-29
/ PRIOR APPLICATION NUMBER: US 60/162,288
/ PRIOR FILING DATE: 1999-10-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 234
/ SOFTWARE: Patent.pn
/ SEQ ID NO 234
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-145-703-234
```

```
Query Match      31.3%; Score 21; DB 7; Length 15;
Best Local Similarity 100.0%; Pred. No. 3.2e+02;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      9 ILGP 12
DB      6 ILGP 9
```

```
RESULT 85
US-11-041-893-274
/ Sequence 274, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahalirae, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ TITLE OF INVENTION: ALTERING AGENTS AND METHODS OF USE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ CURRENT FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ PRIOR FILING DATE: 2004-01-23
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FaetsEQ for Windows Version 4.0
/ SEQ ID NO 274
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Mycobacteria tuberculosis
US-11-041-893-274
```

```
Query Match      31.3%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSPFCILG 11
DB      6 EAGNPFIRISG 15
```

```
RESULT 86
US-11-041-893-275
; Sequence 275, Application US/11041893
; Publication No. US2006002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahatras, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
; FILE REFERENCE: 100123.401
; CURRENT APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 275
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Mycobacteria tuberculosis
US-11-041-893-275

Query Match          31.3%; Score 21; DB 7; Length 15;
Best Local Similarity 50.0%; Pred. No. 3.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      2 EKNSPFCILQ 11
DB      2 EAGNFERISG 11
```

```
RESULT 87
US-10-939-890-99
; Sequence 99, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddi
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
```

```
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 99
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-99
```

```
Query Match          31.3%; Score 21; DB 6; Length 17;
Best Local Similarity 40.0%; Pred. No. 3.6e+02;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;
```

```
QY      1 DEKSNPFCIL 10
DB      7 NEKGMWNCYL 16
```

```
RESULT 88
US-10-939-890-217
; Sequence 217, Application US/10939890
; Publication No. US20050250700A1
; GENERAL INFORMATION:
; APPLICANT: Sato, Aaron K.
; APPLICANT: Sexton, Daniel J.
; APPLICANT: Dransfield, Daniel T.
; APPLICANT: Ladner, Robert C.
; APPLICANT: Arbogast, Christophe
; APPLICANT: Bussac, Philippe
; APPLICANT: Fan, Hong
; APPLICANT: Khurana, Sudha
; APPLICANT: Linder, Karen E.
; APPLICANT: Marinelli, Edmund R.
; APPLICANT: Nanjappan, Palaniappa
; APPLICANT: Nunn, Adrian D.
; APPLICANT: Pillai, Radhakrishna
; APPLICANT: Pochon, Sibylle
; APPLICANT: Ramalingam, Kondareddi
; APPLICANT: Shrivastava, Ajay
; APPLICANT: Song, Bo
; APPLICANT: Swenson, Rolf E.
; APPLICANT: Von Wronski, Mathew A.
; TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
; FILE REFERENCE: D0617.70014US00
; CURRENT APPLICATION NUMBER: US/10/939,890
; PRIOR FILING DATE: 2004-09-13
; PRIOR APPLICATION NUMBER: US 10/661,156
; PRIOR FILING DATE: 2003-09-11
; PRIOR APPLICATION NUMBER: US 10/382,082
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: PCT/US03/06731
; PRIOR FILING DATE: 2003-03-03
; PRIOR APPLICATION NUMBER: US 60/440,411
; PRIOR FILING DATE: 2003-01-15
; PRIOR APPLICATION NUMBER: US 60/360,851
; PRIOR FILING DATE: 2002-03-01
; NUMBER OF SEQ ID NOS: 883
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 217
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Library Isolate
US-10-939-890-217

Query Match          31.3%; Score 21; DB 6; Length 19;
Best Local Similarity 75.0%; Pred. No. 4e+02;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      5 SPFC 8
DB      13 TRFC 16
```

```
RESULT 89
US-11-054-515-2956
; Sequence 2956, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PR523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2956
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2956

Query Match      31.3%; Score 21; DB 7; Length 19;
Best Local Similarity 30.0%; Pred. No. 4e+02;
Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY      2 EKSPECTIG 11
Db      1 EKSQDFPLTG 10

RESULT 90
US-10-997-201A-31
; Sequence 31, Application US/10997201A
; Publication No. US20050249739A1
; GENERAL INFORMATION:
; APPLICANT: Marasco, Wayne
; APPLICANT: Sui, Jinhua
; TITLE OF INVENTION: Antibodies Against SARS-COV and Methods of Use Thereof
; FILE REFERENCE: 20363-026
; CURRENT APPLICATION NUMBER: US/10/997,201A
; PRIOR FILING DATE: 2004-11-24
; PRIOR APPLICATION NUMBER: 60/524,840
; PRIOR FILING DATE: 2003-11-25
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: Patentln Ver. 2.1
; SEQ ID NO 31
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-997-201A-31

Query Match      31.3%; Score 21; DB 6; Length 20;
Best Local Similarity 75.0%; Pred. No. 4.2e+02;
Matches 6; Conservative 0; Mismatches 0; Indels 2; Gaps 1;
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```
QY      5 SPECIIGP 12
Db      6 SFE--LGP 11

RESULT 91
US-11-041-893-264
; Sequence 264, Application US/11041893
; Publication No. US20060002941A1
; GENERAL INFORMATION:
; APPLICANT: Mahalirae, Gregory G.
; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSES
; FILE REFERENCE: 100123,401
; CURRENT APPLICATION NUMBER: US/11/041,893
; PRIOR FILING DATE: 2005-01-24
; PRIOR APPLICATION NUMBER: US 60/616,855
; PRIOR FILING DATE: 2004-10-06
; PRIOR APPLICATION NUMBER: US 60/538,713
; PRIOR FILING DATE: 2004-01-23
; NUMBER OF SEQ ID NOS: 295
; SOFTWARE: fastSeq for Windows Version 4.0
; SEQ ID NO 264
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Mycobacterie tuberculosis
US-11-041-893-264

Query Match      31.3%; Score 21; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 4.2e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      2 EKSPECTIG 11
Db      4 EAGNFERISG 13

RESULT 92
US-11-045-024-2757
; Sequence 2757, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esreban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060,0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
```


;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2757
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2757

Query Match 29.9%; Score 20; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
: |||
Db 3 HSFNC 7

RESULT 93
US-11-045-024-8435
;; Sequence 8435, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Celis, Esleben
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Bpimmune Inc.
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
;; PRIOR FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 8435
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-8435

Query Match 29.9%; Score 20; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
: |||
Db 3 HSFNC 7

RESULT 94
US-11-045-024-10862

;; Sequence 10862, Application US/11045024
;; Publication No. US20050271676A1
;; GENERAL INFORMATION:
;; APPLICANT: Sette, Alessandro
;; APPLICANT: Sidney, John
;; APPLICANT: Southwood, Scott
;; APPLICANT: Livingston, Brian
;; APPLICANT: Chesnut, Robert
;; APPLICANT: Baker, Denise Marie
;; APPLICANT: Celis, Esleben
;; APPLICANT: Kubo, Ralph
;; APPLICANT: Grey, Howard M.
;; APPLICANT: Bpimmune Inc.
;; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
;; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
;; FILE REFERENCE: 2060.0040007
;; CURRENT APPLICATION NUMBER: US/11/045,024
;; PRIOR FILING DATE: 2005-01-28
;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
;; PRIOR FILING DATE: 1993-03-05
;; PRIOR APPLICATION NUMBER: US 08/073,205
;; PRIOR FILING DATE: 1993-06-04
;; PRIOR APPLICATION NUMBER: US 08/103,396
;; PRIOR FILING DATE: 1993-08-06
;; PRIOR APPLICATION NUMBER: US 08/159,184
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/159,339
;; PRIOR FILING DATE: 1993-11-29
;; PRIOR APPLICATION NUMBER: US 08/205,713
;; PRIOR FILING DATE: 1994-03-04
;; PRIOR APPLICATION NUMBER: US 08/347,610
;; PRIOR FILING DATE: 1994-12-01
;; NUMBER OF SEQ ID NOS: 14528
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 10862
;; LENGTH: 8
;; TYPE: PRT
;; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10862

Query Match 29.9%; Score 20; DB 7; Length 8;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
: |||
Db 3 HSFNC 7

RESULT 95
US-10-986-501-241
;; Sequence 241, Application US/10986501
;; Publication No. US20050244845A1
;; GENERAL INFORMATION:
;; APPLICANT: Ruben et al.
;; TITLE OF INVENTION: 90 Human Secreted Proteins
;; FILE REFERENCE: P2013P2C1
;; CURRENT APPLICATION NUMBER: US/10/986,501
;; PRIOR FILING DATE: 2004-11-12
;; PRIOR APPLICATION NUMBER: US/10/621,363
;; PRIOR FILING DATE: 2003-07-18
;; PRIOR APPLICATION NUMBER: 09/969,730
;; PRIOR FILING DATE: 2001-10-06
;; PRIOR APPLICATION NUMBER: 09/774,639
;; PRIOR FILING DATE: 2001-02-01
;; PRIOR APPLICATION NUMBER: 60/238,291
;; PRIOR FILING DATE: 2000-10-06
;; PRIOR APPLICATION NUMBER: 09/244,112
;; PRIOR FILING DATE: 1999-02-04
;; PRIOR APPLICATION NUMBER: PCT/US98/16235
;; PRIOR FILING DATE: 1998-08-04

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/ PRIOR APPLICATION NUMBER: 60/056,371
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,732
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,366
/ PRIOR FILING DATE: 1997-08-19
/ PRIOR APPLICATION NUMBER: 60/056,364
/ PRIOR FILING DATE: 1997-08-19
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ SOFTWARE: Patentln Ver. 2.0
/ SEQ ID NO 241
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-986-501-241

Query Match          29.9%; Score 20; DB 6; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIL 10
   |||
Db 2 NSSDCOL 8

RESULT 96
US-11-010-748A-260
/ Sequence 260, Application US/11010748A
/ Publication No. US20050244421A1
/ GENERAL INFORMATION:
/ APPLICANT: Merck Patent GmbH
/ APPLICANT: STRITTMAYER, Wolfgang
/ APPLICANT: MOLL, Heidrun
/ APPLICANT: SCHAM, Burkhard
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING IMMUNE RESPONSE
/ FILE REFERENCE: MER-136
/ CURRENT APPLICATION NUMBER: US/11/010,748A
/ CURRENT FILING DATE: 2004-12-13
/ PRIOR APPLICATION NUMBER: PCT/EP03/06251
/ PRIOR FILING DATE: 2003-06-13
/ PRIOR APPLICATION NUMBER: EP02013423.5
/ PRIOR FILING DATE: 2002-06-13
/ NUMBER OF SEQ ID NOS: 926
/ SOFTWARE: Patentln version 3.1
/ SEQ ID NO 260
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: HLA-binding peptide of Seq. No. 259
US-11-010-748A-260

Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 25.0%; Pred. No. 5.5e+04;
Matches 2; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 1 DEKNSEFC 8
   |||
Db 2 DDSGEYRC 9

RESULT 97
US-11-045-024-37
/ Sequence 37, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
```

```
/ APPLICANT: Celis, Estebean
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-06-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 37
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-37

Query Match          29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
   |||
Db 1 HSFNC 5

RESULT 98
US-11-045-024-38
/ Sequence 38, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Estebean
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-06-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
```

```
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 38
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-38
```

```
Query Match      29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 NSPEC 8
       :|||
Db      1 HSFNC 5
```

```
RESULT 99
US-11-045-024-2802
/ Sequence 2802, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betsedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 2802
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-2802
```

```
Query Match      29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 NSPEC 8
       :|||
Db      4 HSFNC 8
```

```
RESULT 100
US-11-045-024-6167
/ Sequence 6167, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betsedan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6167
/ LENGTH: 9
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6167
```

```
Query Match      29.9%; Score 20; DB 7; Length 9;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 NSPEC 8
       :|||
Db      1 HSFNC 5
```

Search completed: January 20, 2006, 19:46:31
Job time : 5.84615 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:55:50 ; Search time 6.80769 Seconds

(without alignments)
169.602 Million cell updates/sec

Title: US-09-662-293-5

Perfect score: 67

Sequence: 1 DEKNSPFCILGP 12

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: PIR.80:*
2: PIR2:*
3: PIR3:*
4: PIR4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	27	40.3	14	2	endothelial growth
2	27	40.3	19	2	gamma crystallin I
3	24	35.8	19	2	gamma crystallin I
4	23	34.3	13	2	gamma crystallin I
5	22	32.8	15	2	ig heavy chain DJ
6	22	32.8	16	2	fibronogen alpha C
7	22	32.8	18	2	ig heavy chain CDR
8	22	32.8	19	2	4K protein - pig
9	22	32.8	19	2	4K prothoracicetro
10	22	32.8	15	2	homeobox 4 protein
11	21	31.3	15	2	T-cell receptor be
12	21	31.3	15	2	urogenital tumor m
13	21	31.3	15	2	T-cell receptor be
14	21	31.3	16	2	phospholipase A2 (
15	21	30.6	16	2	gamma crystallin V
16	20	29.9	9	4	L-serine dehydrata
17	20	29.9	16	2	hypothetical E2 pr
18	20	29.9	17	2	amexin 36K chain
19	20	29.9	17	2	T-cell receptor al
20	20	29.9	18	2	T-cell receptor J-
21	20	29.9	18	2	heat-stable entero
22	20	29.9	18	2	heat-stable entero
23	20	29.9	18	2	hepatalin-degradi
24	20	29.9	19	1	ribosomal protein
25	20	29.9	19	1	ancovenin - Strept
26	20	29.9	20	2	cinamycin - Strept
27	20	29.9	20	2	bombyxin-IV chain
28	19.5	29.1	14	2	hypothetical prote
29	19	28.4	10	2	very late antigen-
					ig heavy chain DJ

30	19	28.4	15	2	A43839	beta-tubulin germ-
31	19	28.4	16	2	S57517	T cell receptor be
32	19	28.4	18	2	PH1350	Ig heavy chain DJ
33	19	28.4	18	2	T35141	T-cell receptor de
34	19	28.4	20	2	B44581	bombinin H Met-8 -
35	19	28.4	20	2	C60894	gamma crystallin I
36	19	28.4	20	2	A48394	major fat-globule
37	19	28.4	20	2	A60100	fimbrial antigen C
38	19	28.4	20	2	S50743	proteinase inhibit
39	19	28.4	20	2	S71593	serine proteinase
40	19	28.4	20	2	S08605	hypothetical prote
41	18	26.9	12	2	PH1180	T-cell receptor al
42	18	26.9	12	2	PH1179	T-cell receptor al
43	18	26.9	12	2	PH1181	T-cell receptor al
44	18	26.9	13	1	NTKXAS	T-cell receptor al
45	18	26.9	13	2	I49637	alpha-conotoxin SI
46	18	26.9	14	2	PH0795	deoxynucleotidyltr
47	18	26.9	14	2	PH0804	T-cell receptor al
48	18	26.9	14	2	PH0776	T-cell receptor al
49	18	26.9	14	2	S21747	glutamate dehydrog
50	18	26.9	15	2	S26524	T-cell receptor al
51	18	26.9	15	2	S26523	T-cell receptor al
52	18	26.9	15	2	S26525	T-cell receptor al
53	18	26.9	15	2	PA0020	protein QAL00028 -
54	18	26.9	15	2	PH1762	T cell receptor al
55	18	26.9	15	2	PH0782	T-cell receptor al
56	18	26.9	16	2	F44908	chitinase (EC 3.2.
57	18	26.9	16	2	PH1778	T cell receptor al
58	18	26.9	16	2	A60839	neurokinin A homol
59	18	26.9	17	2	B49404	T-cell receptor be
60	18	26.9	17	2	B44873	caldesmon - rabbit
61	18	26.9	17	2	I49593	cystic fibrosis tr
62	18	26.9	17	2	I84733	gene CPTK protein
63	18	26.9	17	2	PT0234	Ig heavy chain CRD
64	18	26.9	17	2	PH0809	T-cell receptor al
65	18	26.9	18	2	PH1794	T cell receptor al
66	18	26.9	18	2	S36121	lectin - spurge (B
67	18	26.9	18	2	B24867	ecylthorinin II -
68	18	26.9	19	2	A21182	4K prothoracicotro
69	18	26.9	19	2	H61491	seed protein ws-24
70	18	26.9	20	2	S50175	kallikrein (PK-120
71	18	26.9	20	2	PH1783	T cell receptor al
72	18	26.9	20	2	A31516	lectin, galactose/
73	18	26.9	20	2	S29636	jaccalin beta-1 cha
74	18	26.9	20	2	S03987	agglutinin beta-2
75	18	26.9	20	2	B61497	seed protein ws-20
76	18	26.9	20	2	AB0120	insertion element
77	17	25.4	7	2	A33098	244K exantigen -
78	17	25.4	8	4	I54017	granulocyte-colony
79	17	25.4	10	2	S65728	hemoglobin, extrac
80	17	25.4	11	2	PH1583	Ig H chain V-D-J r
81	17	25.4	11	2	I41978	cellIFMamide 9 -
82	17	25.4	11	2	C37196	bradykinin-potent
83	17	25.4	12	2	C20907	ig kappa-l chain J
84	17	25.4	12	2	A49637	MHC class II histo
85	17	25.4	13	2	PT0305	Ig heavy chain CRD
86	17	25.4	13	2	PH0787	T-cell receptor al
87	17	25.4	13	2	B42762	proteaseome endope
88	17	25.4	14	2	PH1615	Ig H chain V-D-J r
89	17	25.4	14	2	PT0210	T-cell receptor al
90	17	25.4	14	2	A41589	25K elastin-bindin
91	17	25.4	14	2	S33802	chaperone, TcPI-re
92	17	25.4	14	2	S68095	calcium-binding pr
93	17	25.4	14	2	B83836	hypothetical prote
94	17	25.4	14	2	S27140	hypothetical prote
95	17	25.4	15	2	PM0004	chlorophyll a/b-bl
96	17	25.4	15	2	PH1342	Ig heavy chain DJ
97	17	25.4	15	2	PT0097	glutathione peroxi
98	17	25.4	15	2	PH1455	T-cell receptor al
99	17	25.4	15	2	PA0008	lectin B2 - Psopho
100	17	25.4	15	2	A61612	allatostatin - tob

ALIGNMENTS

RESULT 1

156493
enothelial growth factor receptors flt [imported] - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: 156493
R/Boocock, C.A.; Charnock-Jones, D.S.; Sharkey, A.M.; McLaren, J.; Barker, P.J.; Wright, J. Natl. Cancer Inst. 87, 506-516, 1995
A/Title: Expression of vascular endothelial growth factor and its receptors flt and KDR
A/Reference number: 156493; PMID:95222657; PMID:7707437
A/Status: preliminary; translated from GB/EWBL/DBBJ
A/Molecule type: mRNA
A/Residues: 1-14 <RBS>
A/Cross-references: UNIPROT:Q16332; UNIPARC:UPI000006EA07; GB:S7812; NID:9998564; PIND:
C/Genetic: flt
A/Gene: flt

Query Match 40.3%; Score 27; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSPECI 9
|:|:|:|:
DB 1 ELNSPECL 8

RESULT 2

A60894
gamma crystallin II - spectracted calman (fragment)
C/Species: Calman crocodilus, Calman sclerops (spectracted calman)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A60894
R/Chlou, S.H.
J. Protein Chem. 7, 527-534, 1988
A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class
A/Reference number: A60894; PMID:89351593; PMID:3255376
A/Accession: A60894
A/Molecule type: protein
A/Residues: 1-19 <CHI>
A/Cross-references: UNIPROT:Q7LZ96; UNIPARC:UPI000017748P
C/Superfamily: beta-crystallin
C/Keywords: duplication; eye lens

Query Match 40.3%; Score 27; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 1 DEKN---SPEC 8
:|:|:|:|:
DB 7 EERNFGGRSTYC 18

RESULT 3

B60894
gamma crystallin IV - spectracted calman (fragment)
C/Species: Calman crocodilus, Calman sclerops (spectracted calman)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: B60894
R/Chlou, S.H.
J. Protein Chem. 7, 527-534, 1988
A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class
A/Reference number: A60894; PMID:89351593; PMID:3255376
A/Accession: B60894
A/Molecule type: protein
A/Residues: 1-19 <CHI>
A/Cross-references: UNIPROT:Q7LZ99; UNIPARC:UPI000017748C
C/Superfamily: beta-crystallin
C/Keywords: duplication; eye lens

Query Match 35.8%; Score 24; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 6.3e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
|:|:|:|:
DB 12 EGRSYEC 18

RESULT 4

PH1316
Ig heavy chain DJ region (clone C388-107) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1316
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; PMID:93094761; PMID:1460419
A/Accession: PH1316
A/Molecule type: DNA
A/Residues: 1-13 <WAS>
A/Cross-references: UNIPARC:UPI000017C23E
C/Keywords: heterotetramer; immunoglobulin

Query Match 34.3%; Score 23; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 6.5e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
|:|:|:|:
DB 6 CDLGP 10

RESULT 5

JP0101
fibrinogen alpha chain - duck (fragment)
N/Contains: fibrinopeptide A
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 30-Jun-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
C/Accession: JP0101
R/Min, Y.; Ping, Z.; Yaoshi, Z.
Sci. Sin. B Chem. Biol. Agric. Med. Earth Sci. 28, 31-35, 1985
A/Title: Purification and primary structures of duck fibrinopeptides A and B.
A/Reference number: A94238
A/Accession: JP0101
A/Molecule type: protein
A/Residues: 1-15 <MIN>
A/Cross-references: UNIPROT:P12801; UNIPARC:UPI000012A74B
C/Superfamily: fibrinogen alpha chain; fibrinogen disulfide ring homology
C/Keywords: blood coagulation; plasma; pyroglutamic acid
F1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 32.8%; Score 22; DB 2; Length 15;
Best Local Similarity 57.1%; Pred. No. 1.2e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSE 7
|:|:|:|:
DB 2 DEKSFQ 8

RESULT 6

PT0224
Ig heavy chain CDR3 region (clone 1-91) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0224
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
A/Reference number: PT0222; PMID:91108337; PMID:1899102
A/Accession: PT0224

A/Molecule type: DNA
 A/Residues: 1-16 <YAM>
 A/Cross-references: UNIPARC:UPI000017C1D6
 A/Title: Identification of differentially expressed members of tobacco homeobox familie
 A/Reference number: JC2057; PMID:94161708; PMID:7509595
 A/Accession: JC2059
 A/Molecule type: DNA
 A/Residues: 1-19 <FEN>
 A/Cross-references: UNIPROT:Q95XV1; UNIPARC:UPI000017B0A8
 A/Experimental source: leaf
 C/Genetics:
 A/Gene: Hot4
 C/Keywords: homeobox

Query Match 32.8%; Score 22; DB 2; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.2e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SFCILGP 12
 Db 6 SYGXILGP 13

RESULT 7
 523950
 45K protein - pig roundworm
 C/Species: Ascaris suum (pig roundworm)
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Jul-1997
 C/Accession: S23950
 R/Komuniecki, R.; Rhee, R.; Bhat, D.; Duran, E.; Sidawy, E.; Song, H.
 Arch. Biochem. Biophys. 296, 115-121, 1992
 A/Title: The pyruvate dehydrogenase complex from the parasitic nematode Ascaris suum: nc
 A/Reference number: S23950; PMID:92296744; PMID:1376597
 A/Accession: S23950
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-18 <KOM>
 A/Cross-references: UNIPARC:UPI000017B698
 A/Note: 13-Arg was also found

Query Match 33.8%; Score 22; DB 2; Length 18;
 Best Local Similarity 55.6%; Pred. No. 1.4e+03;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSPECTILGP 12
 Db 6 SSGHSLGP 14

RESULT 8
 C21182
 4K prothoracicotropic hormone III - silkworm (fragment)
 C/Species: Bombyx mori (silkworm)
 C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 12-Apr-1995
 C/Accession: C21182
 R/Nagabawa, H.; Kataoka, H.; Isegaki, A.; Tamura, S.; Suzuki, A.; Ichizaki, H.; Mizoguchi
 Science 226, 1344-1345, 1984
 A/Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone:
 A/Reference number: A21182
 A/Accession: C21182
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-19 <NAG>
 A/Cross-references: UNIPARC:UPI000017665F
 C/Superfamily: Insulin

Query Match 32.8%; Score 22; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 1.5e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 7 ECIILGP 12
 Db 5 ECCIILGP 10

RESULT 9
 UC2059
 homeobox 4 protein - common tobacco (fragment)
 C/Species: Nicotiana tabacum (common tobacco)
 C/Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 09-Jul-2004

C/Accession: JC2059
 R/Feng, X.H.; Kung, S.D.
 Biochem. Biophys. Res. Commun. 198, 1012-1019, 1994
 A/Title: Identification of differentially expressed members of tobacco homeobox familie
 A/Reference number: JC2057; PMID:94161708; PMID:7509595
 A/Accession: JC2059
 A/Molecule type: DNA
 A/Residues: 1-19 <FEN>
 A/Cross-references: UNIPROT:Q95XV1; UNIPARC:UPI000017B0A8
 A/Experimental source: leaf
 C/Genetics:
 A/Gene: Hot4
 C/Keywords: homeobox

Query Match 32.8%; Score 22; DB 2; Length 19;
 Best Local Similarity 45.5%; Pred. No. 1.5e+03;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECTILGP 11
 Db 2 EKNRRLSETTG 12

RESULT 10
 P28587
 T-cell receptor beta-2 chain T-B2.7 segment - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 16-Aug-1988 #sequence_revision 16-Aug-1988 #text_change 05-Nov-1999
 C/Accession: P28587
 R/Toyonaga, B.; Yoshikai, Y.; Vadasz, V.; Chin, B.; Mak, T.W.
 Proc. Natl. Acad. Sci. U.S.A. 82, 8624-8628, 1985
 A/Title: Organization and sequences of the diversity, joining, and constant region gene
 A/Reference number: A94081; PMID:86094276; PMID:3866244
 A/Accession: P28587
 A/Molecule type: DNA
 A/Residues: 1-15 <TOY>
 A/Cross-references: UNIPARC:UPI0000113C7B; GB:M14159; NID:9338852; PIDN:AAA60681.1; PID
 C/Keywords: T-cell receptor

Query Match 31.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SPECTILGP 12
 Db 1 SYEQYFEP 8

RESULT 11
 A61247
 urogenital tumor maker protein - human (fragment)
 N/Alternate names: p21 protein; replication initiation protein homolog
 C/Species: Homo sapiens (man)
 C/Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 27-Jun-1994
 C/Accession: A61247
 R/Shalitin, C.; Epelbaum, R.; Valansi, C.; Segal, R.; Mekori, T.; Lover, B.; Robinson,
 Int. J. Cancer 49, 861-866, 1991
 A/Title: A novel 21-kDa protein as a serum marker for benign and malignant urogenital t
 A/Reference number: A61247; PMID:92071053; PMID:1959899
 A/Accession: A61247
 A/Molecule type: protein
 A/Residues: 1-15 <SHA>
 A/Cross-references: UNIPARC:UPI000002D270
 C/Keywords: plasma

Query Match 31.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 1.8e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSEFP 7
 Db 8 ERNREFO 13

RESULT 12

153284

T-cell receptor beta 2 chain J region, Jbeta2.7 - rabbit

C/Species: Oryctolagus cuniculus (domestic rabbit)

C/Date: 02-May-1994 #sequence_revision 18-Nov-1994 #text_change 05-Nov-1999

C/Accession: 153284

R/Harindranath, N.; Alexander, C.B.; Mage, R.G.

Mol. Immunol. 28, 881-888, 1991

A/Title: Evolutionarily conserved organization and sequences of germline diversity and

A/Reference number: A53284; PMID:91342655; PMID:1678859

A/Accession: 153284

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-15 <HAR>

A/Cross-references: UNIPARC:UPI0000115418; GB:860737; NID:9233916; PIRIN:AAH19525.1; PTD:

A/Note: Sequence extracted from NCBI backbone (NCBIN:60737, NCBIPI:60747)

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 31.3%; Score 21; DB 2; Length 15;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SPECILGP 12

DB 1 SYEQYFGP 8

RESULT 13

S65520

phospholipase A2 (BC 3.1.1.4) - Malayan spitting cobra (fragment)

N/contains: muscarinic acetylcholine receptor inhibitor

C/Species: Naja naja sputatrix (Malayan spitting cobra)

C/Date: 19-Mar-1997 #sequence_revision 29-Aug-1997 #text_change 05-Oct-2004

C/Accession: S65520

R/Miyoshi, S.; Tu, A.T.

Arch. Biochem. Biophys. 328, 17-25, 1996

A/Title: Phospholipase A(2) from Naja naja sputatrix venom is a muscarinic acetylcholine

A/Reference number: S65520; PMID:96195757; PMID:8638927

A/Accession: S65520

A/Molecule type: protein

A/Residues: 1-16 <MTY>

A/Cross-references: UNIPROT:Q10756; UNIPARC:UPI000013117A

C/Suprafamily: Phospholipase A2

C/Keywords: calcium; carboxylic ester hydrolase; lipid degradation; metalloprotein; pres

Query Match

Best Local Similarity 31.3%; Score 21; DB 2; Length 16;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 KNSFEC 8

DB 6 KNMIQC 11

RESULT 14

D60894

gamma crystallin V - bullfrog (fragment)

C/Species: Rana catesbeiana (bullfrog)

C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004

C/Accession: D60894

R/Chlou, S.H.

J. Protein Chem. 7, 527-534, 1988

A/Title: The protein sequence homology of gamma-crystallins among major vertebrate class

A/Reference number: A60894; PMID:89351593; PMID:3255376

A/Accession: D60894

A/Molecule type: protein

A/Residues: 1-20 <CHI>

A/Cross-references: UNIPROT:Q7LZ97; UNIPARC:UPI000017748E

C/Suprafamily: beta-crystallin

C/Keywords: duplication; eye lens

Query Match

Best Local Similarity 31.3%; Score 21; DB 2; Length 20;

Best Local Similarity 75.0%; Pred. No. 2.4e+03;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 SPEC 8

DB 15 SYEC 18

RESULT 15

S16376

L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus

C/Species: Peptostreptococcus asaccharolyticus

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S16376

R/Grabowski, R.; Buckel, W.

Eur. J. Biochem. 199, 89-94, 1991

A/Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat

A/Reference number: S16224; PMID:91293139; PMID:2065681

A/Accession: S16376

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-16 <EUR>

A/Cross-references: UNIPROT:P33074; UNIPARC:UPI000017ABE6

Query Match

Best Local Similarity 30.6%; Score 20.5; DB 2; Length 16;

Matches 4; Conservative 4; Mismatches 0; Indels 1; Gaps 1;

QY 4 NSPECILGP 12

DB 2 SAFE-VMGP 9

RESULT 16

I73804

hypothetical E2 protein - human papillomavirus type 16 (fragment)

C/Species: human papillomavirus type 16

C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004

C/Accession: I73804

R/Schneider-Maunoury, S.; Croissant, O.; Orth, G.

J. Virol. 61, 3295-3298, 1987

A/Title: Integration of human papillomavirus type 16 DNA sequences: a possible early eve

A/Reference number: I56695; PMID:87311896; PMID:3041049

A/Accession: I73804

A/Status: translated from GB/EMBL/DBJ

A/Molecule type: DNA

A/Residues: 1-9 <SCH>

A/Cross-references: UNIPROT:Q918T3; UNIPROT:Q9YV74; UNIPROT:Q9E841; UNIPROT:Q918T0; UNIP

PROT:Q9YV76; UNIPROT:Q9YV73; UNIPROT:Q9YV75; UNIPROT:Q918U5; UNIPROT:Q9E839; UNIPROT:Q91

96.1; PIR:G553617

C/Comment: This is the hypothetical translation of a viral sequence integrated into the

Query Match

Best Local Similarity 29.9%; Score 20; DB 4; Length 9;

Matches 2; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECT 9

DB 1 DANLUKCL 8

RESULT 17

A26393

amexin 36k chain - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004

C/Accession: A26393

R/Gelsow, M.J.; Fritzsche, U.; Hexham, J.M.; Dash, B.; Johnson, T.

Nature 320, 636-638, 1986

A/Title: A consensus amino-acid sequence repeat in Torpedo and mammalian Ca(2)+-depende

A/Reference number: A93379; PMID:86203621; PMID:2422556

A/Accession: A26393

A/Molecule type: protein

A/Residues: 1-16 <GRI>
A/Cross-references: UNIPROT:Q7M2P4; UNIPARC:UPI000017C456

Query Match 29.9%; Score 20; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.9e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECIL 10
|||
Db 7 DEKRLRITIL 16

RESULT 18

PH1789
T cell receptor alpha chain V region (clone 2PB1 V alpha 24-5) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1789
R/Portelli, S.; Yockey, C.E.; Brenner, M.B.; Balik, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057
A/Accession: PH1789
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-17 <POR>
A/Cross-references: UNIPARC:UPI000017C378

Query Match 29.9%; Score 20; DB 2; Length 17;
Best Local Similarity 40.0%; Pred. No. 3e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
|||
Db 3 CTVSP 7

RESULT 19

S47201
T-cell receptor J-alpha wntv.3 - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 05-Nov-1999
C/Accession: S47201
R/Plaza, A.; Kono, D.H.; Theofilopoulos, A.N.
Submitted to the EMBL Data Library, February 1993
A/Reference number: S40133
A/Accession: S47201
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-17 <FLA>
A/Cross-references: UNIPARC:UPI0000116133; EMBL:X71048; NID:G506944; PIDN:CAA50365.1; PI
C/Keywords: T-cell receptor

Query Match 29.9%; Score 20; DB 2; Length 17;
Best Local Similarity 66.7%; Pred. No. 3e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSP 6
|||
Db 2 DEKLTIF 7

RESULT 20

QHEC2
heat-stable enterotoxin ST-2 - Escherichia coli
C/Species: Escherichia coli
C/Date: 06-Jul-1982 #sequence_revision 06-Jul-1982 #text_change 09-Jul-2004
C/Accession: A01823
R/Chan, S.K.; Giamella, R.A.
J. Biol. Chem. 256, 7744-7746, 1981
A/Title: Amino acid sequence of heat-stable enterotoxin produced by Escherichia coli pat
A/Reference number: A01823; MUID:81264141; PMID:7021541

A/Accession: A01823
A/Molecule type: protein

A/Residues: 1-18 <CHA>
A/Cross-references: UNIPROT:P01560; UNIPARC:UPI000012CDB1
A/Experimental source: strain 18D, serotype 0.42:X86:H37
C/Comment: This enterotoxin is one of several, of differing molecular sizes, produced b
idues of the heat-stable enterotoxin ST-1.
C/Superfamily: heat-stable enterotoxin ST
C/Keywords: enterotoxin; heat-stable protein
F/1-18/Product: heat-stable enterotoxin ST-2 #status experimental <MAT>
F/5-10,6-14,9-17/Disulfide bonds: #status predicted

Query Match 29.9%; Score 20; DB 1; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
|||
Db 1 NTFYC 5

RESULT 21

A60103
heat-stable enterotoxin ST-1a - Citrobacter freundii
C/Species: Citrobacter freundii
C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
C/Accession: A60103
R/Guarino, A.; Giamella, R.; Thompson, M.R.
Infect. Immun. 57, 649-652, 1989
A/Title: Citrobacter freundii produces an 18-amino-acid heat-stable enterotoxin identic
A/Reference number: A60103; MUID:89108617; PMID:2512902
A/Accession: A60103
A/Molecule type: protein
A/Residues: 1-18 <GUA>
A/Cross-references: UNIPROT:Q7M0U3; UNIPARC:UPI000003112P
C/Superfamily: heat-stable enterotoxin ST

Query Match 29.9%; Score 20; DB 2; Length 18;
Best Local Similarity 60.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPEC 8
|||
Db 1 NTFYC 5

RESULT 22

A60915
enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive - rat (fragment)
N/Alternate names: aminocephalinalase; aminopeptidase MII
C/Species: Rattus norvegicus (Norway rat)
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: A60915
R/Dyer, S.H.; Slaughter, C.A.; Orth, K.; Moosaw, C.R.; Hersh, L.B.
J. Neurochem. 54, 547-554, 1990
A/Title: Comparison of the soluble and membrane-bound forms of the puromycin-sensitive
A/Reference number: A60915; MUID:90132681; PMID:229352
A/Accession: A60915
A/Molecule type: protein
A/Residues: 1-18 <DYR>
A/Cross-references: UNIPROT:Q7M076; UNIPARC:UPI00001789A0
A/Note: this sequence represents the N-terminus of both soluble and membrane-associated
C/Superfamily: membrane alanyl aminopeptidase
C/Keywords: hydrolase

Query Match 29.9%; Score 20; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 3.2e+03;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPE 7
|||
Db 2 EKRPPE 7

RESULT 23
S49026
ribosomal protein HS25 (validated) - *Halorcula marismortui* (fragment)
C/Species: *Halorcula marismortui*
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S49026; S63967
R/Engemann, S.; Herfurth, E.; Briesemeister, U.; Grell, G.; Wittmann-Liebold, B.
submitted to the Protein Sequence Database, November 1994
A/Description: Cartography of ribosomal proteins of the 30S subunit from the halophilic
A/Reference number: S49023
A/Accession: S49026
A/Molecule type: protein
A/Residues: 1-18 <ENM>
A/Cross-references: UNIPROT:Q7M532; UNIPARC:UPI000017AEA3
R/Engemann, S.; Noelle, R.; Herfurth, E.; Briesemeister, U.; Grell, G.; Wittmann-Liebold, B.
Eur. J. Biochem. 234, 24-31, 1995
A/Title: Cartography of ribosomal proteins of the 30S subunit from the halophilic *Halorcula marismortui*
A/Reference number: S63964; PMID:96096717; PMID:8529646
A/Accession: S63967
A/Molecule type: protein
A/Residues: 1-18 <ENM>
A/Cross-references: UNIPARC:UPI000017AEA3
C/Keywords: blocked amino end; protein biosynthesis; ribosome

Query Match 29.9%; Score 20; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 3.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12
DB 12 VLGP 15

RESULT 24
EWSMAN
ancovenin - *Streptomyces* sp. (strain A647P-2)
C/Species: *Streptomyces* sp.
C/Date: 12-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C/Accession: A61284
R/Makimäy, T.; Ueki, Y.; Shiba, T.; Kido, Y.; Moroki, Y.
Tetrahedron Lett. 26, 665-668, 1985
A/Title: The structure of ancovenin, a new peptide inhibitor of angiotensin I converting
A/Reference number: A61284
A/Accession: A61284
A/Molecule type: protein
A/Residues: 1-19 <ENM>
A/Cross-references: UNIPROT:P38655; UNIPARC:UPI0000052CC3
C/Superfamily: cinnamycin precursor
C/Keywords: antibiotic; lantibiotic
F/1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F/4-14/Cross-link: an-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F/5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F/6/Modified site: dehydroalanine (Ser) #status experimental

Query Match 29.9%; Score 20; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ILGP 12
DB 5 CSFGP 9

RESULT 25
EWSMCN
cinamycin - *Streptoverficillium cinamomeum*
N/Alternate names: lantibiotic; lantibiotic Ro 09-0198
C/Species: *Streptoverficillium cinamomeum*
C/Date: 30-Sep-1993 #sequence_revision 12-May-1994 #text_change 09-Jul-2004
C/Accession: A45767
R/Naruse, N.; Tenmyo, O.; Tomita, K.; Konishi, M.; Miyaki, T.; Kawaguchi, H.; Fukase, K.
J. Antibiot. 42, 837-845, 1989

A/Title: lantibiotic, a new peptide antibiotic. Production, isolation and properties
A/Reference number: A45767; PMID:89291558; PMID:2544544
A/Accession: A45767
A/Molecule type: protein
A/Residues: 1-19 <ENM>
A/Cross-references: UNIPROT:P29827; UNIPARC:UPI0000052CCP
R/Makimäy, T.; Fukase, K.; Naruse, N.; Konishi, M.; Shiba, T.
Tetrahedron Lett. 29, 4771-4772, 1988
A/Title: lantibiotic, a new peptide effective against Herpes simplex virus: structural
A/Reference number: A53359
A/Contents: annotation; strain L337-2
C/Superfamily: cinnamycin precursor
C/Keywords: antibiotic; beta-hydroxyaspartic acid; lantibiotic
F/1-18/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F/4-14/Cross-link: an-(2S,6R)-lanthionine (Ser-Cys) #status experimental
F/5-11/Cross-link: (2S,3S,6R)-3-methyl-lanthionine (Cys-Thr) #status experimental
F/6-19/Cross-link: (2X,3S)-lysinoalanine (Ser-Lys) #status experimental
F/15/Modified site: erythro-beta-hydroxyaspartic acid (Asp) #status experimental

Query Match 29.9%; Score 20; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 3.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 ILGP 12
DB 5 CSFGP 9

RESULT 26
JTO410
bombyxin-IV chain A - silkworm
C/Species: *Bombyx mori* (silkworm)
C/Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 20-Mar-1998
C/Accession: JTO410
R/Maruyama, K.; Hietter, H.; Nagasawa, H.; Isogai, A.; Tamura, S.; Suzuki, A.; Ishizaki, A.
Agric. Biol. Chem. 52, 3035-3041, 1988
A/Title: Isolation and primary structure of bombyxin-IV, a novel molecular species of bc
A/Reference number: JTO410
A/Accession: JTO410
A/Molecule type: protein
A/Residues: 1-20 <ENM>
A/Cross-references: UNIPARC:UPI0000176661
C/Superfamily: insulin
F/6-11/Diulfide bonds: #status predicted
F/7/Diulfide bonds: interchain (to chain B-10) #status predicted
F/20/Diulfide bonds: interchain (to chain B-22) #status predicted

Query Match 29.9%; Score 20; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.6e+03;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 7 ECLGP 12
DB 5 ECLGP 10

RESULT 27
T26748
hypothetical protein Y39A1B.4 - *Caenorhabditis elegans*
C/Species: *Caenorhabditis elegans*
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C/Accession: T26748
R/Wall, M.
submitted to the EMBL Data Library, January 1998
A/Reference number: Z20258
A/Accession: T26748
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-20 <ENM>
A/Cross-references: UNIPARC:UPI000017B660; EMBL:AL021482; P1DN:CA54436.1; GSPDB:GN0002.
C/Genetic: A/Experimental source: clone Y39A1B
A/Genetic: CESP:Y39A1B.4

A:Map position: 3
A:introns: 16/3

Query Match 29.9%; Score 20; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 3.6e+03;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 1 DEKNSPFCILGP 12
|:|:|
Db 7 DKSISISFLVP 18

RESULT 28

A28018

very late antigen-1 alpha chain - human (fragment)

N/Alternate names: VLA-1 alpha chain

C/Species: Homo sapiens (man)

C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 12-May-1994

C/Accession: A28018

R/Takada, Y.; Strominger, J.L.; Hemler, M.B.

Proc. Natl. Acad. Sci. U.S.A. 84, 3239-3243, 1987

A/Title: The very late antigen family of heterodimers is part of a superfamily of molecu

A/Reference number: A94151; MUID:87204112; PMID:3033641

A/Accession: A28018

A/Molecule type: protein

A/Residues: 1-14 <TAK>

A/Cross-references: UNIPARC:UPI000017C41B

C/Keywords: duplication, heterodimer, membrane protein

Query Match 29.1%; Score 19.5; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 3.1e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 1; Gaps 1;

QY 1 DEKNSPFCILGP 12
|:|:|
Db 4 DVKDSM-TFLGP 14

RESULT 29

PH1345

Ig heavy chain DJ region (clone C100-94) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1345

R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1345

A/Molecule type: DNA

A/Residues: 1-10 <WAS>

A/Cross-references: UNIPARC:UPI000017C226

C/Keywords: the authors translated the stop codon for residue 4 as X

Query Match 28.4%; Score 19; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 2.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12
|:|:|
Db 5 ILGP 8

RESULT 30

A43839

beta-tubulin germ-cell isotype - African clawed frog (fragment)

C/Species: Xenopus laevis (African clawed frog)

C/Date: 10-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 11-Apr-1995

C/Accession: A43839

R/Bieker, J.D.; Yazdani-Bulcky, M.

Differential 50, 15-23, 1992

A/Title: The multiple beta-tubulin genes of Xenopus: isolation and developmental express

A/Reference number: A43839; MUID:92347627; PMID:1379202

A/Accession: A43839

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: nucleic acid

A/Residues: 1-15 <BIE>

A/Cross-references: UNIPARC:UPI000017B7FD

A/Experimental source: cocyte

A/Note: sequence extracted from NCBI backbone (NCBIF:110252)

Query Match 28.4%; Score 19; DB 2; Length 15;
Best Local Similarity 42.9%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSFE 7
|:|:|
Db 1 EERSEFE 7

RESULT 31

S57517

T cell receptor beta chain V region - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 10-Oct-1995 #sequence_revision 17-Nov-1995 #text_change 05-Nov-1999

C/Accession: S57517

R/Burrows, S.R.; Sillis, S.L.; Moss, D.J.; Khanna, R.; Misko, I.S.; Argact, V.P.

submitted to the EMBL Data Library, June 1995

A/Description: T cell receptor repertoire for a viral epitope in humans is diversified

A/Reference number: S57494

A/Accession: S57517

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-16 <BUR>

A/Cross-references: UNIPARC:UPI0000116739; EMBL:Z49924; NID:9887480; PIDN:CAA90170.1; P

C/Keywords: T-cell receptor

Query Match 28.4%; Score 19; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 4.4e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
|:|:|
Db 1 CASGP 5

RESULT 32

PH1350

Ig heavy chain DJ region (clone C100-109R) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1350

R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1350

A/Molecule type: DNA

A/Residues: 1-18 <WAS>

A/Cross-references: UNIPARC:UPI000017C220

A/Note: the authors translated the stop codons for residues 2 and 11 as X

Query Match 28.4%; Score 19; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 4.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12
|:|:|
Db 12 ILGP 15

RESULT 33

I35141

T-cell receptor delta chain V region (105.28) - mouse (fragment)

C/Species: Mus musculus (house mouse)
 C/Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997
 C/Accession: I35141
 R/Stm, G.K.; Augustin, A.
 Cell 61, 397-405, 1990
 A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell receptor
 A/Reference number: A35141; PMID:90242386; PMID:2110506
 A/Accession: I35141
 A/Status: preliminary; not compared with conceptual translation
 A/Molecule type: mRNA
 A/Residues: 1-18 <STM>
 A/Cross-references: UNIPARC:UPI000017C85A
 C/Keywords: T-cell receptor

Query Match 28.4%; Score 19; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 4.9e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CIGP 12
 DB 1 CAGP 5

RESULT 34
 B44581
 bombinin H Met-8 - yellow-bellied toad
 C/Species: Bombina variegata (yellow-bellied toad)
 C/Date: 27-Jun-1994 #sequence_revision 27-Jun-1994 #text_change 09-Jul-2004
 C/Accession: B44581
 R/Mgnogna, G.; Simmaco, M.; Kreil, G.; Barra, D.
 EMBO J. 12, 4829-4832, 1993
 A/Title: Antibacterial and haemolytic peptides containing D-alloisoleucine from the skin
 A/Reference number: S39612; PMID:9403896; PMID:8223491
 A/Accession: B44581
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <MTG>
 A/Cross-references: UNIPROT:P82282; UNIPARC:UPI00001766D2
 C/Superfamily: bombinin H precursor
 C/Keywords: amidated carboxyl end; D-amino acid
 F/2/Modified site: D-allo-isoleucine (Ile) #status experimental
 F/2/Modified site: amidated carboxyl end (Ile) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 20;
 Best Local Similarity 75.0%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12
 DB 1 ILGP 4

RESULT 35
 C60894
 gamma crystallin III - bullfrog (fragment)
 C/Species: Rana catesbeiana (bullfrog)
 C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
 C/Accession: C60894
 R/Chlou, S.H.
 J. Protein Chem. 7, 527-534, 1988
 A/Title: The protein sequence homology of gamma-crystallins among major vertebrate classes
 A/Reference number: A60894; PMID:89351593; PMID:3255376
 A/Accession: C60894
 A/Molecule type: protein
 A/Residues: 1-20 <CHI>
 A/Cross-references: UNIPROT:Q7LZ98; UNIPARC:UPI000017748D
 C/Superfamily: beta-crystallin
 C/Keywords: duplication; eye lens

Query Match 28.4%; Score 19; DB 2; Length 20;
 Best Local Similarity 33.3%; Pred. No. 5.5e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 4; Gaps 1;

QY 1 DEKN---SFEC 8
 DB 7 EDKNFGRCYEC 18

RESULT 36
 A48394
 major fat-globule membrane protein/MGF-E8 homolog - guinea pig (fragment)
 C/Species: Cavia porcellus (guinea pig)
 C/Date: 19-Nov-1993 #sequence_revision 18-Nov-1994 #text_change 31-Oct-1997
 C/Accession: A48394
 R/Mather, I.H.; Banghart, L.R.; Lane, W.S.
 Biochem. Mol. Biol. Int. 29, 545-554, 1993
 A/Title: The major fat-globule membrane proteins, bovine components 15/16 and guinea-pig 11-like sequences.
 A/Reference number: A48394; PMID:93250576; PMID:8485470
 A/Accession: A48394
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-20 <MAT>
 A/Cross-references: UNIPARC:UPI0000177AF6
 A/Experimental source: milk
 A/Note: sequence extracted from NCBI backbone (NCBIP:131440)
 C/Superfamily: milk fat globule protein; discoidin I amino-terminal homology; EGF homology

Query Match 28.4%; Score 19; DB 2; Length 20;
 Best Local Similarity 37.5%; Pred. No. 5.5e+03;
 Matches 3; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 4 NSPECTIG 11
 DB 13 NGCTCLFG 20

RESULT 37
 A60100
 fimbrial antigen CS4 - Escherichia coli (strain B8775) (fragment)
 C/Species: Escherichia coli
 C/Date: 10-Nov-1992 #sequence_revision 10-Nov-1992 #text_change 09-Jul-2004
 C/Accession: A60100
 R/Wolf, M.K.; Andrews, G.P.; Tall, B.D.; McConnell, M.M.; Levine, M.M.; Boedeker, E.C.
 Infect. Immun. 57, 164-173, 1989
 A/Title: Characterization of CS4 and CS6 antigenic components of PCF8775, a putative col
 A/Reference number: A60100; PMID:89079281; PMID:2491834
 A/Accession: A60100
 A/Molecule type: protein
 A/Residues: 1-20 <WOL>
 A/Cross-references: UNIPROT:Q7M077; UNIPARC:UPI00001781C6
 C/Superfamily: CPA1 fimbrial protein
 C/Keywords: fimbria

Query Match 28.4%; Score 19; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 5.5e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 BKNSPEC 8
 DB 2 EKNTVC 8

RESULT 38
 S50743
 proteinase inhibitor (Bowman-Birk) C-II-related protein - potato (fragment)
 N/Alternate names: 10K protein
 C/Species: Solanum tuberosum (potato)
 C/Date: 14-Jul-1995 #sequence_revision 12-Apr-1996 #text_change 09-Jul-2004
 C/Accession: S50743
 R/Mitumori, C.; Yamagishi, K.; Fujino, K.; Kikuta, Y.
 Plant Mol. Biol. 26, 961-969, 1994
 A/Title: Detection of immunologically related Kunitz and Bowman-Birk proteinase inhibi
 A/Reference number: S50743; PMID:95093035; PMID:8000008
 A/Accession: S50743
 A/Molecule type: protein

A/Residues: 1-20 <MT>
A/Cross-references: UNIPROT:Q9S8K0, UNIPARC:UPI000009P9CF

Query Match 28.4%; Score 19; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 5.5e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 1 DDESSKPC 8

RESULT 39

S71593
serine protease inhibitor, 33K - human (fragment)

C/Species: Homo sapiens (man)
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004
C/Accession: S71593
R/Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.

A/Title: Novel extracellular matrix-associated serine protease inhibitors from human
A/Reference number: S71592; PMID:9517768; PMID:7872799
C/Accession: S71593
A/Molecule type: protein

A/Residues: 1-20 <RAO>
A/Cross-references: UNIPROT:Q9UC86, UNIPARC:UPI00000727A3
C/Function:

A/Description: involved in turnover of connective tissues
C/Keywords: serine protease inhibitor

Query Match 28.4%; Score 19; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 5.5e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSPECTIGP 12
DB 9 NNAXITLP 17

RESULT 40

S08605

hypothetical protein 1 estrogen receptor 5'-region - chicken

C/Species: Gallus gallus (chicken)

C/Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change 16-Aug-2004

C/Accession: S08605

R/Kruse, A.; Green, S.; Argos, P.; Kumar, V.; Borner, J.M.; Chambon, P.

EMBO J. 5, 891-897, 1986

A/Title: The chicken oestrogen receptor sequence: homology with v-erbA and the human oes

A/Reference number: S07192; PMID:8624758; PMID:3755102

A/Accession: S08605

A/Status: translation not shown

A/Molecule type: mRNA

A/Residues: 1-20 <KRU>

A/Cross-references: UNIPARC:UPI000011DPID, EMBL:X03805; NID:G63378; PIDN:CAA27431.1; PIR

A/Note: the authors translated the codon TTT for residue 5 as Gly and TTC for residue 16

Query Match 28.4%; Score 19; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 5.5e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPEC 8
DB 11 EPQNRFWC 18

RESULT 41

PH1180

T-cell receptor alpha chain V region (Cw3/5B8) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1180

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto

A/Reference number: S26512; PMID:92364546; PMID:1380061

A/Accession: PH1180

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

A/Cross-references: UNIPARC:UPI000017C39A

Query Match 26.9%; Score 18; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
DB 1 CALG 4

RESULT 42

PH1179

T-cell receptor alpha chain V region (Cw3/HLA1C8) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1179

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto

A/Reference number: S26512; PMID:92364546; PMID:1380061

C/Accession: PH1179

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

A/Cross-references: UNIPARC:UPI000017C3A1

Query Match 26.9%; Score 18; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
DB 1 CALG 4

RESULT 43

PH1181

T-cell receptor alpha chain V region (Cw3/HLA1G6) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1181

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto

A/Reference number: S26512; PMID:92364546; PMID:1380061

C/Accession: PH1181

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-12 <CAS>

A/Cross-references: UNIPARC:UPI000017C3A2

Query Match 26.9%; Score 18; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 5e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
DB 1 CALG 4

RESULT 44

NTKNAS

alpha-conotoxin S1A - cone shell (Conus striatus)

C/Species: Conus striatus (striated cone)

C/Date: 30-Sep-1992 #sequence_revision 30-Sep-1992 #text_change 09-Jul-2004

C/Accession: A40312

R.Myers, R.A.; Zafaralla, G.C.; Gray, W.R.; Abbott, J.; Cruz, L.J.; Olivera, B.M.
 Biochemistry 30, 9370-9377, 1991
 A>Title: alpha-Conotoxins, small peptide probes of nicotinic acetylcholine receptors.
 A/Reference number: A40312; MUID:91369955; PMID:1692838
 A/Accession: A40312
 A/Molecule type: protein
 A/Residues: 1-13 <MYE>

A/Cross-references: UNIPROT:P28878; UNIPARC:UPI0000035428
 C/Comment: This paralytic toxin from a fish-hunting cone snail inhibits the acetylcholin
 C/Superfamily: alpha-conotoxin
 C/Keywords: acetylcholine receptor inhibitor; amidated carboxyl end; postsynaptic neuro
 P/2-7,3-13/Disulfide bonds: #status experimental
 P/13/Modified site: amidated carboxyl end (Cys) #status experimental

Query Match 26.9%; Score 18; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 5 SFFC 8
 DB 10 NFDC 13

RESULT 45
 149637
 deoxynucleotidyltransferase - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C/Accession: I49637
 R/Kotwal, O.; Kaneda, T.; Morishita, R.
 Biochem. Biophys. Res. Commun. 144, 185-190, 1987
 A>Title: Analysis of human terminal deoxynucleotidyl transferase cDNA expressible in man
 A/Reference number: I45884; MUID:87213162; PMID:3579900
 A/Accession: I49637
 A/Status: preliminary; translated from GB/EMBL/DBU
 A/Molecule type: mRNA
 A/Residues: 1-13 <RES>
 A/Cross-references: UNIPROT:Q60517; UNIPARC:UPI0000055AC0; GB:M26145; NID:g951208; PIND:
 A/Genes: DNTT

Query Match 26.9%; Score 18; DB 2; Length 13;
 Best Local Similarity 25.0%; Pred. No. 5.4e+03;
 Matches 2; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 3 KNSPECTL 10
 DB 3 QTRLDCTL 10

RESULT 46
 PH0795
 T-cell receptor alpha chain (KI V-alpha-4.3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0795
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A/Reference number: PH0746; MUID:92078846; PMID:1836010
 A/Accession: PH0795
 A/Molecule type: mRNA
 A/Residues: 1-14 <CAS>
 A/Cross-references: UNIPARC:UPI000017C779; EMBL:X60900
 A/Experimental source: T lymphocyte
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11

DB 1 CALG 4

RESULT 47
 PH0804
 T-cell receptor alpha chain (L4) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0804
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A/Reference number: PH0746; MUID:92078846; PMID:1836010
 A/Accession: PH0804
 A/Molecule type: mRNA
 A/Residues: 1-14 <CAS>
 A/Cross-references: UNIPARC:UPI000017C77A; EMBL:X60913
 A/Experimental source: T lymphocyte
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
 DB 1 CALG 4

RESULT 48
 PH0776
 T-cell receptor alpha chain (M1 V-alpha-8.F3.3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0776
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A>Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A/Reference number: PH0746; MUID:92078846; PMID:1836010
 A/Accession: PH0776
 A/Molecule type: mRNA
 A/Residues: 1-14 <CAS>
 A/Cross-references: UNIPARC:UPI000017C77C; EMBL:X60873
 A/Experimental source: T lymphocyte
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 14;
 Best Local Similarity 75.0%; Pred. No. 5.8e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
 DB 1 CALG 4

RESULT 49
 S21747
 glutamate dehydrogenase [NAD(P)] (EC 1.4.1.3) - Pyrococcus furiosus
 C/Species: Pyrococcus furiosus
 C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004
 C/Accession: S21747
 R/Robb, F.T.; Park, J.B.; Adams, M.W.W.
 Biochem. Biophys. Acta 1120, 267-272, 1992
 A>Title: Characterization of an extremely thermostable glutamate dehydrogenase: a key e
 A/Reference number: S21747; MUID:92247806; PMID:1576153
 A/Accession: S21747
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-14 <ROB>
 A/Cross-references: UNIPROT:Q9UWM2; UNIPARC:UPI0000062915

C/Keywords: oxidoreductase

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 14;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;QY 2 EKNSPFCIL 10
|:|:|:|:
Db 3 EQDPYEIVY 11

RESULT 50

S26524

T-cell receptor alpha chain V region (clone Cw3/5B8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/5B8

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C/Accession: S26524

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26524

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI00001769B9; EMBL:X67975

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/5B8

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;QY 8 CILG 11
|:|:|:|:
Db 1 CALG 4

RESULT 51

S26523

T-cell receptor alpha chain V region (clone Cw3/HLA1C8) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/HLA1C8

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C/Accession: S26523

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26523

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI00001769B8; EMBL:X67974

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1C8

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;QY 8 CILG 11
|:|:|:|:
Db 1 CALG 4

RESULT 52

S26525

T-cell receptor alpha chain V region (clone Cw3/HLA1G6) - mouse (fragment)

C/Species: Mus musculus (house mouse)

A/Variety: clone Cw3/HLA1G6

C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999

C/Accession: S26525

R/Casanova, J.L.; Cerottini, J.C.; Matthes, M.; Necker, A.; Gournier, H.; Barra, C.; Wi

J. Exp. Med. 176, 439-447, 1992

A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell recepto

A/Reference number: S26512; MUID:92364546; PMID:1380061

A/Accession: S26525

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI00001769B8; EMBL:X67976

A/Experimental source: cytolytic T-lymphocyte, clone Cw3/HLA1G6

C/Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: T-cell receptor

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 15;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;QY 8 CILG 11
|:|:|:|:
Db 1 CALG 4

RESULT 53

PA0020

protein QA100028 - Arabidopsis thaliana (fragment)

C/Species: Arabidopsis thaliana (mouse-ear cress)

C/Date: 30-Jun-1992 #sequence_revision 06-Jan-1995 #text_change 06-Jun-1997

C/Accession: PA0020

R/Kamo, M.; Kawakami, T.; Miyatake, N.; Tsugita, A.

submitted to JIPID, July 1994

A/Description: Separation and characterization of Arabidopsis proteins by two-dimension

A/Reference number: PA0001

A/Accession: PA0020

A/Molecule type: protein

A/Residues: 1-15 <KAM>

A/Cross-references: UNIPARC:UPI000017AFB7

A/Experimental source: callus

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 15;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;QY 2 EKNSPFC 7
|:|:|:|:
Db 9 BBSGFE 14

RESULT 54

PH1762

T cell receptor alpha chain V region (clone IV alpha 23-1) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1762

R/Porcelli, S.; Yockey, C.R.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 178, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1762

A/Status: preliminary

A/Molecule type: mRNA

A/Residues: 1-15 <POR>

A/Cross-references: UNIPARC:UPI000017C36D

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 15;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;QY 4 NSPFCILG 11
|:|:|:|:
Db 8 SSKYKIFG 15

RESULT 55

PH0782
T-cell receptor alpha chain (H3 V-alpha-10. TA57) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
C/Accession: PH0782
R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourileky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor gene in a series of class I major histocompatibility complex-I allele exclusion and antigen-specific repertoire.
A/Reference number: PH0746; MUID:92078846; PMID:1636010
A/Accession: PH0782
A/Molecule type: mRNA
A/Residues: 1-15 <CAS>
A/Cross-references: UNIPARC:UPI000017C771; EMBL:X60883
A/Experimental source: T lymphocyte
A/Note: the authors translated the codon TTC for residue 6 as Ieu
C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 15;
Best Local Similarity 75.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
DB 1 CALG 4

RESULT 56

F44908
Chitinase (EC 3.2.1.14), 23.4K - Streptomyces olivaceoviridis (fragment)
C/Species: Streptomyces olivaceoviridis
C/Date: 01-Apr-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: F44908
R/Romaguera, A.; Menge, U.; Breves, R.; Diekmann, H.
J. Bacteriol. 174, 3450-3454, 1992
A/Title: Chitinases of Streptomyces olivaceoviridis and significance of processing for
A/Reference number: A44908; MUID:92276319; PMID:1592803
A/Accession: F44908
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <ROM>
A/Cross-references: UNIPROT:Q9RSK7; UNIPARC:UPI0000088ADC
A/Experimental source: ATCC 11238
A/Note: sequence extracted from NCBI backbone (NCBIRP.104594)
C/Superfamily: lectin-related plant chitinase, hevein chitin-binding domain homology; p
C/Keywords: glycosidase; hydrolase; polysaccharide degradation

Query Match 26.9%; Score 18; DB 2; Length 16;
Best Local Similarity 75.0%; Pred. No. 6.7e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSP 6
DB 10 RNSP 13

RESULT 57

PH1778
T cell receptor alpha chain V region (clone 1PB1 V alpha 24-5) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH1778
R/Porcili, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.
J. Exp. Med. 178, 1-16, 1993
A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1778
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-16 <POR>
A/Cross-references: UNIPARC:UPI000017C36C

Query Match 26.9%; Score 18; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 12
DB 3 CVPF 7

RESULT 58

A60839
neurokinin A homolog - marbled electric ray
N/Alternate names: des-Ser(1), Pro(2) scyllorhinin II
C/Species: Torpedo marmorata (marbled electric ray)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: A60839
R/Conlon, J.M.; Thim, L.
Gen. Comp. Endocrinol. 71, 383-388, 1988
A/Title: Isolation of the tachykinin, Des(Ser(1)Pro(2)) scyllorhinin II from the intestine
A/Reference number: A60839; MUID:89053024; PMID:2847952
A/Accession: A60839
A/Molecule type: protein
A/Residues: 1-16 <CON>
A/Cross-references: UNIPROT:Q7LZ48; UNIPARC:UPI000017BF38
C/Keywords: amidated carboxyl end; neuropeptide; tachykinin
P/6/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 26.9%; Score 18; DB 2; Length 16;
Best Local Similarity 40.0%; Pred. No. 6.7e+03;
Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLG 11
DB 10 DCRVG 14

RESULT 59

B49404
T-cell receptor beta chain VDJ region - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 07-Apr-1994 #sequence_revision 18-Nov-1994 #text_change 23-Jul-1999
C/Accession: B49404
R/Brooks, B.G.; Balk, S.P.; Aupetit, K.; Colonna, M.; Strominger, J.L.; Groh-Spies, V.
Proc. Natl. Acad. Sci. U.S.A. 90, 11787-11791, 1993
A/Title: Human T-cell receptor (TCR) alpha/beta + CD4-CD8- T cells express oligoclonal
A/Reference number: A49404; MUID:94089717; PMID:7505446
A/Accession: B49404
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-17 <BRO>
A/Cross-references: UNIPARC:UPI0000176B42; GB:867400; NID:9455868; PIDN:AMB29275.1; PID
A/Experimental source: alpha/beta + CD4-CD8- T cells
A/Note: sequence extracted from NCBI backbone (NCBIN:141024, NCBIRP.141025)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 17;
Best Local Similarity 30.0%; Pred. No. 7.1e+03;
Matches 3; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 KNSP 12
DB 7 QGGYEQYF 16

RESULT 60

B44873
caldesmon - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
C/Accession: B44873
R/Ikebe, M.; Hornick, T.

Arch. Biochem. Biophys. 288, 538-542, 1991
 A/Title: Determination of the phosphorylation sites of smooth muscle caldesmon by proteolysis
 A/Reference number: A44873; MUID:91378498; PMID:1898046
 A/Accession: B44873

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-17 <IKB>
 A/Cross-references: UNIPROT:Q9TRW1; UNIPARC:UPI0000086A9
 A/Experimental source: skeletal myosin
 A/Note: sequence extracted from NCBI Backbone (NCBIP:63202)
 C/Superfamily: caldesmon

Query Match 26.9%; Score 18; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 7.1e+03;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSP 7
 DB 4 EKQSV 9

RESULT 61

I49593
 cyctic fibrosis transmembrane conductance regulator - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 20-Aug-1999
 C/Accession: I49593
 R/Denatur. B.; Chehab, P.F.
 Hum. Mol. Genet. 3, 1089-1094, 1994
 A/Title: Analysis of the mouse and rat CFTR promoter regions.
 A/Reference number: I49593; MUID:95072572; PMID:7526924
 A/Accession: I49593

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPARC:UPI000016CC99; GB:L04873; NID:G414726; FIDN:AAA73562.1; PID:
 C/Genetic:
 A/Genes: CFTR
 C/Superfamily: cyctic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 26.9%; Score 18; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSP 6
 DB 7 EKASF 11

RESULT 62

I84733
 gene CFTR protein - rat (fragment)
 C/Species: Rattus norvegicus (Norway rat)
 C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 09-Jul-2004
 C/Accession: I84733
 R/Denatur. B.; Chehab, P.F.
 Hum. Mol. Genet. 3, 1089-1094, 1994
 A/Title: Analysis of the mouse and rat CFTR promoter regions.
 A/Reference number: I49593; MUID:95072572; PMID:7526924
 A/Accession: I84733

A/Status: preliminary; translated from GB/EMBL/DBJ
 A/Molecule type: DNA
 A/Residues: 1-17 <RES>
 A/Cross-references: UNIPROT:P34158; UNIPARC:UPI000016CC99; GB:L26098; NID:G425185; FIDN:
 C/Genetic:
 A/Genes: CFTR
 C/Superfamily: cyctic fibrosis transmembrane conductance regulator; ATP-binding cassette

Query Match 26.9%; Score 18; DB 2; Length 17;
 Best Local Similarity 80.0%; Pred. No. 7.1e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSP 6

DB 7 EKASF 11

RESULT 63

PT0234
 Ig heavy chain CRD3 region (clone 1-130) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0234
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Roveya, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0234

A/Molecule type: DNA
 A/Residues: 1-17 <YAM>
 A/Cross-references: UNIPARC:UPI000017C1B0
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 17;
 Best Local Similarity 50.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECLIG 11
 DB 10 FDMWLG 15

RESULT 64

PH0809
 T-cell receptor alpha chain (RF3.10.3) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0809
 R/Casanova, J.L.; Romero, P.; Widmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A/Reference number: PH0746; MUID:92078846; PMID:1896010
 A/Accession: PH0809

A/Molecule type: mRNA
 A/Residues: 1-17 <CAS>
 A/Cross-references: UNIPARC:UPI000017C785; EMBL:X60920
 A/Experimental source: T lymphocyte
 C/Keywords: T-cell receptor

Query Match 26.9%; Score 18; DB 2; Length 17;
 Best Local Similarity 75.0%; Pred. No. 7.1e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILG 11
 DB 1 CALG 4

RESULT 65

PH1794
 T cell receptor alpha chain V region (clone 3DN V alpha 24-4) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
 C/Accession: PH1794
 R/Porcili, S.; Yockey, C.B.; Brenner, M.B.; Balk, S.P.
 J. Exp. Med. 178, 1-16, 1993
 A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057
 A/Accession: PH1794
 A/Status: preliminary
 A/Molecule type: mRNA
 A/Residues: 1-18 <POR>
 A/Cross-references: UNIPARC:UPI000017C382

Query Match 26.9%; Score 18; DB 2; Length 18;
 Best Local Similarity 40.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
 |||
 Db 3 CVTTP 7

RESULT 66

S36121
 lectin - spurge (Euphorbia characias)

C/Species: Euphorbia characias
 C/Date: 09-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C/Accession: S36121
 R/Title: Purification and partial characterization of a mitogenic lectin from the latex
 A/Reference number: S36120; MUID:9357266; PMID:8353129

A/Accession: S36121
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-18 <SN1>

A/Cross-references: UNIPROT:P33888; UNIPARC:UPI00001256C0

Query Match 26.9%; Score 18; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 7.5e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 SPECILGP 12
 |||
 Db 3 SYTPISGP 10

RESULT 67

B24867

scyllorhin II - smaller spotted catshark

C/Species: Scyllorhinus canicula (smaller spotted dogfish)

C/Date: 02-Jun-1988 #sequence_revision 02-Jun-1988 #text_change 09-Jul-2004

C/Accession: B24867

R/Conlon, J.M.; Deacon, C.F.; O'Toole, L.; Thim, L.

FEBS Lett. 200, 111-116, 1986

A/Title: Scyllorhin II and II: two novel tachykinins from dogfish gut.

A/Reference number: A91359; MUID:8612829; PMID:2422058

A/Accession: B24867

A/Molecule type: protein

A/Residues: 1-18 <CON>

A/Cross-references: UNIPROT:P08609; UNIPARC:UPI0000035237

C/Keywords: amidated carboxyl end; neuropeptide

F/18/Modified site: amidated carboxyl end (Met) #status experimental

Query Match 26.9%; Score 18; DB 2; Length 18;
 Best Local Similarity 40.0%; Pred. No. 7.5e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECLIG 11
 |||
 Db 12 DCFVG 16

RESULT 68

A21182

4K prothoracicotropic hormone I - silkworm (fragment)

C/Species: Bombyx mori (silkworm)

C/Date: 03-Aug-1990 #sequence_revision 03-Aug-1990 #text_change 09-Jul-2004

C/Accession: A21182

R/Nagasawa, H.; Kataoka, H.; Iseogi, A.; Tamura, S.; Suzuki, A.; Ishizaki, H.; Mizoguchi

Science 226, 1344-1345, 1984

A/Title: Amino-terminal amino acid sequence of the silkworm prothoracicotropic hormone:

A/Reference number: A21182

A/Accession: A21182

A/Status: preliminary

A/Molecule type: protein
 A/Residues: 1-19 <NAG>
 A/Cross-references: UNIPROT:P26733; UNIPARC:UPI0000176660
 C/Superfamily: Insulin

Query Match 26.9%; Score 18; DB 2; Length 19;
 Best Local Similarity 50.0%; Pred. No. 7.9e+03;
 Matches 3; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 7 ECLIGP 12
 |||
 Db 5 ECCFRP 10

RESULT 69

H61491

seed protein ws-24 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 07-Oct-1994

C/Accession: H61491

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two-d.

A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: H61491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-19 <HR>

A/Cross-references: UNIPARC:UPI000017B071

C/Keywords: glycoprotein; seed

Query Match 26.9%; Score 18; DB 2; Length 19;
 Best Local Similarity 66.7%; Pred. No. 7.9e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFE 7
 |||
 Db 12 EKNSNE 17

RESULT 70

S50175

kallikrein (PK-120) - human

C/Species: Homo sapiens (man)

C/Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995

C/Accession: S50175

R/Pu, X.P.; Iwamoto, A.; Nishimura, H.; Nagasawa, S.

Biochim. Biophys. Acta 1208, 338-343, 1994

A/Title: Purification and characterization of a novel substrate for plasma kallikrein (

A/Reference number: S50175; MUID:95035036; PMID:7947966

A/Accession: S50175

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <PDX>

A/Cross-references: UNIPARC:UPI000017C287

Query Match 26.9%; Score 18; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 8.3e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSFE 7
 |||
 Db 1 EKNGID 6

RESULT 71

PH1783

T cell receptor alpha chain V region (clone 2D9 V alpha 24-4) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999

C/Accession: PH1783

R/Porcell, S.; Yockey, C.E.; Brenner, M.B.; Balk, S.P.

J. Exp. Med. 176, 1-16, 1993

A/Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood

A/Reference number: PH1754; MUID:93301585; PMID:8391057

A/Accession: PH1783

A/Structure: preliminary

A/Molecule type: mRNA

A/Residues: 1-20 <FOR>

A/Cross-references: UNIPARC:UPI000017C376

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 8 ILGP 12

DB 3 CVRP 7

RESULT 72

A31516

lectin, galactose/N-acetylglactosamine-specific - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 18-Jun-1993

C/Accession: A31516

R/II, M.; Kawasaki, T.; Yamashina, I.

Biochem. Biophys. Res. Commun. 155, 720-725, 1988

A/Title: Structural similarity between the macrophage lectin specific for galactose/N-ac

A/Reference number: A31516; MUID:8833956; PMID:3421964

A/Molecule type: protein

A/Residues: 1-20 <IX>

A/Cross-references: UNIPARC:UPI000017C946

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEKN 4

DB 6 EKN 9

RESULT 73

S29636

jacalin beta-1 chain - Artocarpus champeden (fragment)

C/Species: Artocarpus champeden

C/Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C/Accession: S29636

R/NGOC, L.D.; Brillard, M.; Hoebeke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD

A/Reference number: S29635; MUID:93152601; PMID:8427879

A/Accession: S29636

A/Residues: 1-20 <NGO>

A/Cross-references: UNIPROT:Q9S8T0; UNIPARC:UPI00000A4123

A/Experimental source: seed

C/Function: heterotetramer; two alpha and two beta chains

A/Description: seed storage protein

A/Note: lectin for D-galactose-beta-1->3-N-acetylglactosamine, a tumor-associated T-ce

C/Keywords: heterotetramer, lectin, seed, storage protein

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12

DB 11 IVGP 14

RESULT 74

S03987

agglutinin beta-2 chain - Oseage orange

C/Species: MacLura pomifera (Oseage orange)

C/Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 09-Jul-2004

C/Accession: S03987

R/Young, N.M.; Johnston, R.A.Z.; Szabo, A.G.; Watson, D.C.

Arch. Biochem. Biophys. 270, 596-603, 1989

A/Title: Homology of the D-galactose-specific lectins from Artocarpus integrifolia and

A/Reference number: S03983; MUID:89206218; PMID:2705782

A/Accession: S03987

A/Molecule type: protein

A/Residues: 1-20 <YOU>

A/Cross-references: UNIPROT:P18676; UNIPARC:UPI0000111F85

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12

DB 10 IVGP 13

RESULT 75

B61497

seed protein w8-20 - winged bean (fragment)

C/Species: Psophocarpus tetragonolobus (winged bean)

C/Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004

C/Accession: B61497

R/Hirano, H.

J. Protein Chem. 8, 115-130, 1989

A/Title: Microsequence analysis of winged bean seed proteins electrophoretically separated from two di

A/Reference number: A61491; MUID:89351606; PMID:2765119

A/Accession: B61497

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <HIR>

A/Cross-references: UNIPROT:Q9S8J4; UNIPARC:UPI000017B06E

C/Keywords: glycoprotein; seed

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFE 7

DB 12 EKNSNE 17

RESULT 76

AB0120

insertion element protein (partial) [imported] - Yersinia pestis (strain CO92)

C/Species: Yersinia pestis

C/Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C/Accession: AB0120

R/Parikh, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A/Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A/Reference number: AB0001; MUID:21470413; PMID:11586360

A/Accession: AB0120

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-20 <KIR>

A/Cross-references: UNIPROT:Q8ZHC1; UNIPARC:UPI00000CD77D; GB:AL590842; PTDN:CA089824.1

C/Genetics:

A/Gene: im8B

Query Match

Best Local Similarity 26.9%; Score 18; DB 2; Length 20;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSF 6
||:|
Db 8 DEQMSF 13

RESULT 77

A33098
244K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)
C/Species: Plasmodium falciparum
C/Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 09-Jun-2000
C/Accession: A33098
R/Nichols, J.H.; Hager, L.P.
submitted to the Protein Sequence Database, May 1990
A/Reference number: A33098
A/Accession: A33098
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7 <NIC>
A/Cross-references: UNIPARC:UPI000017B5E9

Query Match 25.4%; Score 17; DB 2; Length 7;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12
||:|
Db 2 LGP 4

RESULT 78

I54017
granulocyte-colony stimulating factor precursor - synthetic (fragment)
C/Species: synthetic
A/Note: human gene engineered and expressed in Escherichia coli
C/Date: 28-Jan-2000 #sequence_revision 28-Jan-2000 #text_change 28-Jan-2000
C/Accession: I54017
R/Devlin, P.E.; Drummond, R.J.; Toy, P.; Mark, D.F.; Watt, K.W.; Devlin, J.J.
Gene 65, 13-22, 1988
A/Title: Alteration of amino-terminal codons of human granulocyte-colony-stimulating fac
1.
A/Reference number: I54017; MUID:88284374; PMID:2456256
A/Accession: I54017
A/Status: translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-8 <DEV>
A/Cross-references: UNIPARC:UPI0000000448; GB:M20922; NID:g806638; PIDD:AAA6353.1; PID:

Query Match 25.4%; Score 17; DB 4; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12
||:|
Db 4 LGP 6

RESULT 79

S65728
hemoglobin, extracellular, chain d1 - earthworm (Lumbricus terrestris) (fragment)
C/Species: Lumbricus terrestris (common earthworm)
C/Date: 06-Dec-1996 #sequence_revision 13-Mar-1997 #text_change 31-Dec-2004
C/Accession: S65728
R/Puhtant, K.; Higashiyama, K.; Asao, M.; Hosokawa, K.
Biochim. Biophys. Acta 1292, 273-280, 1996
A/Title: Characterization of the constitutive polypeptides of the extracellular hemoglobin
A/Reference number: S65721; MUID:96176855; PMID:8597573
A/Accession: S65728
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <FUS>
A/Cross-references: UNIPROT:O61233; UNIPARC:UPI000017BD82
C/Superfamily: extracellular hemoglobin

Query Match 25.4%; Score 17; DB 2; Length 10;
Best Local Similarity 50.0%; Pred. No. 6.3e+03;
Matches 2; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 7 ECIL 10
||:|
Db 1 ECLV 4

RESULT 80

PH1583
Ig H chain V-D-J region (wild-type clone 6) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1583
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mlt
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1583
A/Molecule type: DNA
A/Residues: 1-11 <LEV>
A/Cross-references: UNIPARC:UPI000017C6C9
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12
||:|
Db 5 LGP 7

RESULT 81

I41978
Calliphoramide 9 - blowfly fly (Calliphora vomitoria)
C/Species: Calliphora vomitoria
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C/Accession: I41978
R/Duve, H.; Johnsen, A.H.; Sewell, J.C.; Scott, A.G.; Orchard, I.; Rehfeld, J.F.; Thorp
Proc. Natl. Acad. Sci. U.S.A. 89, 2326-2330, 1992
A/Title: Isolation, structure, and activity of -Phe-Met-Arg-Phe-NH-2 neuropeptides (des
A/Reference number: A41978; MUID:92196111; PMID:1549595
A/Accession: I41978
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-11 <DUV>
A/Cross-references: UNIPROT:P41664; UNIPARC:UPI000012A52B
C/Keywords: amidated carboxyl end; neuropeptide
P/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 11;
Best Local Similarity 75.0%; Pred. No. 6.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSF 6
||:|
Db 5 KNSF 8

RESULT 82

C37196
bradykinin-potentiating peptide 3 - island jararaca
C/Species: Bothrops insularis (island jararaca)
C/Date: 14-Feb-1992 #sequence_revision 01-Dec-1992 #text_change 09-Jul-2004
C/Accession: C37196
R/Cintrà, A.C.O.; Vieira, C.A.; Giglio, J.R.
J. Protein Chem. 9, 221-227, 1990
A/Title: Primary structure and biological activity of bradykinin potentiating peptides
A/Reference number: A37196; MUID:90351557; PMID:2386615
A/Accession: C37196

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-11 <CIN>
 A/Cross-references: UNIPROT:P30423; UNIPARC:UPI0000126A91
 C/Keywords: pyroglutamic acid
 F/I/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 11;
 Best Local Similarity 100.0%; Pred. No. 6.9e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LCP 12
 |||
 Db 2 LCP 4

RESULT 83

C20907
 Ig kappa-1 chain J3 region - rabbit
 C/Species: Oryctolagus cuniculus (domestic rabbit)
 C/Date: 10-Aug-1990 #sequence_revision 10-Aug-1990 #text_change 16-Aug-1996
 C/Accession: C20907

R/Emorine, L.; Max, E.E.
 Nucleic Acids Res. 11, 8877-8890, 1983
 A/Title: Structural analysis of a rabbit immunoglobulin kappa2 J-C locus reveals multiple
 A/Reference number: A20907; MUID:84169523; PMID:6324107
 A/Accession: C20907
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-12 <EMO>
 A/Cross-references: UNIPARC:UPI000017C5CF
 C/Keywords: heterotrimer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 12;
 Best Local Similarity 100.0%; Pred. No. 7.6e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 10 LCP 12
 |||
 Db 3 LCP 5

RESULT 84

A49637

MHC class II histocompatibility antigen DRB6 - chimpanzee (fragment)
 C/Species: Pan troglodytes (chimpanzee)
 C/Date: 16-Feb-1996 #sequence_revision 16-Feb-1996 #text_change 09-Jul-2004
 C/Accession: A49637

R/Mayer, W.E.; O'Huigin, C.; Klein, J.
 Proc. Natl. Acad. Sci. U.S.A. 90, 10720-10724, 1993
 A/Title: Resolution of the HLA-DRB puzzle: a case of grafting a de novo-generated exon
 A/Reference number: A49637; MUID:94068473; PMID:8248165
 A/Accession: A49637
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-12 <RES>
 A/Cross-references: UNIPROT:Q07884; UNIPARC:UPI000008A9D0; GB:L19439; NID:9304431; PIDN:
 C/Genetics:
 A/Gene: MHC-DRB6

Query Match 25.4%; Score 17; DB 2; Length 12;
 Best Local Similarity 57.1%; Pred. No. 7.6e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 4 NSPECIL 10
 |||
 Db 4 NSLCLRL 10

RESULT 85

PT0305

Ig heavy chain CRD3 region (clone 5-121) - human (fragment)
 C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C/Accession: PT0305
 R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and
 A/Reference number: PT0222; MUID:91108337; PMID:1899102
 A/Accession: PT0305

A/Molecule type: DNA
 A/Residues: 1-13 <YAM>
 A/Cross-references: UNIPARC:UPI000017C20D
 A/Experimental source: B lymphocyte
 C/Keywords: heterotrimer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 8.2e+03;
 Matches 2; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

OY 6 FEC 8
 |||
 Db 2 FDC 4

RESULT 86

PH0787

T-cell receptor alpha chain (F8) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997
 C/Accession: PH0787

R/Caenova, J.L.; Romero, P.; Midmann, C.; Kourilsky, P.; Maryanski, J.L.
 J. Exp. Med. 174, 1371-1383, 1991
 A/Title: T cell receptor genes in a series of class I major histocompatibility complex-
 allelic exclusion and antigen-specific repertoire.
 A/Reference number: PH0746; MUID:92078846; PMID:1836010
 A/Accession: PH0787
 A/Molecule type: mRNA
 A/Residues: 1-13 <CAS>
 A/Cross-references: UNIPARC:UPI000017C76D; EMBL:X60891
 A/Experimental source: T lymphocyte
 C/Keywords: T-cell receptor

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 100.0%; Pred. No. 8.2e+03;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 CIL 10
 |||
 Db 1 CIL 3

RESULT 87

B42762

proteasome endopeptidase complex (EC 3.4.25.1) subunit 13 - bovine (fragment)
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 17-Feb-2003
 C/Accession: B42762
 R/Dick, L.R.; Moomaw, C.R.; Pramank, B.C.; DeMartino, G.N.; Slaughter, C.A.
 Biochemistry 31, 7347-7355, 1992
 A/Title: Identification and localization of a cysteine1 residue critical for the trypsin
 A/Reference number: B42762; MUID:92378961; PMID:11510924
 A/Accession: B42762

A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-13 <DIC>
 A/Cross-references: UNIPARC:UPI000017CE37
 A/Note: sequence extracted from NCBI backbone (NCBIF:112180)
 C/Keywords: hydrolase

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 44.4%; Pred. No. 8.2e+03;
 Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

OY 1 DEKNSPECT 9
 |||

Db 2 DPEXLPETI 10

RESULT 88

PH1615

Ig H chain V-D-J region (clone B-less 22) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999

C/Accession: PH1615

R/Levinson, D.A.; Campos-Torres, J.; Leder, P.

J. Exp. Med. 178, 317-329, 1993

A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice

A/Reference number: PH1580; MUID:93301609; PMID:8315387

A/Accession: PH1615

A/Molecule type: DNA

A/Residues: 1-14 <LEV>

A/Cross-references: UNIPARC:UPI000017C69E

A/Experimental source: bone marrow pre-B lymphocyte

C/Keywords: immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 75.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKN 4

Db 3 DESN 6

RESULT 89

PT0210

T-cell receptor alpha chain V-J region (4-1-K.1) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C/Accession: PT0210

R/Nakano, N.; Kikuchi, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of islet beta cell-reactive T cells is not restricted

A/Reference number: PT0209; MUID:91217621; PMID:1902501

A/Accession: PT0210

A/Molecule type: mRNA

A/Residues: 1-14 <NAK>

A/Cross-references: UNIPARC:UPI000017C78E

C/Keywords: T-cell receptor

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CIL 10

Db 1 CIL 3

RESULT 90

A41589

25K elastin-binding protein - Staphylococcus aureus (fragment)

C/Species: Staphylococcus aureus

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: A41589

R/Park, P.W.; Roberts, D.D.; Grosso, L.E.; Parke, W.C.; Rosenbloom, J.; Abrams, W.R.; Mc

J. Biol. Chem. 266, 23399-23406, 1991

A/Title: Binding of elastin to Staphylococcus aureus.

A/Reference number: A41589; MUID:92078218; PMID:1744133

A/Accession: A41589

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <PAR>

A/Cross-references: UNIPROT:Q9RSR5; UNIPARC:UPI00000BC64C

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 60.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 KNSFE 7
Db 5 KODFE 9

RESULT 91

S33802

chaperone, TCP1-related - oat

C/Species: Avena sativa (oat)

C/Date: 02-Dec-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C/Accession: S33802

R/Mumme, R.; Gilm, R.; Specht, V.; Eckerskorn, C.; Schiltz, B.; Gatenby, A.A.; Schaefer

Nature 363, 644-648, 1993

A/Title: A TCP1-related molecular chaperone from plants refolds phytochrome to its phot

A/Reference number: S33800; MUID:93288140; PMID:8099715

A/Accession: S33802

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-14 <MDM>

A/Cross-references: UNIPROT:Q7MIG6; UNIPARC:UPI000017B0D7

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LCP 12

Db 7 LCP 9

RESULT 92

S68095

calcium-binding protein, 23k - Orchestia cavimana (fragment)

C/Species: Orchestia cavimana

C/Date: 21-Apr-1997 #sequence_revision 21-Apr-1997 #text_change 09-Jul-2004

C/Accession: S68095

R/Ling, G.; Testeniere, O.; Graf, F.

Biochim. Biophys. Acta 1293, 272-276, 1996

A/Title: Characterization and N-terminal sequencing of a calcium binding protein from ti

A/Reference number: S68095; MUID:96202045; PMID:8620040

A/Accession: S68095

A/Molecule type: protein

A/Residues: 1-14 <LUO>

A/Cross-references: UNIPROT:Q7M3J6; UNIPARC:UPI000017CA5F

C/Keywords: calcium binding

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 60.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNS 5

Db 9 DEKRS 13

RESULT 93

B83836

hypothetical protein BH1490 [imported] - Bacillus halodurans (strain C-125)

C/Species: Bacillus halodurans

C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004

C/Accession: B83836

R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hir

Nucleic Acids Res. 28, 4317-4331, 2000

A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and

A/Reference number: A83650; MUID:20512582; PMID:11058132

A/Accession: B83836

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-14 <STO>

A/Cross-references: UNIPROT:Q9KCS9; UNIPARC:UPI00000C3BC; GB:AP051512; GB:BA000004; NI

A/Experimental source: strain C-125

C/Genetics:

A:Gene: BH1490

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 50.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSF 6
| | |
Db 9 EBASSF 14

RESULT 94

S27140

hypotheetical protein 1 estrogen receptor 5'-region - human

C/Species: Homo sapiens (man)

C/Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 16-Aug-2004

C/Accession: S27140

R/Keaveney, M.; Klug, J.; Gannon, F.

DNA Seq. 2, 347-358, 1992

A/Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene

A/Reference number: S27140; MUID:9307598; PMID:1476547

A/Accession: S27140

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-14 <KEA>

A/Cross-references: UNIPARC:UPI000011DF55; EMBL:X62462; NID:931201; PIND:CAA44319.1; PIR

Query Match 25.4%; Score 17; DB 2; Length 14;

Best Local Similarity 100.0%; Pred. No. 8.8e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12
| | |
Db 12 LGP 14

RESULT 95

PM0004

chlorophyll a/b-binding protein 24.5K - green alga (Dunaliella tertiolecta) (fragment)

N/Alternate names: photosystem II light-harvesting chlorophyll 24.5K protein

C/Species: Dunaliella tertiolecta

C/Date: 04-Sep-1998 #sequence_revision 24-Nov-1999 #text_change 24-Nov-1999

C/Accession: PM0004

R/LaRoche, J.; Bennett, J.; Falkowski, P.G.

Gene 95, 165-171, 1990

A/Title: Characterization of a cDNA encoding for the 28.5-kDa LHClI apoprotein from the

A/Reference number: JMW040; MUID:91065528; PMID:2249775

A/Accession: PM0004

A/Molecule type: protein

A/Residues: 1-15 <LAR>

A/Cross-references: UNIPARC:UPI0000178174

A/Superfamily: chlorophyll a/b-binding protein

C/Keywords: chloroplast; grana; light-harvesting complex; membrane adhesion; membrane pr

Query Match 25.4%; Score 17; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12
| | |
Db 12 LGP 14

RESULT 96

PH1342

Ig heavy chain DJ region (clone C507-95) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1342

R/Wasserman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1342

A/Molecule type: DNA

A/Residues: 1-15 <MAS>

A/Cross-references: UNIPARC:UPI000017C240

C/Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 LGP 12
| | |
Db 10 LGP 12

RESULT 97

PT0097

glutathione peroxidase, non-selenium containing - mouse (fragment)

N/Alternate names: antioxidant protein 2

C/Species: Mus musculus (house mouse)

C/Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 24-Nov-1999

C/Accession: PT0097

R/Kwakam, T.; Uchida, T.; Sakai, T.; Kamo, M.; Morimasa, T.; Tsugita, A.

submitted to JIPID, July 1998

A/Description: Proteome analysis of mouse brain.

A/Reference number: PT0091

A/Accession: PT0097

A/Molecule type: protein

A/Residues: 1-15 <KAW>

A/Cross-references: UNIPARC:UPI000017C66B

A/Experimental source: Brain, striatum

Query Match 25.4%; Score 17; DB 2; Length 15;

Best Local Similarity 66.7%; Pred. No. 9.5e+03;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPF 7
| | |
Db 9 EAPSPF 14

RESULT 98

PH1455

T-cell receptor alpha chain (clone A24/PBF4) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 10-Mar-1994 #sequence_revision 10-Mar-1994 #text_change 15-Mar-2004

C/Accession: PH1455

R/Casanova, J.L.; Martinon, F.; Gournier, H.; Barra, C.; Pannetier, C.; Regnault, A.; K

J. Exp. Med. 177, 811-820, 1993

A/Title: T cell receptor selection by and recognition of two class I major histocompati

A/Reference number: PH1430; MUID:93171821; PMID:8436911

A/Accession: PH1455

A/Molecule type: mRNA

A/Residues: 1-15 <CAS>

A/Cross-references: UNIPARC:UPI000017C762

A/Experimental source: cytolytic T-lymphocyte

C/Keywords: receptor; T-cell

Query Match 25.4%; Score 17; DB 2; Length 15;

Best Local Similarity 100.0%; Pred. No. 9.5e+03;

Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CTL 10
| | |
Db 1 CTL 3

RESULT 99

PA0008

lectin B2 - Peophocarpus scandens (fragment)

C/Species: Peophocarpus scandens

C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004

C/Accession: PA0008

R:Kort, A.A.
 Phytochemistry 27, 2847-2855, 1988
 A/Title: Isolation and characterization of the lectins from the seeds of Psophocarpus sc
 A/Reference number: PA0005
 A/Accession: PA0008
 A/Molecule type: protein
 A/Residues: 1-15 <KOR>
 A/Cross-references: UNIPROT:P22585; UNIPARC:UPI000012E3B8
 A/Experimental source: seed
 C/Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can be
 C/Keywords: lectin

Query Match 25.4%; Score 17; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSFE 7
 | | |
 | | |
 Db 9 NKFE 12

RESULT 100

A61612
 allatostatin - tobacco hornworm
 C/Species: Manduca sexta (tobacco hornworm)
 C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
 C/Accession: A61612
 R/Kramer, S.V.; Toschl, A.; Miller, C.A.; Kataoka, H.; Quistad, G.B.; Li, J.P.; Carney,
 Proc. Natl. Acad. Sci. U.S.A. 88, 9458-9462, 1991
 A/Title: Identification of an allatostatin from the tobacco hornworm Manduca sexta.
 A/Reference number: A61612; MUID:92052112; PMID:1946359
 A/Accession: A61612
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <KRA>
 A/Cross-references: UNIPROT:P42559; UNIPARC:UPI00001258A8
 C/Keywords: neuropeptide; pyroglutamic acid
 F/1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 9.5e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 ECTIGP 12
 : | |
 : | |
 Db 6 QCYFNP 11

Search completed: January 20, 2006, 19:12:12
 Job time : 6.80769 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 39.9231 Seconds
(without alignments)
212.066 Million cell updates/sec

Title: US-09-662-293-5
Perfect score: 67
Sequence: 1 DEKNSFECILGP 12

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	27	40.3	14	2	016332_HUMAN
2	27	40.3	17	2	092633_CHLTR
3	27	40.3	19	2	071286_CAIER
4	26	38.8	18	2	09ERQ0_MOUSE
5	26	38.8	20	2	09DE23_CHICK
6	25	37.3	13	2	08WEKO_CYCCT
7	25	37.3	17	2	08HKG8_GACAR
8	25	37.3	20	2	09S835_PSORB
9	24	35.8	12	2	06DK20_HUMAN
10	24	35.8	13	2	05D4Q9_PRR12
11	24	35.8	13	2	091874_HPV16
12	24	35.8	13	2	091876_HPV16
13	24	35.8	16	2	091871_HPV16
14	24	35.8	16	2	091879_HPV16
15	24	35.8	16	2	091802_HPV16
16	24	35.8	16	2	091804_HPV16
17	24	35.8	16	2	091806_HPV16
18	24	35.8	16	2	091808_HPV16
19	24	35.8	17	1	091808_HPV16
20	24	35.8	19	2	071285_CAIER
21	24	35.8	20	2	04YR89_PLABR
22	24	35.8	12	2	09YR01_GCORO
23	23	34.3	13	2	05F3D0_CHICK
24	23	34.3	16	2	09N0P9_CANFA
25	23	34.3	17	2	08HKE2_GACAR
26	23	34.3	17	2	08HKE6_GACAR
27	23	34.3	17	2	08HKE2_GACAR
28	23	34.3	18	2	04XX11_PLACH
29	23	34.3	20	2	072579_HUMAN
30	23	34.3	20	2	04XN21_PLACH
31	23	34.3	20	2	095M09_PANTR

32	23	34.3	20	2	095MK0_PONPY	095mk0_pongo pygma
33	23	34.3	20	2	095MK1_COIAN	095mk1_colobus ang
34	23	34.3	20	2	095MK2_PAPCY	095mk2_papio cynoc
35	22	32.8	10	1	RCA_PINS	P81094 pinus pinas
36	22	32.8	10	2	07RQJ0_PLAVO	07rqj0_plasmodium
37	22	32.8	11	2	08UDP1_XENLA	08udp1_xenopus lae
38	22	32.8	13	2	06LDS1_BPT3	06lds1_bacterioph
39	22	32.8	14	2	081027_MOUSE	081027_mus musculu
40	22	32.8	14	2	093202_GICRC	093202_porcine cir
41	22	32.8	14	2	077NR3_GICRC	077nr3_porcine cir
42	22	32.8	14	2	077RC0_GICRC	077rc0_porcine cir
43	22	32.8	14	2	077RM6_GICRC	077rm6_porcine cir
44	22	32.8	14	2	077S02_GICRC	077s02_porcine cir
45	22	32.8	14	2	077S09_GICRC	077s09_porcine cir
46	22	32.8	14	2	077S13_GICRC	077s13_bovine cirtc
47	22	32.8	15	1	FIBA_ANAFL	P12801 anas platyr
48	22	32.8	15	2	05RLM1_HUMAN	05rlm1_homo sapien
49	22	32.8	17	2	09TWC6_DIRIM	09twc6_dirofilaria
50	22	32.8	17	2	06OLM0_GINFA	06olm0_influenza a
51	22	32.8	17	2	06OLM1_GINFA	06olm1_influenza a
52	22	32.8	17	2	09DPB5_BRABE	09dpb5_brachydanio
53	22	32.8	19	2	06SE40_DROSI	06se40_drosophila
54	22	32.8	19	2	09TWH8_PARCW	09twh8_parralithode
55	22	32.8	19	2	06OLM2_GINFA	06olm2_influenza a
56	22	32.8	22	2	04X7B9_PLACH	04x7b9_plasmodium
57	21	31.3	10	2	09R791_BORAP	09r791_borrelia af
58	21	31.3	11	2	09R790_BORAP	09r790_borrelia ga
59	21	31.3	14	2	06LEM9_ARATH	06lem9_arabidopsis
60	21	31.3	14	2	056127_GICRC	056127_porcine cir
61	21	31.3	15	2	06LC27_HUMAN	06lc27_homo sapien
62	21	31.3	15	2	09RAU8_FACIC	09rau8_actinobact
63	21	31.3	16	1	PA2_NAUSP	Q10756 naja sputat
64	21	31.3	17	2	Q14316_HUMAN	Q14316_homo sapien
65	21	31.3	17	2	06OL17_GINFA	06ol17_influenza a
66	21	31.3	18	2	06OL19_GINFA	06ol19_influenza a
67	21	31.3	18	2	04X7V0_PLACH	04x7v0_plasmodium
68	21	31.3	19	2	04Y1S4_PLACH	04y1s4_plasmodium
69	21	31.3	19	2	08UH22_CHICK	08uh22_gallus gall
70	21	31.3	19	2	08UVE0_CHICK	08uve0_gallus gall
71	21	31.3	19	2	05PU92_BRABE	05pu92_brachydanio
72	21	31.3	20	1	MHT_BOMMX	P83086 bombina max
73	21	31.3	20	1	MHT_BOMMX	P83087 bombina max
74	21	31.3	20	2	04YTES_PLABE	04ytes_plasmodium
75	21	31.3	20	2	049448_MYCCE	049448_mycoplasma
76	21	31.3	20	2	04G2P1_MYCTU	04g2p1_mycobacteri
77	21	31.3	20	2	06TH87_MOUSE	06th87_mus musculu
78	21	31.3	20	2	07LZ97_MOUSE	07l297_rana catesb
79	20	29.9	12	2	012036_CAVV	012036_caprine art
80	20	29.9	14	2	06LCK3_HUMAN	06lck3_homo sapien
81	20	29.9	15	2	09Y4Z9_HUMAN	09y4z9_homo sapien
82	20	29.9	16	2	07M2P4_PIG	07m2p4_sus scrofa
83	20	29.9	17	2	05B1H5_EMEHI	05b1h5_aespergillus
84	20	29.9	17	2	04XMI0_PLACH	04xmi0_plasmodium
85	20	29.9	17	2	0704V9_BOVIN	0704v9_bos taurus
86	20	29.9	17	2	0712K0_CAPIH	0712k0_capra hircu
87	20	29.9	18	1	HSTB_ECOLI	P01560 escherichia
88	20	29.9	18	2	07M532_HALMA	07m532_haloarcula
89	20	29.9	18	2	07S364_NEUPR	07s364_neurospora
90	20	29.9	18	2	07M0U3_CITPR	07m0u3_citrobacter
91	20	29.9	18	2	07M076_RAT	07m076_rattus norv
92	20	29.9	19	1	DURR_STRGV	P36504 streptococc
93	20	29.9	19	1	DURR_STRGV	P36502 streptococc
94	20	29.9	19	1	LANC_STRS6	P38655 trypanosoma
95	20	29.9	19	2	09TWK8_GTRAP	09twk8_cryptosporo
96	20	29.9	19	2	04X4E2_PLACH	04x4e2_plasmodium
97	20	29.9	19	2	04Y9U4_PLABR	04y9u4_plasmodium
98	20	29.9	19	2	09G197_GPRAB	09g197_saragassum p
99	20	29.9	19	2	0570L9_ARATH	0570l9_arabidopsis
100	20	29.9	20	2	Q16129_HUMAN	Q16129_homo sapien

ALIGNMENTS

```

RESULT 1
Q16332_HUMAN
ID Q16332_HUMAN PRELIMINARY; PRT; 14 AA.
AC Q16332;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE FLT (Fragment).
GN Name=flt;
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OC NCBI_Taxid=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95222657; PubMed=7707437;
RA Boocock C.A., Charnock-Jones D.S., Sharkey A.M., McLaren J.,
RA Barker P.J., Wright K.A., Twentymen P.R., Smith S.K.;
RT "Expression of vascular endothelial growth factor and its receptors
RT flt and KDR in ovarian carcinoma."
RL J. Natl. Cancer Inst. 87:506-516 (1995).
DR EMBL; S77812; AAB34001.1; -; mRNA.
DR PIR; I56493; I56493.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1636 MW; 9141470E2648F62E CRC64;

Query Match 40.3%; Score 27; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 9.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKXSPFCL 9
DB 1 ELSNFECL 8

RESULT 2
Q9ZG33_CHLTR
ID Q9ZG33_CHLTR PRELIMINARY; PRT; 17 AA.
AC Q9ZG33;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
DE Subtilisin/chymotrypsin inhibitor (Fragment).
OS Chlamydia trachomatis.
OC Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
OC NCBI_Taxid=813;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=L2 434B;
RA Wang L., Steenburg S.D., Zheng Y., Larsen S.H.;
RA Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF087336; AAD04110.1; -; Genomic_DNA.
FT NON_TER 17
SQ SEQUENCE 17 AA; 2043 MW; 4FEE704EB041B120 CRC64;

Query Match 40.3%; Score 27; DB 2; Length 17;
Best Local Similarity 83.3%; Pred. No. 1.1e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSP 6
DB 10 DRKNSP 15

RESULT 3
Q7LZ96_CAICR
ID Q7LZ96_CAICR PRELIMINARY; PRT; 19 AA.
AC Q7LZ96;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)

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DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gamma crystallin II (Fragment).
OS Calman crocodilus (Speckled calman) (Calman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Calman.
OC NCBI_Taxid=8499;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89351593; PubMed=3255376;
RA Chion S.H.;
RT "The protein sequence homology of gamma-crystallins among major
RT vertebrate classes and their DNA sequence homology to heat-shock
RT protein genes."
RL J. Protein Chem. 7:527-534 (1988).
DR PIR; A60894; A60894.
DR HSSP; P07320; 1HA4.
DR InterPro; IPR001064; CRYSTALLIN.
DR Pfam; PF00030; CRYSTALL1.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 1.
FT NON_TER 19
SQ SEQUENCE 19 AA; 2236 MW; A95AFC3551E3885A CRC64;

Query Match 40.3%; Score 27; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 1.2e+03;
Matches 6; Conservative 2; Mismatches 0; Indels 4; Gaps 1;

QY 1 DEKN---SFC 8
DB 7 ESKNFQGRSYEC 18

RESULT 4
Q9ER00_MOUSE
ID Q9ER00_MOUSE PRELIMINARY; PRT; 18 AA.
AC Q9ER00;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Amelogenin (Fragment).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_Taxid=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20515040; PubMed=11063035;
RA Snead M.L., Paine M.L., Wen L., Zhu D.-H., Yoshida B., Lei Y.,
RA Chen L., Paine C.T., Burestein J.M., Jitpukdeebudintara S., White S.N.,
RA Bringsas P. Jr.;
RT "Transgene animal model for protein expression and accumulation into
RT forming enamel."
RT Connect. Tissue Res. 38:279-286 (1998).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Snead M.L., Zhu D., Lei Y., Paine M.L.;
RA Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF294397; AAG10078.1; -; Genomic_DNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0007275; P:development; IEA.
DR InterPro; IPR004116; Amelogenin.
DR PANTHER; PTHR10039; Amelogenin; 1.
FT NON_TER 18
SQ SEQUENCE 18 AA; 1913 MW; 302AA3BA4DFB6FC CRC64;

Query Match 38.8%; Score 26; DB 2; Length 18;
Best Local Similarity 66.7%; Pred. No. 1.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECLIG 11
DB 7 FACLIG 12

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RESULT 5

Q9DE23_CHICK PRELIMINARY; PRT; 20 AA.
 ID Q9DE23;
 AC Q9DE23;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE UORP2.
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianine;
 CC Gallus.
 OX NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20528616; PubMed=11073974;
 RX DOI=10.1128/MCB.20.23.8731-8739.2000;
 RA Kobayashi M., Yu R.T., Yasuda K., Umesono K.;
 RT "Cell-type-specific regulation of the retinoic acid receptor mediated by the orphan nuclear receptor RXR."
 RL Mol. Cell. Biol. 20:8731-8739(2000).
 DR EMBL; AF220160; AAC35363.1; -; Genomic DNA.
 SQ SEQUENCE 20 AA; 2261 MW; AA77738B0B3C482 CRC64;

Query Match 38.8%; Score 26; DB 2; Length 20;
 Best Local Similarity 30.0%; Pred. No. 2e+03;

Matches 3; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECIL 10

DB 7 DQLOAFSCV 16

RESULT 6

Q8W6K0_CYCCI PRELIMINARY; PRT; 13 AA.
 ID Q8W6K0;
 AC Q8W6K0;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE NMDH dehydrogenase (Fragment).
 GN Nemeinadi;
 OS Cycas citrinalis (Queen sago).
 CC Mitochondrion.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Cycadophyta; Cycadales; Cycadaceae; Cycas.
 OX NCBI_TaxID=3397;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2155473; PubMed=11697913; DOI=10.1006/mpev.2001.1004;
 RA Gugerli F., Sperisen C., Buchler U., Brunner I., Brodbeck S.,
 RA Palmer J.D., Qiu Y.L.;
 RT "The evolutionary split of Pinaceae from other conifers: evidence from an intron loss and a multigene phylogeny."
 RL Mol. Phylogenet. Evol. 21:167-175(2001).
 DR EMBL; AF227465; AAL38909.1; -; Genomic DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 13 AA; 1339 MW; C00F6BDA894945BD CRC64;

Query Match 37.3%; Score 25; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 SPECILCP 12

DB 3 SYEASIGP 10

RESULT 7

Q8HKG8_9ACAR PRELIMINARY; PRT; 17 AA.
 ID Q8HKG8;
 AC Q8HKG8;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN Name=ND1;
 OS Boophilus geigyl.
 CC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 CC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.
 OX NCBI_TaxID=136141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=2260786; PubMed=12775521; DOI=10.1086/10635150309325;
 RA Murrell A., Campbell N.J.H., Barker S.C.;
 RT "The value of idiosyncratic markers and changes to conserved tRNA sequences from the mitochondrial genome of hard ticks (Acari: Ixodida: Ixodidae) for phylogenetic inference."
 RL Syst. Biol. 52:296-310(2003).
 DR EMBL; AY059200; AAL79403.1; -; Genomic DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 17 AA; 2035 MW; 2E2FE0BFD529C379 CRC64;

Query Match 37.3%; Score 25; DB 2; Length 17;
 Best Local Similarity 57.1%; Pred. No. 2.6e+03;

Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECIL 10

DB 8 NNFICIL 14

RESULT 8

Q9S8J5_PSOTE PRELIMINARY; PRT; 20 AA.
 ID Q9S8J5;
 AC Q9S8J5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
 DE Lectin I (Fragment).
 GN Psophocarpus tetragonolobus (Gua bean) (Asparagus bean).
 OS Psophocarpus tetragonolobus (Gua bean) (Asparagus bean).
 CC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 CC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 CC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
 CC Psophocarpus.
 OX NCBI_TaxID=3891;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95120265; PubMed=7820375;
 RA Yagi F., Sawada R., Inada T., Toyonaga S., Tadara K., Ishinata K.;
 RT "Two isolectins from leaves of winged bean, Psophocarpus tetragonolobus (L.) DC."
 RL Plant Cell Physiol. 35:1087-1095(1994).
 SQ SEQUENCE 20 AA; 2363 MW; 1BF1B347020D3DCE CRC64;

Query Match 37.3%; Score 25; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 3.1e+03;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPECIL 10

DB 12 EKNSNEIL 20

RESULT 9

Q6DKZ0_HUMAN PRELIMINARY; PRT; 12 AA.
 ID Q6DKZ0;
 AC Q6DKZ0;

DT 25-OCT-2004 (TrEMBLrel. 28, Created)
DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
DE DnaU-like heat shock protein (Fragment).
GN Name=DNAJB4;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RX PubMed=15782117;
RA Wang C.C., Tsai M.P., Hong T.M., Chang G.C., Chen C.Y., Yang W.M.,
RA Chen J.C., Yang P.C.;
RT "The transcriptional factor YY1 upregulates the novel invasion
RT suppressor HLI1 expression and inhibits cancer cell invasion";
RL Oncogene 24:4081-4093(2005).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Liver;
RA Wang C.C., Chen J.C., Yang P.C.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY669319; AAT70409.1; -; Genomic DNA.
DR GO; GO:0006457; P:protein folding; IEA.
DR GO; GO:0006986; P:response to unfolded protein; IEA.
KW Heat shock.
FT NON_TER
SQ SEQUENCE 12 AA; 1405 MW; 121CA8B3195EAB4B CRC64;

Query Match 35.8%; Score 24; DB 2; Length 12;
Best Local Similarity 66.7%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 FECLIG 11
:|:|:
Db 5 YXCILG 10

RESULT 10
QSD409.9RHIZ
ID QSD409.9RHIZ PRELIMINARY; PRT; 13 AA.
AC QSD409;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE tRNA-encoded proteolysis-inducing peptide tag (Fragment).
GN Name=STR1;
OS Agrobacterium tumefaciens.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiales; Rhizobium/Agrobacterium group; Agrobacterium.
NCBI_TaxID=358;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NTL4;
RA Williams K.P.;
RT "Phylogenetic analysis of tRNA";
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY911526; AAX12897.1; -; Genomic DNA.
FT NON_TER
SQ SEQUENCE 13 AA; 1304 MW; C47752578BE133D CRC64;

Query Match 35.8%; Score 24; DB 2; Length 13;
Best Local Similarity 40.0%; Pred. No. 3.1e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECIL 10
:|:|:|:
Db 2 NDNNAKCAL 11

RESULT 11

Q918T4.HPV16
ID Q918T4.HPV16 PRELIMINARY; PRT; 13 AA.
AC Q918T4;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF407220; AAL01406.1; -; Genomic DNA.
FT NON_TER
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 35.8%; Score 24; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 3.1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFECLIG 11
:|:|:|:
Db 1 TFKCVSG 7

RESULT 12
Q918T6.HPV16
ID Q918T6.HPV16 PRELIMINARY; PRT; 13 AA.
AC Q918T6;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Cossart Y.B., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
RT cervical cancer isolates from Australia and New Caledonia";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF407219; AAL01403.1; -; Genomic DNA.
FT NON_TER
SQ SEQUENCE 13 AA; 1413 MW; 8AED73A03A52D865 CRC64;

Query Match 35.8%; Score 24; DB 2; Length 13;
Best Local Similarity 42.9%; Pred. No. 3.1e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SFECLIG 11
:|:|:|:
Db 1 TFKCVSG 7

RESULT 13
Q918T1.HPV16
ID Q918T1.HPV16 PRELIMINARY; PRT; 16 AA.
AC Q918T1;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;

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OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
  cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL, AF407221; AL01409.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIG 11
Db 4 TPKCVSG 10

RESULT 14
Q91879_HPV16 PRELIMINARY; PRT; 16 AA.
AC Q91879;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
  cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL, AF407218; AL01400.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIG 11
Db 4 TPKCVSG 10

RESULT 15
Q91802_HPV16 PRELIMINARY; PRT; 16 AA.
AC Q91802;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
  cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).

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DR EMBL, AF407217; AL01397.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIG 11
Db 4 TPKCVSG 10

RESULT 16
Q91804_HPV16 PRELIMINARY; PRT; 16 AA.
AC Q91804;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
  cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL, AF407216; AL01394.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIG 11
Db 4 TPKCVSG 10

RESULT 17
Q91806_HPV16 PRELIMINARY; PRT; 16 AA.
AC Q91806;
DT 01-DEC-2001 (TRENBLREL. 19, Created)
DT 01-DEC-2001 (TRENBLREL. 19, Last sequence update)
DE E1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Watts K.J., Thompson C.H., Coesart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
  cervical cancer isolates from Australia and New Caledonia.";
RL Int. J. Cancer 97:868-874(2002).
DR EMBL, AF407215; AL01391.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIIG 11

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Db          4 TFKCVSG 10

RESULT 18
Q918U8_HPV16
ID Q918U8_HPV16 PRELIMINARY; PRT; 16 AA.
AC Q918U8;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DE B1 protein (Fragment).
OS Human papillomavirus type 16.
OC Viruses; dsDNA viruses, no RNA stage; Papillomaviridae;
OC Alphapapillomavirus.
OX NCBI_TaxID=333760;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21846229; PubMed=11857370;
RA Matte K.J., Thompson C.H., Cosart Y.E., Rose B.R.;
RT "Sequence variation and physical state of human papillomavirus type 16
cervical cancer isolates from Australia and New Caledonia."
RL Int. J. Cancer 97:868-874(2002).
DR EMBL; AF407214; AAL01388.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 16 AA; 1710 MW; 2C7D73A03A17965F CRC64;

Query Match 35.8%; Score 24; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 3.8e+03;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy          5 SPECITLG 11
Db          4 TFKCVSG 10

RESULT 19
CXMAA COMPE STANDARD; PRT; 17 AA.
AC P58926;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Mu-conotoxin Pn1VA.
OS Conus pennaceus (Feathered cone).
OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
OC Apogastropoda; Caenogastropoda; Sorbeoconcha; Hypogastropoda;
OC Neogastropoda; Conoidea; Conus.
OX NCBI_TaxID=37335;
RN [1]
RP PROTEIN SEQUENCE, AND MASS SPECTROMETRY.
RX MEDLINE=95337083; PubMed=7612605;
RA Fainzilber M., Nakamura T., Gaathon A., Lodder J.C., Kitz K.S.,
RA Burlingame A.L., Zlotkin E.;
RT "A new cysteine framework in sodium channel blockin conotoxins";
RL Biochemistry 34:8649-8656(1995).
CC -|- FUNCTION: Mu-conotoxins bind and block voltage-sensitive sodium
channel. Blocks reversibly sodium channels in molluscan neurons,
but has no effect on sodium currents in bovine chromaffin cells or
in rat brain synaptosomes. Induces paralysis in bivalve mollusks
(Mytilus). No effect are observed on fish (Gambusia) and fly
larvae (Sarcophaga). Pn1VA is approximately 6 times more potent
than Pn1VA in blockade of the sodium current in Lymnaea neurons.
CC -|- SUBCELLULAR LOCATION: Secreted.
CC -|- TISSUE SPECIFICITY: Expressed by the venom duct.
CC -|- MASS SPECTROMETRY: MW=1789.5; METHOD=ESI; RANGE=1-17; NOTE=Ref.1.
CC -|- SIMILARITY: Belongs to the conotoxin M superfamily. Mu-type
family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not

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CC removed.
CC -----
CC Direct protein sequencing; Ionic channel inhibitor; Neurotoxin;
KW Sodium channel inhibitor; Toxin.
FT SITE 4
FT DISULFID 12
FT DISULFID 2
FT DISULFID 15
FT DISULFID 8
SQ SEQUENCE 17 AA; 1797 MW; P9B721E0E96B9D82 CRC64;

Query Match 35.8%; Score 24; DB 1; Length 17;
Best Local Similarity 44.4%; Pred. No. 4e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Qy          3 KNSPCTLG 11
Db          3 KTGWCTCLG 11

RESULT 20
Q7LZ29 CAICR PRELIMINARY; PRT; 19 AA.
ID Q7LZ29 CAICR PRELIMINARY; PRT; 19 AA.
AC Q7LZ29;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Gamma crystallin IV (Fragment).
OS Catman crocodilus (Speckled catman) (Catman sclerops).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Cichliformes; Cichlidae; Atherinomorpha; Atherinidae;
OC NCBI_TaxID=8499;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=89351593; PubMed=3255376;
RA Chlou S.H.;
RT "The protein sequence homology of gamma-crystallins among major
RT vertebrate classes and their DNA sequence homology to heat-shock
RT protein genes."
RL J. Protein Chem. 7:527-534(1988).
DR PIR; B60894; B60894.
DR InterPro; IPR01064; Crystallin.
DR Pfam; PF00030; Crystallin.
DR PROSITE; PS50915; CRYSTALLIN_BETAGAMMA; 1.
FT NON TER 1
FT NON TER 1
SQ SEQUENCE 19 AA; 2325 MW; 26DAE30ADBFB23FF CRC64;

Query Match 35.8%; Score 24; DB 2; Length 19;
Best Local Similarity 57.1%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy          2 EKNSPFC 8
Db          12 EGRSYEC 18

RESULT 21
Q4YR89_PLABR PRELIMINARY; PRT; 20 AA.
ID Q4YR89_PLABR PRELIMINARY; PRT; 20 AA.
AC Q4YR89;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
DE ORFNames=PB107323.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX Hall N., Karas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

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RA Quidell M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses.";
 RL Science 307:82-86 (2005).
 CC -1 CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL, CAAT01002802; CAH99438.1; -; Genomic_DNA.
 KM Hypothetical protein.
 DR EMBL, CAAT01002802; CAH99438.1; -; Genomic_DNA.
 FT NON_TER
 SQ SEQUENCE 20 AA; 2708 MW; DF40072FE75148D CRC64;

Query Match 35.8%; Score 24; DB 2; Length 20;
 Best Local Similarity 71.4%; Pred. No. 4.8e+03;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIL 10
 DB 2 NPFICIL 8

RESULT 22
 Q9YFJ1_9CORO PRELIMINARY; PRT; 12 AA.
 ID Q9YFJ1_9CORO PRELIMINARY; PRT; 12 AA.
 AC Q9YFJ1_9CORO PRELIMINARY; PRT; 12 AA.
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Matrix glycoprotein (Fragment).
 OS Avian infectious bronchitis virus.
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Nidovirales;
 OC Coronaviridae; Coronavirinae.
 OC NCBI_TaxID=11120;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=UK12;
 RX MEDLINE=88171451; PubMed=2832526;
 RA Cavanagh D., Davis P.J.;
 RT "Evolution of Avian Coronavirus IBV: sequence of the matrix
 RL J. Gen. Virol. 69:621-629 (1988).
 DR EMBL, D00415; BAA20959.1; -; Genomic_RNA.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1224 MW; 02D5B87F8D51B1A4 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 4.4e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 4 NSPECIL 11
 DB 5 NTINCTIL 12

RESULT 23
 Q5F3D0_CHICK PRELIMINARY; PRT; 13 AA.
 ID Q5F3D0_CHICK PRELIMINARY; PRT; 13 AA.
 AC Q5F3D0_CHICK PRELIMINARY; PRT; 13 AA.
 DT 10-MAY-2005 (TREMBlrel. 30, Created)
 DT 10-MAY-2005 (TREMBlrel. 30, Last sequence update)
 DT 10-MAY-2005 (TREMBlrel. 30, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=RCJMB04_21c11;
 OS Gallus gallus (Chicken).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinoptera; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=CB; TISSUE=Bursa;

RA Caldwell R.B., Kierzek A.M., Arakawa H., Bezubov Y., Zaim J.,
 RA Pichler P., Kutter S., Blagoderetki A., Kostovska D., Kotter M.,
 RA Pichler J., Carninci P., Hayashizaki Y., Buerstedde J.M.,
 RT "Full-length cDNAs from chicken bursa lymphocytes to facilitate
 RT gene function analysis.";
 RL Genome Biol. 6:R6-R6 (2005).
 DR EMBL, AJ851720; CAH65354.1; -; mRNA.
 KM Hypothetical protein.
 SQ SEQUENCE 13 AA; 1550 MW; 6ADCBB330C4D4B1B CRC64;

Query Match 34.3%; Score 23; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 4.7e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 EKNSFE 7
 DB 6 EENGFE 11

RESULT 24
 Q9N0F9_CANFA PRELIMINARY; PRT; 16 AA.
 ID Q9N0F9_CANFA PRELIMINARY; PRT; 16 AA.
 AC Q9N0F9_CANFA PRELIMINARY; PRT; 16 AA.
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Class II beta-tubulin (Fragment).
 OS Canis familiaris (Dog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
 OC Canis.
 OC NCBI_TaxID=9615;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC Aral K.;
 RL EMBL, AB022055; BAA96410.2; -; mRNA.
 DR EMBL, AB022055; BAA96410.2; -; mRNA.
 FT NON_TER
 SQ SEQUENCE 16 AA; 1813 MW; 7BEC91EDC77B5E1F CRC64;

Query Match 34.3%; Score 23; DB 2; Length 16;
 Best Local Similarity 57.1%; Pred. No. 5.8e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSFE 7
 DB 2 DEGEFE 8

RESULT 25
 Q8HKE2_9ACAR PRELIMINARY; PRT; 17 AA.
 ID Q8HKE2_9ACAR PRELIMINARY; PRT; 17 AA.
 AC Q8HKE2_9ACAR PRELIMINARY; PRT; 17 AA.
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN Name=ND1;
 OS Rhizoclephalus punctatus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhizoclephalus.
 OC NCBI_TaxID=72860;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC MEDLINE=22660766; PubMed=12775521; DOI=10.1080/10635150309325;
 RA Murrell A., Campbell N.J.H., Barker S.C.;
 RT "The value of idiosyncratic markers and changes to conserved tRNA
 RT sequences from the mitochondrial genome of hard ticks (Acari: Ixodidae;
 RT Ixodidae) for phylogenetic inference.";
 RL Syst. Biol. 52:296-310 (2003).
 DR EMBL, AY059231; AAL79429.1; -; Genomic_DNA.

DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2069 MW; 15AFEP9B3743422 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECT 9
 DB 8 NMFICI 13

RESULT 25

Q8HKF6_9ACAR PRELIMINARY; PRT; 17 AA.
 ID Q8HKF6;
 AC Q8HKF6;

DT 01-MAR-2003 (TREMBLrel. 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE NADH dehydrogenase subunit 1 (Fragment).

GN Name=ND1;

OS Rhipicephalus eversti.

OC Mitochondrion.

OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;

OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Rhipicephalus.

OC NCBI_TaxID=60190;

NP NUCLEOTIDE SEQUENCE.

RA MEDLINE=22660786; PubMed=12775521; DOI=10.1080/10635150309325;

RA Murrell A., Campbell N.J.H., Barker S.C.;

RT "The value of idiosyncratic markers and changes to conserved tRNA

sequences from the mitochondrial genome of hard ticks (Acari: Ixodida:

RT Ixodidae) for phylogenetic inference.";

RL Syst. Biol. 52:296-310(2003).

DR EMBL; AY059219; AL79415.1; -; Genomic_DNA.

GO; GO:0005739; C:mitochondrion; IEA.

KM Mitochondrion.

FT NON_TER 1

SQ SEQUENCE 17 AA; 2071 MW; 15AFEDCC1743422 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECT 9
 DB 8 NMFICI 13

RESULT 27
 Q8HKH2_9ACAR PRELIMINARY; PRT; 17 AA.
 ID Q8HKH2;
 AC Q8HKH2;
 DT 01-MAR-2003 (TREMBLrel. 23, Created)
 DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
 DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)
 DE NADH dehydrogenase subunit 1 (Fragment).
 GN Name=ND1;
 OS Boophilus decoloratus.
 OC Mitochondrion.
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Arachnida; Acari;
 OC Parasitiformes; Ixodida; Ixodidae; Ixodidae; Boophilus.
 OC NCBI_TaxID=60189;
 NP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=22660786; PubMed=12775521; DOI=10.1080/10635150309325;
 RA Murrell A., Campbell N.J.H., Barker S.C.;

DR EMBL; AY059197; AL79399.1; -; Genomic_DNA.
 DR GO; GO:0005739; C:mitochondrion; IEA.
 KM Mitochondrion.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2130 MW; 8E7FE0A737438DD CRC64;

Query Match 34.3%; Score 23; DB 2; Length 17;
 Best Local Similarity 66.7%; Pred. No. 6.2e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSPECT 9
 DB 8 NMFICI 13

RESULT 28

Q4XXL1_PLACH PRELIMINARY; PRT; 18 AA.
 ID Q4XXL1;
 AC Q4XXL1;

DT 13-SEP-2005 (TREMBLrel. 31, Created)

DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)

DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)

DE Hypothetical protein (Fragment).

GN ORFNames=PC10478.00.0;

OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

OC NCBI_TaxID=5825;

NP NUCLEOTIDE SEQUENCE.

RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,

RA Beriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,

RA James K., Rutherford K., Harris B., Harris D., Churcher C.,

RA Chail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,

RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,

RA Janse C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden K.S.,

RT "A comprehensive survey of the Plasmodium life cycle by genomic,

RT transcriptomic, and proteomic analyses.";

RL Science 307:82-86(2005).

CC -!- CAUTION: The sequence shown here is derived from an

EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is

preliminary data.

DR EMBL; CAJ01002428; CAH78350.1; -; Genomic_DNA.

KM Hypothetical protein.

FT NON_TER 1

SQ SEQUENCE 18 AA; 2124 MW; 754D7D9B16643A74 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 18;
 Best Local Similarity 57.1%; Pred. No. 6.6e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 6 FBCTIGP 12
 DB 2 FVCTVRP 8

RESULT 29
 Q7Z579_HUMAN PRELIMINARY; PRT; 20 AA.
 ID Q7Z579;
 AC Q7Z579;
 DT 01-OCT-2003 (TREMBLrel. 25, Created)
 DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
 DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
 DE 5-hydroxytryptamine receptor 2C variant b (Fragment).
 GN Name=HTR2C;
 OS Homo sapiens (human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 OC NCBI_TaxID=9606;
 NP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=22651194; PubMed=12767050; DOI=10.1002/jcp.10287;
 RA Stomniski A., Pilschik A., Zbytek B., Tobin D.J., Kauser S.,

RA Wortman J.;
 RT "Functional activity of serotonergic and melatonergic systems
 expressed in the skin."
 RL J. Cell. Physiol. 196;144-153(2003).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Piarick A.V., Slominski A.;
 RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY114104; AAW78371.1; -; mRNA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2232 MW; EA74DCAFD4BCBB9 CRC64;
 Query Match 34.3%; Score 23; DB 2; Length 20;
 Best Local Similarity 62.5%; Pred. No. 7.3e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 4 EKNSPEC 11
 DB 8 NSFOIGS 15

RESULT 30
 Q4XN21 PLACH PRELIMINARY; PRT; 20 AA.
 ID Q4XN21 PLACH PRELIMINARY;
 AC Q4XN21
 DT 13-SEP-2005 (Tremblrel. 31, Created)
 DT 13-SEP-2005 (Tremblrel. 31, Last sequence update)
 DT 13-SEP-2005 (Tremblrel. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORNames=PC108623.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karas M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Berriman M., Florens L., Jansen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Duggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; CAJ01004522; CAH81691.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 20 AA; 2470 MW; 4730C7869162447F CRC64;
 Query Match 34.3%; Score 23; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 7.3e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EKNSPEC 9
 DB 12 KSNFLBCT 19

RESULT 31
 Q95MJ9_PANTR PRELIMINARY; PRT; 20 AA.
 ID Q95MJ9_PANTR PRELIMINARY;
 AC Q95MJ9
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Growth hormone receptor (Fragment).
 OS Pan troglodytes (Chimpanzee).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Pan.
 OX NCBI_TaxID=9598;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=21265430; PubMed=11371582;
 RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.;
 RT "Episodic evolution of growth hormone in primates and emergence of the
 RT species specificity of human growth hormone receptor."
 RL Mol. Biol. Evol. 18:945-953(2001).
 DR EMBL; AF339077; AAK62304.1; -; Genomic_DNA.
 DR HSSP; P10912; 3HR.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2412 MW; 3BD9F94636B54BE7 CRC64;
 Query Match 34.3%; Score 23; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 7.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EKNSPEC 8
 DB 4 ERRTFSC 10

RESULT 32
 Q95MKO_PONPY PRELIMINARY; PRT; 20 AA.
 ID Q95MKO_PONPY PRELIMINARY;
 AC Q95MKO
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)
 DE Growth hormone receptor (Fragment).
 OS Pongo pygmaeus (Orangutan).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OX NCBI_TaxID=9600;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.;
 RT "Episodic evolution of growth hormone in primates and emergence of the
 RT species specificity of human growth hormone receptor."
 RL Mol. Biol. Evol. 18:945-953(2001).
 DR EMBL; AF339076; AAK62303.1; -; Genomic_DNA.
 DR HSSP; P10912; 1AXI.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER 1 1
 SQ SEQUENCE 20 AA; 2366 MW; 3FC9F95C86B38BE7 CRC64;
 Query Match 34.3%; Score 23; DB 2; Length 20;
 Best Local Similarity 42.9%; Pred. No. 7.3e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EKNSPEC 8
 DB 4 ERRTFSC 10

RESULT 33
 Q95MKI_COLAN PRELIMINARY; PRT; 20 AA.
 ID Q95MKI_COLAN PRELIMINARY;
 AC Q95MKI
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-JUN-2003 (Tremblrel. 24, Last annotation update)
 DE Growth hormone receptor (Fragment).
 OS Colobus angolensis (Angolan colobus).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Colobinae; Colobus.
OX NCBI_TaxID=54131;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21265430; PubMed=11371582;
RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.;
RT "Epilodic evolution of growth hormone in primates and emergence of the
RT species specificity of human growth hormone receptor.";
RL Mol. Biol. Evol. 18:945-953(2001).
DR EMBL; AF339075; AAK62302.1; -; Genomic_DNA.
DR HSSP; P10912; IAXI.
DR GO; GO:0004872; F:receptor activity; IEA.
KM Receptor.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2359 MW; 3FC9ECA636B38BE7 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
Db 4 ERETFSC 10

RESULT 34
ID Q95MK2_PAPCY PRELIMINARY; PRT; 20 AA.
AC Q95MK2;
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Growth hormone receptor (Fragment).
OS Papio cynocephalus (Yellow baboon).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
OC Cercopitheciidae; Cercopitheciinae; Papio.
OX NCBI_TaxID=9556;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=21265430; PubMed=11371582;
RA Liu J.-C., Makova K.D., Adkins R.M., Gibson S., Li W.-H.;
RT "Epilodic evolution of growth hormone in primates and emergence of the
RT species specificity of human growth hormone receptor.";
RL Mol. Biol. Evol. 18:945-953(2001).
DR EMBL; AF339074; AAK62301.1; -; Genomic_DNA.
DR HSSP; P10912; IAXI.
DR GO; GO:0004872; F:receptor activity; IEA.
KM Receptor.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2339 MW; 3FC9P94636B38BE7 CRC64;

Query Match 34.3%; Score 23; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 7.3e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
Db 4 ERETFSC 10

RESULT 35
ID RCA_PINPS STANDARD; PRT; 10 AA.
AC P81084;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Ribulose biphosphate carboxylase/oxygenase activase, chloroplast
DE (Rubisco activase) (RA) (Water stress responsive protein 4)

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DE (Fragment).
DE Pinus pinaster (Maritime pine).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus;
OX NCBI_TaxID=71647;
RN [1]
RP PROTEIN SEQUENCE.
RX TISSUE=Needle;
RX MEDLINE=98418576; PubMed=9747804; DOI=10.1006/A.1006006132120;
RA Costa P., Bahman N., Frigerio J.-M., Kremer A., Plomion C.;
RT "Water-deficit-responsive proteins in maritime pine.";
RL Plant Mol. Biol. 38:587-596(1998).
RN [2]
RP PROTEIN SEQUENCE.
RC TISSUE=Needle;
RX MEDLINE=99274088; PubMed=10344291;
RX DOI=10.1002/(SICI)1522-2683(19990101)20:4<1098::AID-ELPS1098>3.3.CO;2-Q;
RA Costa P., Plomion C., Bauw G., Dubos C., Bahman N., Kremer A.,
RA Frigerio J.-M., Plomion C.;
RT "Separation and characterization of needle and xylem maritime pine
RT proteins.";
RL Electrophoresis 20:1098-1108(1999).
CC -I- FUNCTION: Activation of Rubisco (ribulose-1,5-bisphosphate
CC carboxylase/oxygenase; EC 4.1.1.39) involves the ATP-dependent
CC carboxylation of the epsilon-amino group of lysine leading to a
CC carbamate structure (By similarity).
CC -I- SUBCELLULAR LOCATION: Chloroplast stroma (By similarity).
CC -I- INDUCTION: By water stress.
CC -I- SIMILARITY: Belongs to the Rubisco activase family.
CC
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC
CC ATP-binding; Chloroplast; Direct protein sequencing;
KM Nucleotide-binding.
FT NON_TER 1
FT NON_TER 10
FT NON_TER 10
SQ SEQUENCE 10 AA; 1171 MW; C0A506D2C72B1E46 CRC64;

Query Match 32.8%; Score 22; DB 1; Length 10;
Best Local Similarity 66.7%; Pred. No. 5.6e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECIL 10
Db 1 SFOCEL 6

RESULT 36
ID Q7ROUO_PLAYO PRELIMINARY; PRT; 10 AA.
AC Q7ROUO;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Hypothetical protein (Fragment).
GN Name=PY01107;
OS Plasmodium yoelii yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_TaxID=73239;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=17XNL;
RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
RA Carlton J.M., Angluol S.V., Suh B.B., Kooli T.W., Perera M.,
RA Silva J.C., Ernolava M.D., Allen J.E., Selengut J.P., Koo H.L.,
RA Peterson J.D., Pop M., Kosack D.S., Shumway M.F., Bidwell S.L.,
RA Shallow S.J., van Aken S.B., Riedmuller S.B., Feldblyum T.V.,
RA Cho J.K., Quackenbush J., Sedegah M., Shoabli A., Cummings L.M.,
RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,

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RA Cunningham D.A., Pfeleer P.R., Bergman L.W., Vaidya A.B.,
 RA van Lin L.H., Jansen C.J., Waters A.P., Smith H.O., White O.R.,
 RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.T.,
 RA Carucci D.J.,
 RT "Genome sequence and comparative analysis of the model rodent malaria
 parasite *Plasmodium yoelii yoelii*." ,
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL, AAB01000292; EAA030307.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON TER
 SQ SEQUENCE 10 AA; 1225 MW; 1F0267BB10572724 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 5.6e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECIL 10
 Db 7 ECIL 10

RESULT 37
 080UP1_XENLA PRELIMINARY; PRT; 11 AA.

AC 080UP1;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Beta-TrCP protein (Fragment).
 OS Name-beta-TrCP;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_Taxid=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Ballarino M.;
 RT "Analisi strutturale e funzionale del gene beta-TrCP in *Xenopus laevis*." ,
 RL Thesis (2001), Department of Genetics e Biologia Molecolare,
 RL University of Rome La Sapienza, Rome, Italy.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Carnevali P.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ428930; CAD21927.1; -; Genomic_DNA.
 FT NON TER
 SQ SEQUENCE 11 AA; 1195 MW; CEB938BE35BEA5B9 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 11;
 Best Local Similarity 57.1%; Pred. No. 6.1e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 FSCSLGP 12
 Db 4 FSCSLGP 10

RESULT 38
 06LDS1_BPT3
 ID 06LDS1_BPT3 PRELIMINARY; PRT; 13 AA.
 AC 06LDS1;
 DT 05-JUN-2004 (TREMBlrel. 27, Created)
 DT 05-JUN-2004 (TREMBlrel. 27, Last sequence update)
 DT 05-JUN-2004 (TREMBlrel. 27, Last annotation update)
 DE RNA polymerase III (Fragment).
 OS Bacteriophage T3.
 OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Podoviridae;
 OC T3-like viruses.

OX NCBI_Taxid=10759;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=86221699; PubMed=3011596; DOI=10.1016/0378-1119(86)90098-3;
 RA Morris C.E., Klement J.F., McAllister W.T.;
 RT "Cloning and expression of the bacteriophage T3 RNA polymerase gene." ,
 RL Gene 41:193-200(1986).
 DR EMBL, M22609; AAA63781.1; -; Genomic_DNA.
 FT NON TER
 SQ SEQUENCE 13 AA; 1567 MW; 16F2BD5EA021054 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 13;
 Best Local Similarity 80.0%; Pred. No. 7.3e+03;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EKNSF 6
 Db 8 EKNSF 12

RESULT 39
 081027_MOUSE PRELIMINARY; PRT; 14 AA.

AC 081027;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Kinesin KIFCI (Fragment).
 OS Name=KIFCI;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=129/Sv;
 RA Nagataja R., Brathwaite M.E., Abe K.;
 RL Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF528162; AAO27574.1; -; Genomic_DNA.
 FT NON TER
 SQ SEQUENCE 14 AA; 1474 MW; 225CE886C694FA8 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 40.0%; Pred. No. 7.8e+03;
 Matches 2; Conservative 3; Mismatches 0; Indels 0; Gaps 0;

Qy 7 ECILG 11
 Db 3 QCVIG 7

RESULT 40
 093202_9CIRC
 ID 093202_9CIRC PRELIMINARY; PRT; 14 AA.
 AC 093202; Q9YU34;
 DT 01-NOV-1998 (TREMBlrel. 08, Created)
 DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)
 DT 01-FEB-2005 (TREMBlrel. 29, Last annotation update)
 DE ORF11.
 OS Porcine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_Taxid=46221;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Porcine circovirus Type II;
 RX MEDLINE=86418498; PubMed=9747725;
 RA Mehan B.M., McNeill F.M., Todd D., Kennedy S., Jewhurst V.,
 RA Ellis J.A., Haasard L.E., Clark E.G., Haines D.M., Allan G.M.;
 RT "Characterisation of novel circovirus DNAs associated with wasting
 RT syndromes in pigs." ,
 RL J. Gen. Virol. 79:2171-2199(1998).
 DR EMBL, AF055394; AAC35336.1; -; Genomic_DNA.

DR EMBL: AF055392; AAC35316.1; -; Genomic DNA.
 DR EMBL: AF055393; AAC35326.1; -; Genomic DNA.
 DR EMBL: AF055391; AAC35305.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 41
 Q77NR3_9CIRC
 ID Q77NR3_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77NR3;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 GN Name=ORF11;
 OS Porcine circovirus 2.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85708;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Wellenbergh G.J., Pesch S., Berntsen F.W., Steverink P.J.G.M.,
 RA Hunneman W., Van der Vorst T.J.K., Peperkamp N.H.M.T., Ohlinger V.F.,
 RA Schipper R., Van Oirschot J.T., de Jong M.F.;
 RL Submitted (Nov-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF201897; AAC41230.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 42
 Q77RC0_9CIRC
 ID Q77RC0_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77RC0;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-D.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=86385;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF117753; AAD12313.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 43
 Q77RM6_9CIRC
 ID Q77RM6_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77RM6;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-B.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85709;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF103999; AAD03080.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 44
 Q77S02_9CIRC
 ID Q77S02_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77S02;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-E.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF103999; AAD03080.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 45
 Q77S09_9CIRC
 ID Q77S09_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77S09;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-C.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85543;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF112862; AAD03090.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 46
 Q77S02_9CIRC
 ID Q77S02_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77S02;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-E.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85544;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF103999; AAD03080.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 47
 Q77S09_9CIRC
 ID Q77S09_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77S09;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-C.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85543;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF103999; AAD03080.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RESULT 48
 Q77S09_9CIRC
 ID Q77S09_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77S09;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Porcine circovirus type 2-C.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85543;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=20142849; PubMed=10680656;
 RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus.";
 RL Can. J. Vet. Res. 64:44-52(2000).
 DR EMBL: AF103999; AAD03080.1; -; Genomic DNA.
 SQ SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECT 9
 : ||: ||
 Db 2 NNKNHYEVI 10

RA Hamel A.L., Lin L.L., Sachvie C., Grudecki E., Nayyar G.P.S.;
 RT "PCR detection and characterization of type-2 porcine circovirus";
 CC J. Vet. Res. 64:44-52(2000)
 DR EMBL, AF109398; AAD03069.1; -; Genomic DNA.
 SO SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
 Db 2 NNNKHYEVI 10

RESULT 46
 Q77S13_9CIRC
 ID Q77S13_9CIRC PRELIMINARY; PRT; 14 AA.
 AC Q77S13;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE ORF-11.
 OS Bovine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=85542;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hamel A.L., Nayyar G.P.S.;
 RL Submitted (FEBS-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AF109397; AAD11937.1; -; Genomic DNA.
 SO SEQUENCE 14 AA; 1747 MW; 00F50DC89AEBF20B CRC64;

Query Match 32.8%; Score 22; DB 2; Length 14;
 Best Local Similarity 44.4%; Pred. No. 7.8e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DEKNSPECI 9
 Db 2 NNNKHYEVI 10

RESULT 47
 FIBA_ANAPL
 ID FIBA_ANAPL STANDARD; PRT; 15 AA.
 AC P12801;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 01-FEB-2005 (Rel. 46, Last annotation update)
 DE Fibrinogen alpha chain [Contains: Fibrinopeptide A] (Fragment).
 GN Name=Fga;
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 OX NCBI_TaxID=8839;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=85168193; PubMed=3983613;
 RA Min Y., Ping Z., Yaoshi Z.;
 RT "Purification and primary structures of duck fibrinopeptides A and B";
 RL Sci. Sin., Ser. B, Chem. Biol. Agric. Med. Barth Sci. 28:31-35(1985).
 CC -1- FUNCTION: Fibrinogen has a double function: yielding monomers that
 CC polymerize into fibrin and acting as a cofactor in platelet
 CC aggregation.
 CC -1- SUBUNIT: Heterohexamer; disulfide linked. Contains 2 sets of 3
 CC nonidentical chains (alpha, beta and gamma). The 2 heterochains
 CC are in head to head conformation with the N-termini in a small
 CC central domain (by similarity).
 CC -1- DOMAIN: A long coiled coil structure formed by 3 polypeptide
 CC chains connects the central nucleolus to the C-terminal domains
 CC (distal nucleolus). The long C-terminal ends of the alpha chains
 CC fold back, contributing a fourth strand to the coiled coil

CC structure.
 CC -1- PPM: Conversion of fibrinogen to fibrin is triggered by thrombin,
 CC which cleaves fibrinopeptides A and B from alpha and beta chains,
 CC and thus exposes the N-terminal polymerization sites responsible
 CC for the formation of the soft clot.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC PIR; JP0101; JP0101.
 DR Blood coagulation; Coiled coil; Direct protein sequencing; Plasma;
 KW Pyrolydione carboxylic acid. Fibrinopeptide A.
 FT PEPTIDE 1 15
 FT MOD RES 1 1 Pyrolydione carboxylic acid.
 FT NON TER 15 15
 SO SEQUENCE 15 AA; 1580 MW; D78A51FF88B40373 CRC64;

Query Match 32.8%; Score 22; DB 1; Length 15;
 Best Local Similarity 57.1%; Pred. No. 8.4e+03;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DEKNSPE 7
 Db 2 DGRSFO 8

RESULT 48
 Q5RLM1_HUMAN
 ID Q5RLM1_HUMAN PRELIMINARY; PRT; 15 AA.
 AC Q5RLM1;
 DT 01-FEB-2005 (TrEMBLrel. 29, Created)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
 DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
 DE Neuronal acetylcholine receptor alpha-4 subunit (Fragment).
 GN Name=CHRNA4;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
 OC Mammalia; Butheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Qi Y.F., Shan K.R., Ren X.L., Xu Y., Zhang T., Li Y.;
 RT "Research of association between genetic polymorphisms of CHRNA4 and
 RT Alzheimer's Disease";
 RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AY816234; AAV66461.1; -; Genomic DNA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 DR InterPro; IPR006202; Neur_chan_LBD.
 DR Pfam; PF02931; Neur_chan_LBD; 1.
 KW Receptor.
 FT NON TER 1 1
 FT NON TER 15 15
 SO SEQUENCE 15 AA; 1852 MW; 9DB55FDACC3614E5 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 8.4e+03;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEKN 4
 Db 1 DEKN 4

RESULT 49
 Q9TWC6_DIRIM
 ID Q9TWC6_DIRIM PRELIMINARY; PRT; 17 AA.
 AC Q9TWC6;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

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DT 01-JUN-2002 (TrEMBLrel. 21, last annotation update)
DE 22L kDa excretory-secretory protein (Fragment).
OC Dirofilaria immitis (Canine heartworm).
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Spirurida; Filarioidea;
OC Onchocercidae; Dirofilaria.
OX NCBI_TaxID=6287;
RN (1)
RP PROTEIN SEQUENCE.
RX MEDLINE=96258562; Pubmed=8992320; DOI=10.1016/0166-6851(95)02533-2;
RA Frank G.R., Griewe R.B.,
RT "Purification and characterization of three larval excretory-secretory
RL proteins of Dirofilaria immitis."
RL Mol. Biochem. Parasitol. 75:221-229(1996).
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 2048 MW; 478557C5392BAE7 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 9.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 6 CILKP 10

RESULT 50
O6QLM0_9INFA PRELIMINARY; PRT; 17 AA.
ID O6QLM0_9INFA PRELIMINARY; PRT; 17 AA.
AC O6QLM0;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Neuraminidase (Fragment).
OS Influenza A virus (A/chicken/Thailand/W3Nf/2004(H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=264511;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Oraveerakul K., Keawcharoen J., Wattanadorn S., Khanda S.,
RA Paphavast T., Theamboonlers A., Poovorawan Y.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY535026; AAS57879.1; -; Genomic RNA.
DR GO; GO:0016020; C:integral to membrane; IEA.
DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; Neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Glycosidase; Hydrolase; Transmembrane.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1954 MW; F35F7F3FFD8AF26F CRC64;

Query Match 32.8%; Score 22; DB 2; Length 17;
Best Local Similarity 33.3%; Pred. No. 9.5e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECTLGP 12
DB 1 NSRSGPEMTWDP 12

RESULT 51
O6QLM1_9INFA PRELIMINARY; PRT; 17 AA.
ID O6QLM1_9INFA PRELIMINARY; PRT; 17 AA.
AC O6QLM1;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)

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DE Neuraminidase (Fragment).
OS Influenza A virus (A/chicken/Thailand/LV1NF/2004(H5N1)).
OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
OC Influenzavirus A.
OX NCBI_TaxID=264510;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Oraveerakul K., Keawcharoen J., Wattanadorn S., Khanda S.,
RA Paphavast T., Thongmee C., Theamboonlers A., Poovorawan Y.;
RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY535025; AAS57878.1; -; Genomic RNA.
DR GO; GO:0016020; C:integral to membrane; IEA.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
DR InterPro; IPR001860; Glyco_hydro_34.
DR Pfam; PF00064; Neur; 1.
DR ProDom; PD000431; Glyco_hydro_34; 1.
KW Glycosidase; Hydrolase; Transmembrane.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1954 MW; F35F7F3FFD8AF26F CRC64;

Query Match 32.8%; Score 22; DB 2; Length 17;
Best Local Similarity 33.3%; Pred. No. 9.5e+03;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECTLGP 12
DB 1 NSRSGPEMTWDP 12

RESULT 52
O9DPB5_BRARE PRELIMINARY; PRT; 17 AA.
ID O9DPB5_BRARE PRELIMINARY; PRT; 17 AA.
AC O9DPB5;
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Ptz-F1 alpha isoform 1 (Fragment).
GN Name=n5a2; Synonym=sf1a;
OS Brachydanio rerio (Zebrafish) (Danio rerio).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC Cyprinidae; Danio.
OX NCBI_TaxID=7955;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=20277948; Pubmed=10816440; DOI=10.1042/0264-6021:3480439;
RA Lin W., Wang H.W., Sun C., Liu D., Hew C.L., Chung B.;
RT "Zebrafish ftz-f1 gene has two promoters, is alternatively spliced,
RT and is expressed in digestive organs."
RL Biochem. J. 348:439-446(2000).
DR EMBL; AF286364; AAG28162.1; -; Genomic DNA.
DR ZFIN; ZDB-GENE-990415-79; nr5a2.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1932 MW; FA22C4B4FD2C8F41 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 17;
Best Local Similarity 62.5%; Pred. No. 9.5e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECTLGP 11
DB 3 SSFSESLG 10

RESULT 53
O6SR40_DROSI PRELIMINARY; PRT; 19 AA.
ID O6SR40_DROSI PRELIMINARY; PRT; 19 AA.
AC O6SR40;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

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DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Desol (Fragment).
 OS Drosophila simulans (Fruit fly).
 CC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 CC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 CC Ephyridiidae; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7240;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX PubMed14762063; DOI=10.1101/gr.1329204;
 RA Halligan D.L., Byrne-Walker A., Andolfatto P., Keightley P.D.;
 RT "Patterns of evolutionary constraints in intronic and intergenic DNA
 of *Drosophila*.";
 RL Genome Res. 14:273-279(2004).
 DR EMBL; AY459578; AAC3028.1; -; Genomic_DNA.
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2068 MW; D13CFB2A110C762C CRC64;
 Query Match 32.8%; Score 22; DB 2; Length 19;
 Best Local Similarity 40.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 3 KNSFPCILGP 12
 Db 3 KKKLNLVLP 12

RESULT 54
 Q9TWH8_PACM PRELIMINARY; PRT; 19 AA.
 ID Q9TWH8_PACM PRELIMINARY;
 AC Q9TWH8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-MAY-2000 (TrEMBLrel. 14, Last annotation update)
 DE Carboxypeptidase PC (Fragment).
 OS Paratithodes cantschaticus (Kamchatka crab) (Red king crab).
 CC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 CC Eumalacostraca; Eucarida; Decapoda; Pleocyemata; Anomura; Paguroidea;
 CC Lithodidae; Paratithodes.
 OX NCBI_TaxID=6741;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95305881; PubMed=7786315;
 RA Rudenskaya G.N., Kopenko O.G., Isaev V.A., Stepanov V.M.,
 RA Dunaevskii I.A.B.;
 RT "[Isolation and properties of carboxypeptidase from the Kamchatka crab
 Paratithodes cantschaticus].";
 RL Bioorg. Khim. 21:249-255(1995).
 SQ SEQUENCE 19 AA; 2213 MW; 2D7B894F238D5670 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 19;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 DEKNS 5
 Db 11 DEKNS 15

RESULT 55
 O6QLM2_GINPA PRELIMINARY; PRT; 19 AA.
 ID O6QLM2_GINPA PRELIMINARY;
 AC O6QLM2;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Neuraminidase (Fragment).
 OS Influenza A virus (A/chicken/Thailand/KP1NF/2004(H5N1)).
 CC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 CC Influenzavirus A.
 OX NCBI_TaxID=264509;
 RN [1]

RP NUCLEOTIDE SEQUENCE.
 RA Oraveerakul K., Keavcharoen J., Wattanadorn S., Khanda S.,
 RA Paphavasit T., Theamboonlers A., Poovorawan Y.;
 RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY535024; AAC57877.1; -; Genomic RNA.
 DR GO; GO:0016021; C:Integral to membrane; IEA.
 DR GO; GO:0016020; C:membrane; IEA.
 DR GO; GO:0004308; F:exo-alpha-sialidase activity; IEA.
 DR GO; GO:0016798; F:hydrolyase activity, acting on glycosyl bonds; IEA.
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.
 DR InterPro; IPR001860; Glyco_hydro_34.
 DR Pfam; PF00064; Neur_1.
 DR ProDom; PD000431; Glyco_hydro_34; 1.
 KM Glycosidase; Hydrolase; Transmembrane.
 FT NON_TER 1
 FT NON_TER 19
 SQ SEQUENCE 19 AA; 2142 MW; F33310F96DBAF26F CRC64;
 Query Match 32.8%; Score 22; DB 2; Length 19;
 Best Local Similarity 33.3%; Pred. No. 1.1e+04;
 Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSFCILGP 12
 Db 3 NSRSGFEMIDP 14

RESULT 56
 O4X7B9_PLACH PRELIMINARY; PRT; 20 AA.
 ID O4X7B9_PLACH PRELIMINARY;
 AC O4X7B9;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC405454.00.0;
 OS Plasmodium chabaudi.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karrae M., Ratne J.D., Carlton J.M., Kool J.T.W.A.,
 RA Bettman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajendram M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jase C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 transcriptomic, and proteomic analyses.";
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL; CAJ01009247; CAH87207.1; -; Genomic_DNA.
 KM Hypothetical protein.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 20 AA; 2432 MW; C6C090AB73A055F9 CRC64;

Query Match 32.8%; Score 22; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 1.1e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 3 KNSFE 7
 Db 15 KNSFE 19

RESULT 57
 Q9R791_BORAF PRELIMINARY; PRT; 10 AA.
 ID Q9R791_BORAF PRELIMINARY;
 AC Q9R791;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Outer surface protein C (Fragment).
 GN Name=ospC;
 OS Borrelia afzelii.
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Borrelia burgdorferi group.
 OX NCBI_TaxID=29518;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=US461;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 ROSA P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 plasmid structure and targeted inactivation of the ospC gene."
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL; U93699; AAC4552.1; -; Genomic DNA.
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 RT NON_TER
 FT SEQUENCE 10 AA; 1118 MW; 480864C5B731A43 CRC64;
 SQ
 Query Match 31.3%; Score 21; DB 2; Length 10;
 Best Local Similarity 44.4%; Pred. No. 8.5e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EKNSPECTL 10
 DB 2 KKNLTSAIIL 10

RESULT 58
 Q9R790_BORGA
 ID Q9R790_BORGA PRELIMINARY; PRT; 11 AA.
 AC Q9R790;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Outer surface protein C (Fragment).
 GN Name=ospC;
 OS Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia;
 OC Borrelia burgdorferi group.
 OX NCBI_TaxID=29519;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=G25;
 RX MEDLINE=97426044; PubMed=9282748;
 RA Tilly K., Casjens S., Stevenson B., Bono J.L., Samuels D.S., Hogan D.,
 ROSA P.;
 RT "The Borrelia burgdorferi circular plasmid cp26: conservation of
 plasmid structure and targeted inactivation of the ospC gene."
 RL Mol. Microbiol. 25:361-374(1997).
 DR EMBL; U93700; AAC4553.1; -; Genomic DNA.
 DR GO; GO:0009279; C:outer membrane (sensu Gram-negative Bacteria); IEA.
 DR GO; GO:0006952; P:defense response; IEA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 RT NON_TER
 FT SEQUENCE 11 AA; 1250 MW; 0868D864C5B731A4 CRC64;
 SQ
 Query Match 31.3%; Score 21; DB 2; Length 11;
 Best Local Similarity 44.4%; Pred. No. 9.4e+03;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
 QY 2 EKNSPECTL 10
 DB 2 KKNLTSAIIL 10

RESULT 59

Q6LEMG_ARATH
 ID Q6LEMG_ARATH PRELIMINARY; PRT; 14 AA.
 AC Q6LEMG;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE RNA polymerase beta subunit (Fragment).
 GN Name=rpob;
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsie.
 OX NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=97304680; PubMed=9161043;
 RA Inada H., Seki M., Morikawa H., Nishimura M., Iba K.;
 RT "Existence of three regulatory regions each containing a highly
 conserved motif in the promoter plastid-encoded RNA polymerase gene
 (rpob)."
 RL Plant J. 11:883-890(1997).
 DR EMBL; D84552; BAA21502.1; -; Genomic DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 14 AA; 1405 MW; 7195255E0082917B CRC64;
 SQ
 Query Match 31.3%; Score 21; DB 2; Length 14;
 Best Local Similarity 45.5%; Pred. No. 1.2e+04;
 Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;
 QY 1 DEKNSPECTL 11
 DB 4 DEKGTSAIPG 14

RESULT 60
 O56127_9CIRC
 ID O56127_9CIRC PRELIMINARY; PRT; 14 AA.
 AC O56127;
 DT 01-JUN-1998 (TReMBLrel. 06, Created)
 DT 01-JUN-1998 (TReMBLrel. 06, Last sequence update)
 DT 01-DIC-2001 (TReMBLrel. 19, Last annotation update)
 DE ORF1; predicted 1.8 kda protein.
 OS Porcine circovirus.
 OC Viruses; ssDNA viruses; Circoviridae; Circovirus.
 OX NCBI_TaxID=46221;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=pms PCV;
 RX MEDLINE=98241772; PubMed=9573301;
 RA Hamel A.L., Lin L.L., Nayyar G.P.;
 RT "Nucleotide sequence of porcine circovirus associated with postweaning
 multisystemic wasting syndrome in pigs."
 RL J. Virol. 72:5262-5267(1998).
 DR EMBL; AF027217; AAC59472.1; -; Genomic DNA.
 DR InterPro; IPR001800; Lipoprotein_6.
 DR Pfam; PF01441; Lipoprotein_6; 1.
 RT NON_TER
 FT SEQUENCE 14 AA; 1761 MW; 00F50DC89EBAF20B CRC64;
 SQ
 Query Match 31.3%; Score 21; DB 2; Length 14;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 KNSPECT 9
 DB 4 KKHYEVI 10

RESULT 61
 O6LCZ7_HUMAN
 ID O6LCZ7_HUMAN PRELIMINARY; PRT; 15 AA.
 AC O6LCZ7;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)

DT 05-JUN-2004 (TRENBLREL. 27, Last sequence update)
 DT 01-FEB-2005 (TRENBLREL. 29, Last annotation update)
 DE Interleukin-8 receptor type B (Fragment).
 OS Name=IL8RB;
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 CC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=95014476; PubMed=7929358;
 RA Ahuja S.K., Shetty A., Tiffany H.L., Murphy P.M.;
 RT "Comparison of the genomic organization and promoter function for
 human interleukin-8 receptors A and B."
 RL J. Biol. Chem. 269:26381-26389(1994).
 DR EMBL/ U11873; AAA64381.1; -; mRNA.
 DR EMBL/ U11874; AAA64382.1; -; mRNA.
 DR EMBL/ U11875; AAA64383.1; -; mRNA.
 DR EMBL/ U11876; AAA64384.1; -; mRNA.
 DR EMBL/ U11877; AAA64385.1; -; mRNA.
 DR EMBL/ U11878; AAA64386.1; -; mRNA.
 DR EMBL/ U11872; AAA64380.1; -; mRNA.
 DR GO: 0004872; P:receptor activity; IEA.
 KW Receptor.
 FT NON TER.
 SQ SEQUENCE 15 AA; 1929 MW; 8937AF0B93D4F48C CRC64;
 Query Match 31.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 1.3e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 EKNSFE 7
 DB 7 ESDSFE 12

RESULT 62
 Q9R4U8 ACICA PRELIMINARY; PRT; 15 AA.
 AC Q9R4U8;
 DT 01-MAY-2000 (TRENBLREL. 13, Created)
 DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
 DT 01-JUN-2000 (TRENBLREL. 14, Last annotation update)
 DE Malonate decarboxylase beta subunit (Fragment).
 OS Acinetobacter calcoaceticus.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
 OC Moraxellaceae; Acinetobacter.
 OC NCBI_TaxID=471;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95050812; PubMed=7961952;
 RA Kim Y.S., Byun H.S.;
 RT "Purification and properties of a novel type of malonate decarboxylase
 from Acinetobacter calcoaceticus."
 RL J. Biol. Chem. 269:29636-29641(1994).
 SQ SEQUENCE 15 AA; 1790 MW; 03388040DB71DE8D CRC64;
 Query Match 31.3%; Score 21; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 1.3e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 3 KNSP 6
 DB 7 KNSP 10

RESULT 63
 PA2_NAJSR STANDARD; PRT; 16 AA.
 ID PA2_NAJSR
 AC Q10756;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Phospholipase A2 (EC 3.1.1.4) (Phosphatidylcholine 2-acylhydrolase)
 DE (Muscarinic inhibitor) (Fragment).
 OS Naja sputatrix (Malayan spitting cobra).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
 CC Elapidae; Elapinae; Naja.
 OC NCBI_TaxID=33626;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC TISUB-Venom;
 RA MEDLINE=96195757; PubMed=8638927; DOI=10.1006/abbi.1996.0137;
 RA Miyoshi S.-I., Tu A.T.;
 RT "Phospholipase A2 from Naja naja sputatrix venom is a muscarinic
 acetylcholine receptor inhibitor."
 RL Arch. Biochem. Biophys. 328:17-25(1996).
 CC -1- FUNCTION: PA2 catalyzes the calcium-dependent hydrolysis of the 2-
 acyl groups in 3-sn-phosphoglycerides. Blocks neuromuscular
 transmission at the postsynaptic site. Binds to the muscarinic
 acetylcholine receptor.
 CC -1- CATALYTIC ACTIVITY: Phosphatidylcholine + H(2)O = 1-
 acylglycerophosphocholine + a carboxylate.
 CC -1- COFACTOR: Binds 1 calcium ion (By similarity).
 CC -1- SUBUNIT: Monomer.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the phospholipase A2 family. Group I
 subfamily.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation -
 the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.
 CC PIR: S65520; S65520.
 DR HSHP; P00598; IPOA.
 DR InterPro: IPR001211; PhospholipaseA2.
 DR Pfam; PF00068; Phospholip_A2_1; 1.
 DR PROSITE; PS00119; PA2_ASP; PARTIAL.
 DR PROSITE; PS00118; PA2_HIS; PARTIAL.
 KW Acetylcholine receptor inhibitor; Calcium; Direct protein sequencing;
 KW Hydrolyase; Lipid degradation; Neurotoxin; Postsynaptic neurotoxin;
 KW Toxin.
 FT NON TER.
 SQ SEQUENCE 16 AA; 1969 MW; 9AC1F9834B585F0 CRC64;
 Query Match 31.3%; Score 21; DB 1; Length 16;
 Best Local Similarity 50.0%; Pred. No. 1.4e+04;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 3 KNSPEC 8
 DB 6 KNNIQC 11

RESULT 64
 Q14316 HUMAN PRELIMINARY; PRT; 17 AA.
 ID Q14316
 AC Q14316;
 DT 01-NOV-1996 (TRENBLREL. 01, Created)
 DT 01-JUN-2004 (TRENBLREL. 24, Last sequence update)
 DT 01-MAY-2004 (TRENBLREL. 26, Last annotation update)
 DE Factor IX protein (Fragment).
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
 CC Homo.
 OC NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88327116; PubMed=3416069;
 RA Reitsma P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,

RA Brlet E.;
 RT "The putative factor IX gene promoter in hemophilia B Leyden."
 RL Blood 72:1074-1076(1988).
 DR EMBL: X55008; CAB38245.2; -; Genomic_DNA.
 DR HSS: P00734; IUMA.
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1807 MW; 73887873A971A4F1 CRC64;

Query Match
 Best Local Similarity 31.3%; Score 21; DB 2; Length 17;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 8 CILG 11
 DB 11 CILG 14

RESULT 65
 ID O6QL7_9INFA PRELIMINARY; PRT; 17 AA.
 AC O6QL7;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Neuraminidase (Fragment).
 OS Influenza A virus (A/Thailand/BK29NF/2004(H5N1)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A.
 OC NCBI_TaxID=264514;
 RN [1]
 RP NCLECTIDE SEQUENCE.
 RA Oraveerakul K., Keawcharoen J., Wattanodorn S., Pattanarangsarn S.,
 Paphavast T., Theamboonlers A., Poovorawan Y.;
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY355029; AA557882.1; -; Genomic_RNA.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0016020; C: membrane; IEA.
 DR GO: GO:0004308; F: exo-alpha-sialidase activity; IEA.
 DR GO: GO:0016798; F: hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO: GO:0005975; P: carbohydrate metabolism; IEA.
 DR InterPro: IPR001860; Glyco_hydro_34.
 DR Pfam: PF0064; Neur; 1.
 DR Prodom: PD000431; Glyco_hydro_34; 1.
 KM Glycosidase; Hydrolase; Transmembrane.
 RT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2003 MW; EBB82F3FFD8AF26F CRC64;

Query Match
 Best Local Similarity 31.3%; Score 21; DB 2; Length 17;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPECTIGP 12
 DB 3 RSGFEMIMDP 12

RESULT 66
 ID O6QL9_9INFA PRELIMINARY; PRT; 17 AA.
 AC O6QL9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Neuraminidase (Fragment).
 OS Influenza A virus (A/chicken/Thailand/LV3NF/2004(H5N1)).
 OC Viruses; ssRNA negative-strand viruses; Orthomyxoviridae;
 OC Influenzavirus A.
 OC NCBI_TaxID=264512;
 RN [1]
 RP NCLECTIDE SEQUENCE.
 RA Oraveerakul K., Keawcharoen J., Wattanodorn S., Khanda S.,
 Paphavast T., Theamboonlers A., Poovorawan Y.;

RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY355027; AA557880.1; -; Genomic_RNA.
 DR GO: GO:0016021; C: integral to membrane; IEA.
 DR GO: GO:0016020; C: membrane; IEA.
 DR GO: GO:0004308; F: exo-alpha-sialidase activity; IEA.
 DR GO: GO:0016798; F: hydrolase activity, acting on glycosyl bonds; IEA.
 DR GO: GO:0005975; P: carbohydrate metabolism; IEA.
 DR InterPro: IPR001860; Glyco_hydro_34.
 DR Pfam: PF0064; Neur; 1.
 DR Prodom: PD000431; Glyco_hydro_34; 1.
 KM Glycosidase; Hydrolase; Transmembrane.
 RT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2003 MW; EBB82F3FFD8AF26F CRC64;

Query Match
 Best Local Similarity 31.3%; Score 21; DB 2; Length 17;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 KNSPECTIGP 12
 DB 3 RSGFEMIMDP 12

RESULT 67
 ID Q4X7V0_PLACH PRELIMINARY; PRT; 18 AA.
 AC Q4X7V0;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC405248.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5825;
 RN [1]
 RP NCLECTIDE SEQUENCE.
 RA Hall N., Kariya M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 Berrieman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 James K., Rutherford K., Harris B., Harris D., Churcher C.,
 Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 Jansz C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RA "A comprehensive survey of the Plasmodium life cycle by genomic,
 transcriptomic, and proteomic analyses."
 RT Science 307:82-86(2005).
 RL Science 307:82-86(2005).
 CC -!- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 preliminary data.
 DR EMBL: CAJ01009092; CAH87026.1; -; Genomic_DNA.
 KM Hypothetical protein.
 RT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 18 AA; 2225 MW; 2E5832A217F96845 CRC64;

Query Match
 Best Local Similarity 75.0%; Score 21; DB 2; Length 18;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 FECTI 9
 DB 15 FDCI 18

RESULT 68
 ID Q4Y1S4_PLACH PRELIMINARY; PRT; 19 AA.
 AC Q4Y1S4;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC103036.00.0;

OS Plasmodium chabaudi.
 OC Buxaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Biwell S.L., Rajandream N.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA James C.J., Barrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86 (2005).
 CC -! CAUTION: The sequence shown here is derived from an
 CC EMBL/Genbank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; CA01001723; CAH76886.1; -; Genomic_DNA.
 CC KW Hypothetical protein.
 CC FT NON TER 1
 SQ SEQUENCE 19 AA; 2211 MW; EP1P95ACE6A07PFP4 CRC64;
 QY Query Match 31.3%; Score 21; DB 2; Length 19;
 DB Best Local Similarity 42.9%; Pred. No. 1.6e+04;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 QY 3 KNSPECI 9
 DB 11 KNAILCV 17
 RESULT 69
 OS CHICK
 ID OSU92_CHICK PRELIMINARY; PRT; 19 AA.
 AC OSU92;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DE TGF-beta4 (Fragment).
 OS Gallus gallus (Chicken).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RA Li H., Deeb N., Zhou H., Ashwell C.M., Lamont S.J.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF459837; AAL67517.1; -; Genomic_DNA.
 DR EMBL; AF459838; AAL67518.1; -; Genomic_DNA.
 FT NON TER 1
 FT NON TER 19
 SQ SEQUENCE 19 AA; 2046 MW; 1250C1CBFE03C2F7 CRC64;
 QY Query Match 31.3%; Score 21; DB 2; Length 19;
 DB Best Local Similarity 60.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CILGP 12
 DB 3 CEMGP 7
 RESULT 70
 OS CHICK
 ID OSU92_CHICK PRELIMINARY; PRT; 19 AA.
 AC OSU92;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DE TGF-beta4 (Fragment).
 OS Gallus gallus (Chicken).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RA Li H., Deeb N., Zhou H., Ashwell C.M., Lamont S.J.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF459837; AAL67517.1; -; Genomic_DNA.
 DR EMBL; AF459838; AAL67518.1; -; Genomic_DNA.
 FT NON TER 1
 FT NON TER 19
 SQ SEQUENCE 19 AA; 2046 MW; 1250C1CBFE03C2F7 CRC64;

OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 OC Gallus.
 OC NCBI_TaxID=9031;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RA Li H., Deeb N., Zhou H., Ashwell C.M., Lamont S.J.;
 RL Submitted (DEC-2001) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF459837; AAL67517.1; -; Genomic_DNA.
 DR EMBL; AF459838; AAL67518.1; -; Genomic_DNA.
 FT NON TER 1
 FT NON TER 19
 SQ SEQUENCE 19 AA; 2033 MW; 1315C1CBFE03C2F7 CRC64;
 QY Query Match 31.3%; Score 21; DB 2; Length 19;
 DB Best Local Similarity 60.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 8 CILGP 12
 DB 3 CEMGP 7
 RESULT 71
 OS BRAB
 ID OSU92_BRAB PRELIMINARY; PRT; 19 AA.
 AC OSU92;
 DT 01-FEB-2005 (TREMBlrel. 29, Created)
 DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
 DE T-cell factor 7 isoform D (Fragment).
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=AB;
 RA PubMed:15765502; DOI=10.1002/dvdy.20330;
 RA Velden B.S., Grierson M.J., Sand R.S., Dorak R.I.;
 RT "Expression pattern of zebrafish tcf7 suggests unexplored domains of
 RT wnt/beta-catenin activity."
 RL Dev. Dyn. 233:233-239 (2005).
 DR EMBL; AY825027; AAV84017.1; -; mRNA.
 DR ZFIN; ZDB-GENE-050222-4; tcf7.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 19 AA; 2239 MW; 30C5948AC4B9B9A2 CRC64;
 QY Query Match 31.3%; Score 21; DB 2; Length 19;
 DB Best Local Similarity 60.0%; Pred. No. 1.6e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 NSFEC 8
 DB 14 NSLDC 18
 RESULT 72
 OS BOMMX
 ID MHT_BOMMX STANDARD; PRT; 20 AA.
 AC P83086;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Maxima-hc (Maxima-7).
 OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
 OC Buxaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
 OC NCBI_TaxID=161274;
 RN [1]
 RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE

RP SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
RT "Isolation and structural characterisation of antimicrobial peptides
from the venom of the Chinese large-webbed bell toad (Bombina
maxima).";
RL Submitted (JUL-2001) to Swiss-Prot.
CC -1- FUNCTION: Has antimicrobial activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- SIMILARITY: Belongs to the bombin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amphibian defense peptide; Antibiotic; Antimicrobial;
KW Direct protein sequencing.
SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6B2F949 CRC64;
Query Match 31.3%; Score 21; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 ILGP 12
DB 1 ILGP 4

RESULT 73
MHU_BOMMX STANDARD; PRT; 20 AA.
ID MHU_BOMMX
AC P83087;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Maximin-Hu (Maximin-8)
OS Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Archaeobatrachia; Bombinatoridae; Bombina.
OX NCBI_TaxID=161274;
RN [1]
RP PROTEIN SEQUENCE, FUNCTION, SUBCELLULAR LOCATION, AND TISSUE
RP SPECIFICITY.
RC TISSUE=Skin secretion;
RA Chen T.B., McClean S., Orr D.F., Bjourson A.J., Rao P.F., Shaw C.;
RT "Isolation and structural characterisation of antimicrobial peptides
from the venom of the Chinese large-webbed bell toad (Bombina
maxima).";
RL Submitted (JUN-2001) to Swiss-Prot.
CC -1- FUNCTION: Has antimicrobial activity.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Expressed by the skin glands.
CC -1- SIMILARITY: Belongs to the bombin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
CC Amphibian defense peptide; Antibiotic; Antimicrobial;
KW Direct protein sequencing.
SQ SEQUENCE 20 AA; 1977 MW; EC7541AD6B2F949 CRC64;
Query Match 31.3%; Score 21; DB 1; Length 20;
Best Local Similarity 100.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 ILGP 12
DB 1 ILGP 4

DB 1 ILGP 4

RESULT 74
Q4YU5_PLABE PRELIMINARY; PRT; 20 AA.
ID Q4YU5_PLABE
AC Q4YU5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB105963.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Kariya M., Raine J.D., Carlton J.M., Koof J.T.W.A.,
RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajadream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses";
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAI01002380; CAH98362.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 20 AA; 2265 MW; 1322E950F0B057BF CRC64;
Query Match 31.3%; Score 21; DB 2; Length 20;
Best Local Similarity 37.5%; Pred. No. 1.7e+04;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
QY 3 KNSPECIL 10
DB 1 KXHMOCIT 8

RESULT 75
Q49448_MYCGE PRELIMINARY; PRT; 20 AA.
ID Q49448_MYCGE
AC Q49448;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Uncertain (Fragment).
OS Mycoplasma genitalium.
OC Bacteria; Firmicutes; Mollicutes; Mycoplasmataceae; Mycoplasma.
OX NCBI_TaxID=2097;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94075230; PubMed=8253680;
RA Peterson S.N., Hu P.-C., Bock K.F., Hutchison C.A. III;
RT "A survey of the Mycoplasma genitalium genome by using random
RT sequencing";
RL J. Bacteriol. 175:7918-7930(1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Peterson S.N.;
RT "Characterization and analysis of the Mycoplasma genitalium genome.";
RL Thesis (1992), Microbiology and Immunology, University of North
Carolina Medical School.
DR EMBL; U01744; AAD10557.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 20 AA; 2424 MW; BF8CE399592F014 CRC64;
Query Match 31.3%; Score 21; DB 2; Length 20;

Best Local Similarity 57.1%; Pred. No. 1.7e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 3 KNSPECI 9
Db 14 KVSFLCV 20

RESULT 76

Q4GZP1_MYCTU PRELIMINARY; PRT; 20 AA.
AC Q4GZP1;
DT 13-SEP-2005 (TREMBLrel. 31, Created)
DT 13-SEP-2005 (TREMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Hypothetical protein RV3136 (Fragment).
GN Name=RV3136;
OS Mycobacterium tuberculosis.
OC Bacteria; Actinobacteria; Actinobacteridae; Mycobacteriales;
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium;
OC Mycobacterium tuberculosis complex.
OX NCBI_TaxID=1773;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RA Menendez M.C., Buxton R.S., Stavropoulos E., Evans J.,
RA Gascogne-Binzi D., Barlow R.B.L., Hawkey P.M., Colston M.,
RT "Genomic characterization by DNA microarray analysis of prevalent
RT clinical strains of Mycobacterium tuberculosis in the South Asian
RT community of the UK indicates a common evolutionary origin."
RL Submitted (JUL-2005) to the EMBL/GenBank/DBJ databases.
RN [2]
RP NUCLEOTIDE SEQUENCE.

RA Menendez C.;
RL Submitted (JAN-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL, AJ879178, CAIS1329.1; -, Genomic_DNA.
KM Hypothetical protein.
FT NON_TER 20
SQ SEQUENCE 20 AA; 2166 MW; B6D1A559B33CA2F CRC64;

Query Match 31.3%; Score 21; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.7e+04;
Matches 5; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

Qy 2 EKXSPECILGP 12
Db 9 EVNSARMYTCP 19

RESULT 77

Q6TH87_MOUSE PRELIMINARY; PRT; 20 AA.
AC Q6TH87;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Mu oploid receptor variant 8 (Fragment).
GN Name=Opml; Synonym=Opnm;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Eumarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.

RC TRS8UB-whole brain;
RX PubMed=1499152; DOI=10.1007/s00109-003-0514-z;
RA Kram T.M., Baar C., Rakvag T.T., Kaasa S., Krokan H.B., Skorge P.,
RT "Genetic analysis of the murine micro oploid receptor: increased
RT complexity of Opm gene splicing."
RL J. Mol. Med. 82:250-255(2004).
DR EMBL, AY397681, AAR28085.1; -, mRNA.

DR MGI:97441; Opm1.
DR GO: GO:0016021; C:integral to membrane, TAS.
DR GO: GO:0005624; C:membrane fraction; IDA.
DR GO: GO:0004968; F:mu-oploid receptor activity; IDA.
DR GO: GO:0007610; P:behavior; IMP.
DR GO: GO:0007191; P:dopamine receptor, adenylylate cyclase activa. . .; IDA.
DR GO: GO:0007193; P:G-protein signaling, adenylylate cyclase inh. . .; IDA.
KW Receptor.
FT NON_TER 1
SQ SEQUENCE 20 AA; 2160 MW; EBD8381A9DE5B0B CRC64;

Query Match 31.3%; Score 21; DB 2; Length 20;
Best Local Similarity 42.9%; Pred. No. 1.7e+04;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 SPECILG 11
Db 1 SIVCVG 7

RESULT 78

Q7L297_RANCA PRELIMINARY; PRT; 20 AA.
ID Q7L297;
AC Q7L297;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Gamma crystallin V (Fragment).
OS Rana catesbeiana (Bull frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana;
OC Aquarana.
OX NCBI_TaxID=8400;
RN [1]
RP PROTEIN SEQUENCE.

RX MEDLINE=89351593; PubMed=3255376;
RA Chlou S.H.;
RT "The protein sequence homology of gamma-crystallins among major
RT vertebrate classes and their DNA sequence homology to heat-shock
RT protein genes."
RL J. Protein Chem. 7:527-534(1988).
DR HSP; P08209; 1BLP.
DR PIR; D60894; D60894.
DR InterPro; IPR01064; Crystallin.
DR Pfam; PF00030; Crystall; 1.
DR PROSITE; PSS0915; CRYSTALLIN_BETAGAMMA; 1.
FT NON_TER 1
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2386 MW; E24FBAE30914FB23 CRC64;

Query Match 31.3%; Score 21; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.7e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 SPEC 8
Db 15 SYEC 18

RESULT 79

O12036_CAVY PRELIMINARY; PRT; 12 AA.
ID O12036;
AC O12036;
DT 01-JUL-1997 (TREMBLrel. 04, Created)
DT 01-JUL-1997 (TREMBLrel. 04, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN Name=env;
OS Caprine arthritis encephalitis virus (CAEV).
OC Viruses; Retroviridae; Retroviridae; Lentivirus;
OC Ovis/caprine lentivirus.
OX NCBI_TaxID=11660;
RN [1]

```

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE-97296261; PubMed-9151845;
RA Turelli P., Guiguen P., Mornex J.F., Vigne R., Querat G.;
RT "dUTPase-minus caprine arthritis-encephalitis virus is attenuated for
RT pathogenesis and accumulates G-to-A substitutions.";
RL J. Virol. 71:4522-4530(1997).
DR EMBL; U81390; AAC57905.1; -; Genomic RNA.
DR GO; GO:0019031; C:Viral envelope; IEA.
KM Envelope protein.
FT NON_TER
SQ SEQUENCE 12 AA; 1398 MW; 8D24228CA3733455 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 1.6e+04;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 EKNSPEC 8
DB 4 ESNKWTCT 10

RESULT 80
Q6LCK3 HUMAN PRELIMINARY; PRT; 14 AA.
AC Q6LCK3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Amloride-sensitive epithelial sodium channel gamma subunit
DE (Fragment).
OS Name=SCN1G;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
RX NCBI_TaxID=9606;
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE-96415199; PubMed-8824247; DOI=10.1074/jbc.271.42.26062;
RA Thomas C.P., Doggett N.A., Fisher R., Stokes J.B.;
RT "Genomic organization and the 5' flanking region of the gamma subunit
RT of the human amloride-sensitive epithelial sodium channel.";
RL J. Biol. Chem. 271:26062-26066(1996).
DR EMBL; U53853; AAC50761.1; -; Genomic DNA.
DR GO; GO:0005216; F:ion channel activity; IEA.
KM Ion channel.
FT NON_TER
SQ SEQUENCE 14 AA; 1536 MW; 97F3F771ACD52945 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 14;
Best Local Similarity 57.1%; Pred. No. 1.8e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 NSPECIT 10
DB 6 NSIEMML 12

RESULT 81
Q9Y4Z9 HUMAN PRELIMINARY; PRT; 15 AA.
AC Q9Y4Z9;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-NOV-1999 (TrEMBLrel. 12, Last annotation update)
DE PANCA protein (Fragment).
OS Name=PCNA;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
RX NCBI_TaxID=9606;

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RN [1]
RP NUCLEOTIDE SEQUENCE.
RA D'Apollito M., Ianzano L., Savino M., Rommens J., Zelante L.,
RA Savota A.;
RT Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
RL EMBL; AJ131189; CAB46099.1; -; Genomic DNA.
DR EMBL; AJ131189; CAB46099.1; -; Genomic DNA.
FT NON_TER
SQ SEQUENCE 15 AA; 1590 MW; 8732D75A24DC44F0 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 15;
Best Local Similarity 60.0%; Pred. No. 2e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 6 CTCGP 10

RESULT 82
Q7M2P4 PIG PRELIMINARY; PRT; 16 AA.
AC Q7M2P4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Annexin 36k chain (Fragment).
OS Sus scrofa domestica (domestic pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Suina; Suidae;
OC Sus.
RX NCBI_TaxID=9825;
RP PROTEIN SEQUENCE.
RX MEDLINE-86203621; PubMed-2422556;
RA Geisow M.J., Fritsche U., Hexham J.M., Dash B., Johnson T.;
RT "A consensus amino-acid sequence repeat in Torpedo and mammalian
RT Ca(2+)-dependent membrane-binding proteins.";
RL Nature 320:636-638(1986).
DR PIR; A26393; A26393.
FT NON_TER
SQ SEQUENCE 16 AA; 1801 MW; A7554408D57CF129 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 2.1e+04;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 1 DEKNSPECIT 10
DB 7 DEDRLIBITL 16

RESULT 83
Q5BIH5 EMENI PRELIMINARY; PRT; 17 AA.
AC Q5BIH5;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DT 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DE Hypothetical protein.
OS ORFNames=AN5605.2;
OS Apeerygillus nidulans FGSC A4.
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Eurotiiales; Trichocomaceae; Emericella.
RX NCBI_TaxID=227321;
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FGSC A4;
RA Birren B., Nusbaum C., Abouelleil A., Allen N., Anderson S.,
RA Arachchi H.M., Barna N., Baatien V., Bloom T., Boguslavsky L.,
RA Boukhalter B., Butler J., Calvo S.E., Camarata U., Chang J.,
RA Choepel Y., Collamore A., Cook A., Cooke P., Corum B., Deatellano K.,
RA Diaz J.S., Dodge S., Dooley K., Dorris L., Elkins T., Engels R.,
RA Erickson J., Faro S., Ferreira P., Fitzgerald M., Gage D., Galagan J.,

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RA Gardyna S., Gnerre S., Graham L., Grand-Pierre N., Hafez N.,
 RA Hagopian D., Hagos R., Hall J., Horton L., Hulme W., Iliev I.,
 RA Jaffe D., Johnson R., Jones C., Kamel M., Kamet A., Karatas A.,
 RA Kells C., Landers T., Levine R., Lindblad-Toh K., Liu G., Lui A.,
 RA Ma L.-J., Mabbitt E., McCarty M., McDonald P., Major J., Manning J.,
 RA Matthews C., Mauceli E., McCarthy M., Meldrum J., Menais L.,
 RA Mhova T., Mienna V., Murphy T., Naylor J., Nguyen C., Nicol R.,
 RA Nielsen C.B., Norbu C., O'Connor T., O'Donnell P., O'Neill D.,
 RA Oliver J., Peterson K., Phunkhang P., Pierre N., Purcell S.,
 RA Raghupathi A., Ramasamy U., Raymond C., Reta R., Rise C., Rogov P.,
 RA Roman J., Schauer S., Schupbach R., Seaman S., Severy P., Shtromov S.,
 RA Smith C., Spencer B., Stange-Thomann N., Stojanovic N., Stubbs M.,
 RA Talamas J., Testaye S., Theodore J., Topham K., Travers M.,
 RA Vesiliev H., Venkatarman V.S., Viel R., Vo A., Wang S., Wilson B.,
 RA Wu X., Wyman D., Young G., Zainoun J., Zembek U., Zimmer A., Zody M.,
 RA Zander B.,
 RT "genome sequence of Aspergillus nidulans."
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 KW EMBL; AACD0100097; EAA62195.1; -; Genomic_DNA.
 KM Hypothetical protein.
 SQ SEQUENCE 17 AA; 1874 MW; B279D1966C71F967 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 6 FECL 10
 Db 4 FDCAL 8

RESULT 84
 Q4XMI0_PLACH PRELIMINARY; PRT; 17 AA.
 ID Q4XMI0_PLACH PRELIMINARY; PRT; 17 AA.
 AC Q4XMI0_PLACH PRELIMINARY; PRT; 17 AA.
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC108836.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 CC NCBI_TaxID=5825;
 RX NCBI_TaxID=5825;
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Bertman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Hartle D., Churchev C.,
 RA Qaill M.A., Ormond D., Doggett J., Truman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jans C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86 (2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 KW EMBL; CAJ01004645; CAH81882.1; -; Genomic_DNA.
 KM Hypothetical protein.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 2060 MW; F407D2F3398B1E09 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 4 NSPEC 8
 Db 10 NNFCV 14

RESULT 85
 Q704V9_BOVIN PRELIMINARY; PRT; 17 AA.
 ID Q704V9_BOVIN PRELIMINARY; PRT; 17 AA.
 AC Q704V9_BOVIN PRELIMINARY; PRT; 17 AA.
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Signal transducer and activator of transcription 3 (Fragment).
 GN Name=Stat3;
 OS Bos taurus (Bovine).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 CC Pecora; Bovidae; Bovinae; Bos.
 CC NCBI_TaxID=9913;
 RX NCBI_TaxID=9913;
 RP NUCLEOTIDE SEQUENCE.
 RA Seyfert H.M., Wheeler T.T., Molenaar A., Pitra C.,
 RL Submitted (JAN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ220667; CAF06194.1; -; Genomic_DNA.
 FT NON_TER 1
 SQ SEQUENCE 17 AA; 1863 MW; AA9BCEFCDC255F CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;
 Best Local Similarity 33.3%; Pred. No. 2.2e+04;
 Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

Qy 1 DEKNSPECIATP 12
 Db 5 DMELTSECATSP 16

RESULT 86
 Q712K0_CAPI PRELIMINARY; PRT; 17 AA.
 ID Q712K0_CAPI PRELIMINARY; PRT; 17 AA.
 AC Q712K0_CAPI PRELIMINARY; PRT; 17 AA.
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Alpha s2-casein precursor (Fragment).
 GN Name=csn12;
 OS Capra hircus (Goat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
 CC Pecora; Bovidae; Caprinae; Capra.
 CC NCBI_TaxID=9925;
 RX NCBI_TaxID=9925;
 RP NUCLEOTIDE SEQUENCE.
 RA TISSUE=Blood;
 RC MEDLINE=33216130; PubMed=8462880; DOI=10.1016/0378-1119(93)90336-2;
 RA Boudol C.;
 RT "Sequence of the goat alpha s2-casein-encoding cDNA."
 RL Gene 125:235-236 (1993).
 CC [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Blood;
 RX MEDLINE=21313038; PubMed=11419340;
 RA Ramuno L., Longobardi E., Pappalardo M., Rando A., Di Gregorio P.,
 RA Cosenza G., Mariani P., Pastore N., Marina P.;
 RT "An allele associated with a non detectable amount of as2 casein in
 RT goat milk."
 RL Anim. Genet. 32:19-26 (2001).
 DR EMBL; AJ242924; CAB44499.1; -; Genomic_DNA.
 DR GO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0005215; F:transporter activity; IEA.
 DR InterPro; IPR001588; Casein.
 DR PROSITE; PS00306; CASIN_ALPHA_BETA; 1.
 KW SIGNAL.
 FT CHAIN 1 15 Potential.
 FT NON_TER 16 >17 Alpha s2-casein.
 SQ SEQUENCE 17 AA; 1953 MW; C76CC285A9B94551 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 2.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 6 PECTL 10
 | | |
 | | |
 DB 6 PCTCL 10

RESULT 87
 HSTB_ECOLI STANDARD; PRT; 18 AA.
 AC P01560;
 DT 21-UTL-1986 (Rel. 01, Created)
 DT 21-UTL-1986 (Rel. 01, Last sequence update)
 DT 05-UTL-2004 (Rel. 44, Last annotation update)
 DE Heat-stable enterotoxin ST-2 (ST-B).
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OX NCBI_TaxID=562;
 RN [1]
 RP PROTEIN SEQUENCE.
 RC STRAIN=O42:K86:H37 / 18D / ETEC;
 RA MEDLINE=81264141; PubMed=7021541;
 RA Chan S.-K., Giamella R.A.;
 RT "Amino acid sequence of heat-stable enterotoxin produced by
 RT Escherichia coli pathogenic for man."
 RL J. Biol. Chem. 256:7744-7746(1981).
 RN [2]
 RP DISULFIDE BONDS.
 RX MEDLINE=87191003; PubMed=3552731; DOI=10.1016/0014-5793(87)80134-5;
 RA Shimoniishi Y., Hidaaka Y., Koizumi M., Hane M., Almoto S., Takeda T.,
 RA Miwatani T.; Takeda Y.;
 RT "Mode of disulfide bond formation of a heat-stable enterotoxin (STh)
 RT produced by a human strain of enterotoxigenic Escherichia coli."
 RL FEBS Lett. 215:165-170(1987).
 CC -1- FUNCTION: Toxin which activates the particulate form of guanylate
 CC cyclase and increases cyclic GMP levels within the host intestinal
 CC epithelial cells.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- SIMILARITY: Belongs to the heat-stable enterotoxin family.
 CC
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.

DR PIR; A01823; QHEC2.
 DR HSSP; P01559; 1ETN.
 DR InterPro; IPR001489; Enterotoxin HS.
 DR Pfam; PF02048; Enterotoxin HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 KM Direct protein sequencing; Enterotoxin; Toxin.
 FT DISULFID 5 10
 FT DISULFID 6 14
 FT DISULFID 9 17
 SQ SEQUENCE 18 AA; 1978 MW; DDC975F49D600650 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 18;
 Best Local Similarity 60.0%; Pred. No. 2.4e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 NSFEC 8
 | | |
 | | |
 DB 1 NTFFC 5

RESULT 88
 Q7M532 HALMA PRELIMINARY; PRT; 18 AA.

AC Q7M532;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Ribosomal protein HS25 (fragment).
 OS Halobaculum marismortui (Halobacterium marismortui).
 OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;
 OC Halobacteriaceae; Halobaculum.
 OX NCBI_TaxID=2238;
 RN [1]
 RP PROTEIN SEQUENCE.
 RA Engemann S., Herfurth E., Briesemeister U., Grellle G.,
 RA Witzmann-Liebold B.;
 RL Submitted (NOV-1994) to the PIR data bank.
 RN [2]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96096717; PubMed=8529646;
 RA Engemann S., Noelle R., Herfurth E., Briesemeister U., Grellle G.,
 RA Witzmann-Liebold B.;
 RT "Cartography of ribosomal proteins of the 30S subunit from the
 RT halophilic Halobaculum marismortui and complete sequence analysis of
 RT protein HS26."
 RL Eur. J. Biochem. 234:24-31(1995).
 DR PIR; S49026; S49026.
 FT NON TER 1 1
 FT NON TER 18 18
 SQ SEQUENCE 18 AA; 2008 MW; F66720F002BAEDCD CRC64;

Query Match 29.9%; Score 20; DB 2; Length 18;
 Best Local Similarity 75.0%; Pred. No. 2.4e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 ILGP 12
 | | |
 | | |
 DB 12 VLGP 15

RESULT 89
 Q7S364 NEUCR
 ID Q7S364 NEUCR PRELIMINARY; PRT; 18 AA.
 AC Q7S364;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Predicted protein.
 GN Name=NC008586.1;
 OS Neurospora crassa.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Sordariaceae; Neurospora.
 OX NCBI_TaxID=5141;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=OR74A;
 RA Galagan J.E., Calvo S.E., Borkovich K.A., Selker E.U., Read N.D.,
 RA Jaffe D., Fitzhugh W., Ma L.-J., Smirnov S., Puccelli S., Rehman B.,
 RA Bikins T., Engels R., Wang S., Nielsen C.B., Butler J., Endrizzi M.,
 RA Qui D., Ianakiev P., Pedersen D., Nelson M., Washburne M.,
 RA Selitrenikoff C.P., Kinsey J.A., Braun E.L., Zelter A., Schulte U.,
 RA Kothe G.O., Jedd G., Mewes W., Staben C., Marcotte E., Greenberg D.,
 RA Roy A., Foley K., Naylor J., Thomann N., Barrett R., Greer S.,
 RA Kamal M., Kamyssele M., Mauceli E., Bielke C., Rudd S., Frieman D.,
 RA Krysotova S., Rasmussen C., Metznerberg R.L., Perkins D.D., Kroken S.,
 RA Cogoni C., Macino G., Catchside D., Li W., Pratt R.J., Osmant S.A.,
 RA Desouza C.C., Glaes L., Orbach M.U., Berglund U., Voelker R.,
 RA Yarden O., Plamann M., Seiler S., Dunlap J., Radford A., Aramayo R.,
 RA Natvig D.O., Alex L.A., Mannhaupt G., Ebdole D.J., Pretlag M.,
 RA Paulsen I., Sachs M.S., Lander E.S., Nussbaum C., Birren B.;
 RT "The Genome Sequence of the Filamentous Fungus Neurospora crassa."
 RL Nature 0:0-0(2003).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 CC EMBL; AABX01000413; EAA29868.1; -; genomic_DNA.

SQ SEQUENCE 18 AA; 2108 MW; 015D9CC527B1B7 CRC64;
 Query Match 29.9%; Score 20; DB 2; Length 18;
 Best Local Similarity 80.0%; Pred. No. 2.4e+04;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DEKNS 5
 Db 10 DPKNS 14
 RESULT 90
 Q7M0U3_CITPR
 ID Q7M0U3_CITPR PRELIMINARY; PRT; 18 AA.
 AC Q7M0U3
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Heat-stable enterotoxin ST-1a.
 OS Citrobacter freundii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OC NCBI_TaxID=546;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=89108617; PubMed=2912902;
 RA Guarino A., Giannella R., Thompson M.R.;
 RT "Citrobacter freundii produces an 18-amino-acid heat-stable
 RT enterotoxin identical to the 18-amino-acid Escherichia coli heat-
 RT stable enterotoxin (ST 1a)."
 RL Infect. Immun. 57:649-652(1989).
 DR PIR; A60103; A60103.
 DR HSSP; P01559; 1ETN.
 DR DR CO; GO:0005576; C:extracellular region; IEA.
 DR GO; GO:0009405; P:pathogenesis; IEA.
 DR InterPro; IPR001489; Enterotoxin_HS.
 DR Pfam; PF02048; Enterotoxin_HS; 1.
 DR PROSITE; PS00273; ENTEROTOXIN_H_STABLE; 1.
 SQ SEQUENCE 18 AA; 1978 MW; D4D875F49D60064F CRC64;
 Query Match 29.9%; Score 20; DB 2; Length 18;
 Best Local Similarity 60.0%; Pred. No. 2.4e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 4 NSPEC 8
 Db 1 NTFYC 5
 RESULT 91
 Q7M076_RAT
 ID Q7M076_RAT PRELIMINARY; PRT; 18 AA.
 AC Q7M076
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Enkephalin-degrading aminopeptidase (EC 3.4.-.-), puromycin-sensitive
 DE (fragment).
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OC NCBI_TaxID=10116;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=90132681; PubMed=2299352;
 RA Dyer S.H., Slaughter C.A., Orth K., Moomaw C.R., Heresh L.B.;
 RT "Comparison of the soluble and membrane-bound forms of the puromycin-
 RT sensitive enkephalin-degrading aminopeptidases from rat."
 RL J. Neurochem. 54:547-554(1990).
 DR PIR; A60915; A60915.
 FT NON_TER 1 1
 FT NON_TER 16 16

SQ SEQUENCE 18 AA; 2172 MW; 100BA08632399CC3 CRC64;
 Query Match 29.9%; Score 20; DB 2; Length 18;
 Best Local Similarity 66.7%; Pred. No. 2.4e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 2 EKNSFE 7
 Db 2 EKNSFE 7
 RESULT 92
 DURA_STRGV
 ID DURA_STRGV STANDARD; PRT; 19 AA.
 AC P36504;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 13-SEP-2005 (Rel. 48, Last annotation update)
 DE Lanthibiotic duramycin (Leucopentin) (Antibiotic PA48009).
 OS Streptococcus thermophilus.
 OC Bacteria; Actinobacteria; Actinobacteriales; Actinomycetales;
 OC Streptococcaceae; Streptococcaceae; Streptococcus.
 OC NCBI_TaxID=68215;
 RN [1]
 RP PROTEIN SEQUENCE, AND STRUCTURE BY NMR.
 RC STRAIN=PA-48009;
 RX MEDLINE=9107438; PubMed=2272918;
 RA Hayashi F., Nagashima K., Terui Y., Kawamura Y., Matsumoto K.,
 RA Itazaki H.;
 RT "The structure of PA48009, the revised structure of duramycin."
 RL J. Antibiot. 43:1421-1430(1990).
 RN [2]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=9107436; PubMed=2125590;
 RA Frederix A., Fendrich G., Markl F., Markl W., Gruner J.,
 RA Raschdorf F., Peter H.H.;
 RT "Duramycin B and C, two new lantibiotics containing antibiotics as
 RT inhibitors of phospholipase A2. Structural revision of duramycin and
 RT cinnamycin."
 RL J. Antibiot. 43:1403-1412(1990).
 CC -1- FUNCTION: Acts as inhibitor of phospholipase A2.
 CC -1- PM: Maturation of lantibiotics involves the enzymic conversion of
 CC Thr, and Ser into dehydrated AA and the formation of thioether
 CC bonds with cysteine or the formation of dialkylamine bonds with
 CC lysine. This is followed by membrane translocation and cleavage of
 CC the modified precursor.
 CC -1- SIMILARITY: Belongs to the type B lantibiotic family.
 CC -----
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 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC KW Antibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;
 KW Lantibiotic; Thioether bond.
 FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
 FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
 FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
 FT CROSSLINK 6 19 Lysinalanine (Ser-Lys).
 SQ SEQUENCE 19 AA; 2069 MW; 012951AE27362F00 CRC64;
 Query Match 29.9%; Score 20; DB 1; Length 19;
 Best Local Similarity 60.0%; Pred. No. 2.5e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 8 CILGP 12
 Db 5 CSFGP 9
 RESULT 93
 DURA_STRGV

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ID DURB_STRGW STANDARD; PRT; 19 AA.
AC P36502;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lanthibiotic duramycin B.
OS Streptococcicillium sp. (strain R2075).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=35759;
RN 1;
RP PROTEIN SEQUENCE.
RX MEDLINE=91107436; PubMed=2125590;
RA Frederhagen A., Fendrich G., Markl F., Markl W., Gruner J.,
RA Raschdorf F., Peter H.H., Gruner J.,
RT "Duramycin B and C, two new lanthionine containing antibiotics as
RT inhibitors of phospholipase A2. Structural revision of duramycin and
RT cinamycin.",
RL J. Antibiot. 43:1403-1412 (1990).
RN 2;
RP STRUCTURE BY NMR.
RA Zimmermann N., Freund S., Frederhagen A., Jung G.,
RT "Solution structure of the lanthibiotics duramycin B and C.",
RL (in) Schneider C.H., Eberle A.N. (eds.),
RL Peptides 1992, pp.519-520, Bescm Science Publishers, Leiden (1993).
RN 3;
RP STRUCTURE BY NMR.
RX MEDLINE=93387292; PubMed=8375380;
RA Zimmermann N., Freund S., Frederhagen A., Jung G.,
RT "Solution structures of the lanthibiotics duramycin B and C.",
RL Bur. J. Biochem. 216:419-428 (1993).
CC -1- FUNCTION: Acts as inhibitor of phospholipase A2.
CC -1- PTM: Maturation of lanthibiotics involves the enzymic conversion of
CC Thr. and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -1- SIMILARITY: Belongs to the type B lanthibiotic family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Antibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;
KM Lanthibiotic; Thioether bond.
FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2063 MW; 0133445E27362F00 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 5 CSFGP 9

RESULT 94
LANC_STRS6 STANDARD; PRT; 19 AA.
ID LANC_STRS6
AC P38655;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Lanthibiotic ancoventin.
OS Streptomyces sp. (strain A647P-2).
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycinae; Streptomycetaceae; Streptomyces.

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OX NCBI_TaxID=72591;
RN 1;
RP PROTEIN SEQUENCE.
RA Wakamiya T., Ueki Y., Shiba T., Kido Y., Moroki Y.,
RT "The structure of ancoventin, a new peptide inhibitor of angiotensin I
RT converting enzyme.",
RL Tetrahedron Lett. 26:665-668 (1985).
CC -1- FUNCTION: Acts as an inhibitor of angiotensin I converting enzyme.
CC -1- PTM: Maturation of lanthibiotics involves the enzymic conversion of
CC Thr. and Ser into dehydrated AA and the formation of thioether
CC bonds with cysteine or the formation of dialkylamine bonds with
CC lysine. This is followed by membrane translocation and cleavage of
CC the modified precursor.
CC -1- SIMILARITY: Belongs to the type B lanthibiotic family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
KW Antibiotic; Antimicrobial; Bacteriocin; Direct protein sequencing;
KM Lanthibiotic; Thioether bond.
FT CROSSLINK 1 18 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 4 14 Lanthionine (Ser-Cys).
FT CROSSLINK 5 11 Beta-methylanthionine (Cys-Thr).
FT CROSSLINK 6 19 Lysinoalanine (Ser-Lys).
SQ SEQUENCE 19 AA; 2033 MW; F434299E2736286A CRC64;

Query Match 29.9%; Score 20; DB 1; Length 19;
Best Local Similarity 60.0%; Pred. No. 2.5e+04;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 8 CILGP 12
DB 5 CSFGP 9

RESULT 95
Q9TWS_9TRY PRELIMINARY; PRT; 19 AA.
ID Q9TWS_9TRY
AC Q9TWS8;
DT 01-MAY-2000 (TRENBLrel. 13, Created)
DT 01-MAY-2000 (TRENBLrel. 13, Last sequence update)
DT 01-MAR-2004 (TRENBLrel. 26, Last annotation update)
DE Haploglobin-related protein beta subunit (Fragment).
OS Trypanosoma brucei.
OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN 1;
RP PROTEIN SEQUENCE.
RX MEDLINE=95232503; PubMed=7716520;
RA Smith A.B., Bako J.D., Hajduk S.L.,
RT "Killing of trypanosomes by the human haploglobin-related protein.",
RL Science 268:284-286 (1995).
SQ SEQUENCE 19 AA; 2055 MW; 65BD135667C94056 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 2.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DEKNSP 6
DB 7 DAKGSP 12

RESULT 96
Q4XAE2_PLACH PRELIMINARY; PRT; 19 AA.
ID Q4XAE2_PLACH
AC Q4XAE2;
DT 13-SEP-2005 (TRENBLrel. 31, Created)
DT 13-SEP-2005 (TRENBLrel. 31, Last sequence update)

```

DT 13-SEP-2005 (TReMBLrel. 31, Last annotation update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PC401441.00.0;
 OS Plasmodium chabaudi.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NC NCBI_TaxID=5825;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jans C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAJ01007305; CAJ05554.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2106 MW; F29C6EAB8D6C461A CRC64;

Query Match 29.9%; Score 20; DB 2; Length 19;
 Best Local Similarity 75.0%; Pred. No. 2.5e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

DT 13-SEP-2005 (TReMBLrel. 31, Created)
 DT 13-SEP-2005 (TReMBLrel. 31, Last sequence update)
 DE Hypothetical protein (Fragment).
 GN ORFNames=PA403980.00.0;
 OS Plasmodium berghel.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
 NC NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jans C.J., Barrall B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAJ01007305; CAJ05554.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2106 MW; F29C6EAB8D6C461A CRC64;

Query Match 29.9%; Score 20; DB 2; Length 19;
 Best Local Similarity 75.0%; Pred. No. 2.5e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

RESULT 98
 09G197_9PHAB
 ID 09G197_9PHAB PRELIMINARY; PRT; 19 AA.
 AC 09G197;
 DT 01-MAR-2001 (TReMBLrel. 16, Created)
 DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Ribulose-1,5-bisphosphate carboxylase/oxygenase large subunit
 DE (Fragment).
 GN Name=rbcl;
 OS Sargassum polycystum.
 OC Chloroplast.
 OC Eukaryota; stramenopiles; Phaeophyceae; Fuciales; Sargassaceae;
 OC Sargassum.
 NC NCBI_TaxID=127578;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=nepl27;
 RA Phillips N.E.;
 RT "Molecular phylogenetic analysis of the pan-pacific genus Sargassum
 RT (Fuciales, Phaeophyceae)."
 RL Thesis (1998), University of Hawaii.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=nepl27;
 RA Phillips N.E.; Smith C.M., Norden C.W.;
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF244344; AAF98113.1; -; Genomic_DNA.
 GO GO:0009507; C:chloroplast; IEA.
 KW Chloroplast.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2108 MW; A02FD2B6DD66A57 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 19;
 Best Local Similarity 100.0%; Pred. No. 2.5e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

DT 10-MAY-2005 (TReMBLrel. 30, Created)
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
 DE Hypothetical protein (Fragment).
 GN Arabidopsis thaliana (Mouse-ear cress).
 OC Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosid II; Brassicales; Brassicaceae; Arabidopsis.
 NC NCBI_TaxID=3702;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Totoki Y., Seki M., Ishida J., Nakajima M., Enju A., Kamiya A.,
 RA Narusaka M., Shin-i T., Nakagawa M., Sakamoto N., Oishi K., Kohara Y.,
 RA Kobayashi M., Toyoda T., Konagaya A., Sakaki Y., Sakurai T., Iida K., Akiyama K.,
 RA Satou M., Toyoda T., Konagaya A., Carninci P., Kawai J.,
 RA Hayashizaki Y., Shinozaki K.;
 RT "Large-scale analysis of RIKEN Arabidopsis full-length (RAFL) cDNAs."
 RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AK220689; BMD93761.1; -; mRNA.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 19 AA; 2146 MW; 5DC5F79C9FAA6C37 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 19;
 Best Local Similarity 60.0%; Pred. No. 2.5e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 SPECI 9
: |||
Db 3 TPSCI 7

RESULT 100

016129 HUMAN
ID 016129 HUMAN PRELIMINARY; PRT; 20 AA.
AC 016129;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, last annotation update)
DE Protein tyrosine phosphatase (Fragment).
GN Name=PTPGL;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=94156037; PubMed=7509295; DOI=10.1016/0014-5793(94)80420-6;
RA Takekawa M., Itoh F., Hinoda Y., Adachi M., Ariyama T., Inazawa J.,
RA Imai K., Yachi A.;
RT "Chromosomal localization of the aberrant transcripts in human colon cancer
RT and characterization of the protein tyrosine phosphatase G1 gene
RT cell".
RL FEBS Lett. 339:222-228(1994).
DR EMBL, S69183; AAB30046.1; -; mRNA.
FT NON TER 20 20
SQ SEQUENCE 20 AA; 2428 MW; 473AB954F158A78B CRC64;
Query Match 29.9%; Score 20; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 2.6e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
QY 2 EKNSPECTL 10
: |||
Db 2 KKNRYKDL 10

Search completed: January 20, 2006, 19:11:10
Job time : 41.9231 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:14 ; Search time 68.0192 Seconds
(without alignments)
116.273 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DAEPRHGYLLTAIVSPCK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 243163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 880474

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

A_Geneseq_21:*

1: geneseqp19808:*

2: geneseqp19908:*

3: geneseqp20008:*

4: geneseqp20018:*

5: geneseqp20028:*

6: geneseqp20038:*

7: geneseqp20048:*

8: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	3	AAV52515
2	96	100.0	18	5	AAU96319
3	38	39.6	10	2	AAV47095
4	35.5	37.0	19	9	ADM43819
5	34	35.4	15	5	ABU14737
6	34	35.4	15	5	ABU14493
7	34	35.4	15	5	ABU14856
8	34	35.4	15	5	ABU14620
9	34	35.4	15	5	ABU14316
10	34	35.4	15	5	ABU14777
11	34	35.4	15	8	ADL21730
12	34	35.4	15	8	ADL22014
13	34	35.4	15	8	ADL21857
14	34	35.4	15	8	ADL21553
15	34	35.4	15	8	ADL21974
16	34	35.4	15	8	ADL22093
17	34	35.4	15	8	ADL22093
18	34	35.4	15	8	ADL22093
19	34	35.4	15	8	ADL22093
20	34	35.4	15	8	ADL22093
21	34	35.4	15	8	ADL22093
22	34	35.4	15	8	ADL22093
23	34	35.4	15	8	ADL22093
24	34	35.4	15	8	ADL22093

25	33	34.4	17	5	ABG67141	ADG67141 HCV pepti
26	33	34.4	18	2	AAW45412	AAW45412 N-termina
27	32	33.3	12	5	AAE26395	AAE26395 Human GPR
28	32	33.3	16	2	AAW45125	AAW45125 Human car
29	31	32.3	9	5	AAU74686	AAU74686 Human can
30	31	32.3	9	7	ABR82211	ABR82211 Human can
31	31	32.3	15	2	AAV13274	AAV13274 Naturally
32	31	32.3	18	7	ADR40700	ADR40700 KDR & VEG
33	31	32.3	18	8	ADK57606	ADK57606 Cyclic KD
34	31	32.3	20	5	AAU73345	AAU73345 Human DR as
35	31	32.3	20	9	ADZ25579	ADZ25579 Human pro
36	31	32.3	20	9	ADZ25579	ADZ25579 Pig 3-ali
37	31	32.3	20	9	ADZ25579	ADZ25579 Peptide f
38	30	31.2	11	4	AAE26607	AAE26607 Beta-ahoe
39	30	31.2	11	6	ABU79065	ABU79065 Amyloid f
40	30	31.2	11	6	ABW00199	ABW00199 Controll p
41	30	31.2	12	5	AAE26397	AAE26397 Human GPR
42	30	31.2	14	8	ADU04328	ADU04328 Human imm
43	30	31.2	19	2	AAE04059	AAE04059 Reagent o
44	30	31.2	20	2	AAV29388	AAV29388 Fetal 3D
45	30	31.2	20	8	ADU04264	ADU04264 Human imm
46	29	30.2	6	8	ADU037698	ADU037698 Binding p
47	29	30.2	6	8	ADU028220	ADU028220 Captur s
48	29	30.2	6	8	ADU030397	ADU030397 6-mer pep
49	29	30.2	6	8	ADU030397	ADU030397 Tagged po
50	29	30.2	6	9	ADZ46403	ADZ46403 Antigenic
51	29	30.2	11	5	AAE30513	AAE30513 Therapeut
52	29	30.2	11	5	AAE30513	AAE30513 HER-2 mim
53	29	30.2	11	8	ADU67980	ADU67980 T. thermo
54	29	30.2	11	8	ADU67980	ADU67980 T. thermo
55	29	30.2	11	8	ADU67980	ADU67980 T. thermo
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57	29	30.2	11	8	ADU67980	ADU67980 T. thermo
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64	29	30.2	11	8	ADU67980	ADU67980 T. thermo
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75	29	30.2	11	8	ADU67980	ADU67980 T. thermo
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78	29	30.2	11	8	ADU67980	ADU67980 T. thermo
79	29	30.2	11	8	ADU67980	ADU67980 T. thermo
80	29	30.2	11	8	ADU67980	ADU67980 T. thermo
81	29	30.2	11	8	ADU67980	ADU67980 T. thermo
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91	29	30.2	11	8	ADU67980	ADU67980 T. thermo
92	29	30.2	11	8	ADU67980	ADU67980 T. thermo
93	29	30.2	11	8	ADU67980	ADU67980 T. thermo
94	29	30.2	11	8	ADU67980	ADU67980 T. thermo
95	29	30.2	11	8	ADU67980	ADU67980 T. thermo
96	29	30.2	11	8	ADU67980	ADU67980 T. thermo
97	29	30.2	11	8	ADU67980	ADU67980 T. thermo

98	28	29.2	6	8	ADR49871	6-mer pep
99	28	29.2	6	8	ADS95517	Tagged po
100	28	29.2	6	8	ADS95525	Tagged po

ALIGNMENTS

RESULT 1

ID AAY52515 standard; peptide, 18 AA.

XX AAY52515/

DT 22-FEB-2000 (first entry)

DE House dust mite allergen protein (map) A/B fragment map(5).

XX Mite allergen protein; map; high molecular weight; HMW-map; allergy;

KM house dust mite; IGE; immunoglobulin E; allergen; mapA; mapB;

KM hypersensitivity reaction; therapy; treatment; diagnosis; human; feline;

XX canine; veterinary; antibody; vaccine; immunisation.

OS Dermatophagoides farinae.

XX WO954349-A2.

PD 28-OCT-1999.

PF 16-APR-1999; 99WO-US008524.

PR 17-APR-1998; 98US-00062013.

PR 13-MAY-1998; 98US-0085295P.

PR 02-SEP-1998; 98US-0098909P.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2000-052700/04.

XX Novel high molecular weight Dermatophagoides nucleic acid polypeptides

XX used to modify an animal's hypersensitivity to mite allergens.

XX Claim 3; Page 69; 154pp; English.

XX Sequences AAY5510-Y5522 represent proteolytic fragments of

XX Dermatophagoides farinae high molecular weight mite allergen protein (HMW

XX -map) composition. The HMW-map composition was isolated from a D. farinae

XX homogenate by gel filtration, with each fraction being analysed for the

XX presence of proteins that bound to IGE present in mite-allergic dog

XX antiserum. The HMW-map composition comprises mapA (a 109 kD protein) and

XX mapB (98 kD). Mite allergenic proteins and peptides, and nucleic acids

XX encoding them, may be used in therapeutic compositions to modify an

XX animal's hypersensitivity reaction to mite allergens. Animals that may be

XX created include mammals and birds, especially felines, canines, equines,

XX humans, other pets, and work or domestic animals. The proteins or

XX fragments may also be used to diagnose allergies via a skin test. The

XX proteins and peptides can also be used to raise antibodies, which have a

XX variety of potential uses. For example, they can be used as vaccines to

XX passively immunise animals against dust mite hypersensitivity, as

XX positive controls in test kits and as tools to recover desired dust mite

XX allergens from a mixture of proteins

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 96; DB 3; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFEPHGYLLTAAVSPGK 18

DB 1 DAFEPHGYLLTAAVSPGK 18

RESULT 2
ID AAU96319 standard; peptide, 18 AA.

XX AAU96319/

DT 15-JUL-2002 (first entry)

DE Der HMW-map polypeptide #6.

XX Der HMW-map; American house dust mite; anti-allergic; mite; IGE;

KM mite allergenic protein; immunoglobulin E; hypersensitivity;

XX immunocomplex formation.

XX Dermatophagoides farinae.

XX WO200222807-A2.

PD 21-MAR-2002.

PF 14-SEP-2001; 2001WO-US028730.

PR 14-SEP-2000; 2000US-00662293.

XX (HESK-) HESKA CORP.

XX Mccall CA, Hunter SW, Weber ER;

XX WPI; 2002-351888/38.

XX New mite allergenic protein isolated from Dermatophagoides, designated

XX Der HMW-map protein, useful as a vaccine for treating mite allergy.

XX Claim 12; Page 70; 161pp; English.

XX The invention relates to an isolated mite allergenic protein of

XX Dermatophagoides, designated Der HMW-map protein, and its related nucleic

XX acid. The Der HMW-map protein is useful for eliciting an immune response

XX against Der HMW-map protein. The protein or a reagent comprising a non-

XX proteinaceous epitope is useful for identifying an animal (e.g., dog,

XX cat) susceptible to or having an allergic response to a mite. A

XX therapeutic composition is useful for desensitising a host animal to an

XX allergic response to a mite. The DNA and protein can be used in the

XX detection of anti-Der HMW-map antibodies in animal fluids, and inhibition

XX of immunoglobulin (Ig)E or Der HMW-map protein activity associated with a

XX disease. Antibodies that bind to Der HMW-map are useful for inhibiting

XX binding of proteins to IGE, to prevent immunocomplex formation, thus

XX reducing hypersensitivity responses to mite allergens, and as vaccines

XX against mite allergen hypersensitivity. Sequences AAU96314-AAU96342

XX represent Der HMW-map polypeptides of the invention

XX Sequence 18 AA;

SQ

Query Match 100.0%; Score 96; DB 5; Length 18;

Best Local Similarity 100.0%; Pred. No. 1.6e-09;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAFEPHGYLLTAAVSPGK 18

DB 1 DAFEPHGYLLTAAVSPGK 18

RESULT 3

ID AAY47095 standard; peptide, 10 AA.

XX AAY47095/

AC AAY47095;

DT 01-DEC-1999 (first entry)

XX Immunogenic peptide having a human leukocyte antigen binding motif #1706.

XX Human leukocyte antigen; binding; immunogenic; glycoprotein; MHC; HLA;
 KW immune response; T cell activation; major histocompatibility complex;
 KW cytotoxic T lymphocyte; CTL; tumour rejection; viral infection; cancer;
 KW prostate cancer; hepatitis B; hepatitis C; AIDS; renal carcinoma;
 KW vaccine; immunisation.
 OS Synthetic.
 OS Homo sapiens.
 XX MO9945954-A1.
 PN 16-SEP-1999.
 PD 13-MAR-1998; 98WO-US005039.
 PF 13-MAR-1998; 98WO-US005039.
 PR 13-MAR-1998; 98WO-US005039.
 XX (EPIM-) EPIMUNE INC.
 PA
 PI Sette A, Kubo RT, Sidney J, Celis E, Grey HM, Southwood S;
 DR WPI, 1999-551214/46.
 XX New immunogenic peptides with HLA binding motif, useful in treatment and
 PT diagnosis of cancers and viral diseases.
 XX Claim 1, Page 93; 150pp; English.
 PS
 XX AA45390 to AA48224 represent specifically claimed immunogenic peptides
 CC having a human major histocompatibility complex (MHC) Class I (also known
 CC as human leukocyte antigen (HLA)) binding motif. The immunogenic peptides
 CC can bind to a specific HLA allele (i.e. HLA-A subtypes HLA-A2.1, A1, A3.2
 CC or A24.1 or HLA-B or C) and induce a cytotoxic T cell response against
 CC the antigen from which the peptide is derived. Cytotoxic T lymphocytes
 CC (CTLs) which destroy antigen-bearing cells are normally induced by an
 CC antigen in the form of a peptide fragment bound to a HLA molecule, rather
 CC than the intact foreign antigen itself, and are particularly important in
 CC tumour rejection and in fighting viral infections. The peptides are
 CC therefore useful therapeutically to treat or prevent viral infections and
 CC cancers in mammals (especially humans) e.g. prostate cancer, hepatitis B
 CC and C, AIDS, and renal carcinoma. They can be administered as vaccines to
 CC elicit an immune response in individuals susceptible or otherwise at risk
 CC of viral infection or cancer, or used to treat chronic or acute
 CC conditions. They are also useful diagnostically, and can be used to
 CC induce a cytotoxic T cell response, by contacting a cytotoxic T cell with
 CC the peptide e.g. to produce CTLs ex vivo for infusion back into a
 CC patient. The polynucleotides encoding the immunogenic peptides are also
 CC useful therapeutically and for immunisation as above
 CC
 XX Sequence 10 AA;
 SQ
 Query Match 39.6%; Score 38; DB 2; Length 10;
 Best Local Similarity 75.0%; Pred. No. 12;
 Matches 6; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 1 DAREPFCY 8
 Db 3 DGEFNGY 10
 RESULT 4
 ID ADW43819 standard; peptide; 19 AA.
 AC
 XX ADW43819;
 XX
 DT 24-MAR-2005 (first entry)
 XX
 DE Mouse chemerin peptide SEQ ID NO 43.
 XX
 KW gene therapy; diagnosis; cell signaling; gene therapy;
 KW lymphoproliferative disease; dermatological disease; dermatological;

KW hemostatic; inflammation; antiinflammatory; hematological disease;
 KW immune disorder; neoplasm; cardiovascular-gen.; can-gen.;
 KW neurological disease; hyperproliferative disorders; cytostatic; chemerin.
 XX
 OS Mus musculus.
 XX MO200500875-A2.
 PN 06-JAN-2005.
 PD 25-JUN-2004; 2004WO-EP006945.
 PF 25-JUN-2003; 2003US-00603566.
 PR 25-JUN-2003; 2003US-00603566.
 XX (EURO-) EUROSCREEN SA.
 PA
 PI Wltamer V, Communi D, Dethaux M, Parmentier M, Loison C;
 PI Ooms FDR;
 XX WPI; 2005-058121/06.
 DR
 XX
 PT New Chemerin polypeptides, useful for diagnosing and treating a disease,
 PT e.g. neoplasms, hypergammaglobulinemia, paraproteinemias, purpura,
 PT sarcoidosis, Sezary Syndrome, Waldenstrom's Macroglobulinemia, Gaucher's
 PT Disease, or histiocytosis.
 XX
 XX Example 2; SEQ ID NO 43; 183pp; English.
 PS
 XX The invention describes a polypeptide (I) of up to 50 amino acids where
 CC the polypeptide binds specifically to a chemerin polypeptide. Also
 CC described are: a nucleic acid sequence encoding (I); an expression vector
 CC comprising the coding sequence of the nucleic acid; a transgenic animal
 CC transduced with the expression vector; a (therapeutic) composition
 CC comprising (I) and an isolated Chemerin polypeptide or a nucleic acid
 CC sequence of (I); an antibody that selectively binds to (I); identifying
 CC an agent that modulates the interaction between a Chemerin polypeptide
 CC and a Chemerin polypeptide; detecting the presence, in a sample, of an
 CC agent that modulates the interaction between a Chemerin polypeptide and a
 CC Chemerin polypeptide in a sample; identifying an agent that modulates
 CC the function of Chemerin polypeptide; detecting the presence, in a
 CC sample, of an agent that modulates the function of Chemerin polypeptide;
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin (polypeptide) signaling; a kit, for screening agents that
 CC modulate the signaling activity of Chemerin polypeptide or for
 CC diagnosing a disease or disorder characterized by dysregulation of
 CC Chemerin polypeptide signaling, comprising an isolated Chemerin
 CC polypeptide, (I), an isolated polynucleotide encoding (I), a cell
 CC transformed with a polynucleotide encoding (I), and its packaging
 CC materials; a non-human mammal transgenic for a Chemerin polynucleotide
 CC encoding (I); identifying an antibody inhibiting Chemerin activation;
 CC and an in vitro method of inhibiting cell proliferation. The
 CC (therapeutic) composition or expression vector is useful for preparing a
 CC medicament for ex vivo gene therapy or for in vivo gene therapy or a
 CC medicament for inhibiting cell proliferation, where the medicament is
 CC used for treating a disease, e.g. neoplasms, hypergammaglobulinemia,
 CC lymphoproliferative diseases, disorders, and/or conditions,
 CC paraproteinemias, purpura, sarcoidosis, Sezary Syndrome, Waldenstrom's
 CC Macroglobulinemia, Gaucher's Disease, histiocytosis, and any other
 CC hyperproliferative disease. The polypeptides and polynucleotides and
 CC methods are useful for diagnosing and treating the cited diseases. This
 CC is the amino acid sequence of a mouse chemerin peptide used to analyse
 CC processing of immature chemerin.
 CC
 XX Sequence 19 AA;
 SQ
 Query Match 37.0%; Score 35.5; DB 9; Length 19;
 Best Local Similarity 46.7%; Pred. No. 69;
 Matches 7; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
 QY 4 EPHGYLTAAVSPGK 18
 : | | | | |
 : | | | | |
 : | | | | |
 : | | | | |
 Db 6 DPHGYLT-----PGQ 15

RESULT 5
ABJ14737
ID ABJ14737 standard; peptide; 15 AA.
XX
AC ABJ14737;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3363.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 208; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLITRAVSPGK 18
|:|:|:|:|
Db 1 GHILINGTNP GK 12
XX
RESULT 6
ABJ14493
ID ABJ14493 standard; peptide; 15 AA.
XX
AC ABJ14493;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3119.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PT

XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 203; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLITRAVSPGK 18
|:|:|:|:|
Db 2 GHILINGTNP GK 13
XX
RESULT 7
ABJ14856
ID ABJ14856 standard; peptide; 15 AA.
XX
AC ABJ14856;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3482.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX
DR WPI; 2002-713510/77.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
SQ

XX PS Disclosure; Page 211; 274pp; English.
XX CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
SQ Sequence 15 AA;
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTTAAVSPGK 18
|:|:|:|:|
Db 2 GHILNSGTNPGK 13
RESULT 8
ABJ14620
ID ABJ14620 standard; peptide; 15 AA.
AC ABJ14620;
XX 10-DEC-2002 (first entry)
XX DE Human 125P5C8 epitope #3246.
XX KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
XX KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX OS Homo sapiens.
XX PN WO200272785-A2.
XX PD 19-SEP-2002.
XX PS 13-MAR-2002; 2002MO-US007855.
XX PR 14-MAR-2001; 2001US-00809638.
XX PA (AGEN-) AGENSYS INC.
XX PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
XX PI Morrison RK, Morrison K, Jakobovits A, Jakobovits A;
XX DR WPI; 2002-713510/77.
XX PT New composition comprising a substance that modulates the status of
XX PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
XX PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX PS Disclosure; Page 206; 274pp; English.
XX CC The present invention relates to compositions comprising a substance that
XX CC modulates the status of 125P5C8 or a molecule that is modulated by
XX CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
XX CC composition is useful for treating cancer, particularly prostate,
XX CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
XX CC and/or a nucleotide sequence encoding the protein is useful for
XX CC immunising a mammal against cancer. The present sequence is a 125P5C8
XX CC epitope shown in the exemplification of the invention
SQ Sequence 15 AA;
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18
|:|:|:|:|
Db 1 GHILNSGTNPGK 12
RESULT 9
ABJ14316
ID ABJ14316 standard; peptide; 15 AA.
XX ABJ14316;
XX AC 10-DEC-2002 (first entry)
XX DE Human 125P5C8 epitope #2942.
XX KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
XX KM bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX OS Homo sapiens.
XX PN WO200272785-A2.
XX PD 19-SEP-2002.
XX PS 13-MAR-2002; 2002MO-US007855.
XX PR 14-MAR-2001; 2001US-00809638.
XX PA (AGEN-) AGENSYS INC.
XX PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
XX PI Morrison RK, Morrison K, Jakobovits A, Jakobovits A;
XX DR WPI; 2002-713510/77.
XX PT New composition comprising a substance that modulates the status of
XX PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
XX PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX PS Disclosure; Page 199; 274pp; English.
XX CC The present invention relates to compositions comprising a substance that
XX CC modulates the status of 125P5C8 or a molecule that is modulated by
XX CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
XX CC composition is useful for treating cancer, particularly prostate,
XX CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
XX CC and/or a nucleotide sequence encoding the protein is useful for
XX CC immunising a mammal against cancer. The present sequence is a 125P5C8
XX CC epitope shown in the exemplification of the invention
SQ Sequence 15 AA;
Query Match 35.4%; Score 34; DB 5; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTTAAVSPGK 18
|:|:|:|:|
Db 3 GHILNSGTNPGK 14
RESULT 10
ABJ14777
ID ABJ14777 standard; peptide; 15 AA.
XX ABJ14777;
XX AC 10-DEC-2002 (first entry)
XX DE Human 125P5C8 epitope #3403.
XX KM Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;

XX	bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX	
OS	Homo sapiens.
XX	
PN	WO200272785-A2.
XX	
PD	19-SEP-2002.
XX	
PP	13-MAR-2002; 2002WO-US007855.
XX	
PR	14-MAR-2001; 2001US-00809638.
XX	
PA	(AGEN-) AGENSYS INC.
XX	
PI	Faris M, Chailita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
XX	Morrison RK, Morrison K, Jakobovits A;
DR	WPI, 2002-713510/77.
XX	
PT	New composition comprising a substance that modulates the status of
XX	125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PR	treating or preventing cancer that expresses or over expresses 125P5C8.
XX	
PS	Disclosure; Page 209; 274pp; English.
XX	
CC	The present invention relates to compositions comprising a substance that
XX	modulates the status of 125P5C8 or a molecule that is modulated by
CC	125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC	composition is useful for treating cancer, particularly prostate, the
CC	bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC	and/or a nucleotide sequence encoding the protein is useful for
CC	immunising a mammal against cancer. The present sequence is a 125P5C8
CC	epitope shown in the exemplification of the invention
XX	
SO	Sequence 15 AA;
Query Match	35.4%; Score 34; DB 5; Length 15;
Best Local Similarity	41.7%; Pred. No. 95;
Matches	5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
Oy	7 GYLITRAVSPGK 18 4 GHLINSTGPNPK 15
Db	
RESULT 11	
ADL21730	
ID	ADL21730 standard; peptide; 15 AA.
XX	
AC	ADL21730;
XX	
DT	20-MAY-2004 (first entry)
XX	
DE	125P5C8 protein-related peptide #2978.
XX	
KM	125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX	
OS	Unidentified.
XX	
PN	US2003219444-A1.
XX	
PD	27-NOV-2003.
XX	
PP	13-MAR-2002; 2002US-00099460.
XX	
PR	14-MAR-2001; 2001US-00809638.
XX	
PA	(FARI/) FARIS M.
XX	(CHAL/) CHAILITA-BID P M.
PA	(HUBE/) HUBERT R S.
XX	(AFAR/) AFAR D E H.
PA	(RAIT/) RAITANO A B.
XX	(GEWM/) GE W.

```

PA      (MORR/) MORRISON R K.
PA      (MORR/) MORRISON K J M.
PA      (JAKO/) JAKOBOVITS A.
PI      Faris M, Chailita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI      Morrison RK, Morrison KJM, Jakobovits A;
XX      MPI; 2004-021932/02.
DR
XX
XX      New composition comprising a substance that modulates the status of
PT      12SP5C8 gene or a molecule that is modulated by 12SP5C8, useful for
PT      diagnosing or treating cancer.
SQ
Sequence 15 AA;
CC      The invention comprises a composition which contains a substance that can
CC      modulate the status of 12SP5C8 (12SP5C8 is a novel cancer-associated
CC      gene/protein), or a molecule that is modulated by 12SP5C8. The
CC      composition of the invention is useful for diagnosing or treating cancer.
CC      The present amino acid sequence represents a 12SP5C8-related peptide
CC      which was used in an example of the invention.
XX
XX      Example 51; Page 124; 183pp; English.
XX
XX      The invention comprises a composition which contains a substance that can
CC      modulate the status of 12SP5C8 (12SP5C8 is a novel cancer-associated
CC      gene/protein), or a molecule that is modulated by 12SP5C8. The
CC      composition of the invention is useful for diagnosing or treating cancer.
CC      The present amino acid sequence represents a 12SP5C8-related peptide
CC      which was used in an example of the invention.
XX
XX      Sequence 15 AA;
SQ
Query Match          35.4%; Score 34; DB 8; Length 15;
Best Local Similarity 41.7%; Pred. NO. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY      7 GYLTTAAVSPGK 18
        ||:::|||||
DB      2 GHLLNGTNPgk 13
RESULT 12
ADL22014
ID      ADL22014 standard; peptide; 15 AA.
XX
AC      ADL22014;
XX
DT      20-MAY-2004 (first entry)
DE      12SP5C8 protein-related peptide #3262.
XX
KM      12SP5C8; cancer-associated gene; cancer-associated protein; cancer.
OS      Unidentified.
XX
FN      US2003219444-A1.
XX
PD      27-NOV-2003.
XX
PF      13-MAR-2002; 2002US-00099460.
PR      14-MAR-2001; 2001US-00809638.
XX
XX      (FARI/) FARIS M.
XX      (CHAL/) CHAILITA-BID P M.
XX      (HUBE/) HUBERT R S.
XX      (AFAR/) AFAR D B H.
XX      (RAIT/) RAITANO A B.
XX      (GEWU/) GE W.
XX      (MORR/) MORRISON R K.
XX      (MORR/) MORRISON K J M.
XX      (JAKO/) JAKOBOVITS A.
PI      Faris M, Chailita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI      Morrison RK, Morrison KJM, Jakobovits A;
XX      MPI; 2004-021932/02.
XX
XX      New composition comprising a substance that modulates the status of
PT      12SP5C8 gene or a molecule that is modulated by 12SP5C8, useful for
PT      diagnosing or treating cancer.
```

XX Example 51, Page 128, 183pp; English.
PS
XX The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
SQ Sequence 15 AA;
Query Match 35.4%; Score 34; DB 8; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTTAAVSPGK 18
DB 4 GHILNSGTNPGK 15
RESULT 13
ADL21857
XX ADL21857 standard; peptide; 15 AA.
XX
AC ADL21857;
XX
DT 20-MAY-2004 (first entry)
XX
DE 125P5C8 protein-related peptide #3105.
XX
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
XX
PD 27-NOV-2003.
XX
PF 13-MAR-2002; 2002US-00099460.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PI (PARI/) PARIS M.
XX
PI (CHAL/) CHALLITA-BID P M.
XX
PA (HUBE/) HUBERT R S.
XX
PA (AFAR/) AFAR D B H.
XX
PA (RAIT/) RAITANO A B.
XX
PA (GEWW/) GE W.
XX
PA (MORR/) MORRISON R K.
XX
PA (MORR/) MORRISON K J M.
XX
PA (JAKO/) JAKOBOVITS A.
XX
PI Farie M, Challita-Bid PM, Hubert RS, Afar DBH, Raitano AB, Ge W,
PI Morrison RK, Morrison KM, Jakobovits A;
PI MPI, 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
PS Example 51, Page 126, 183pp; English.
XX
CC The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
SQ Sequence 15 AA;

Query Match 35.4%; Score 34; DB 8; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTTAAVSPGK 18
DB 1 GHILNSGTNPGK 12
RESULT 14
ADL21553
XX ADL21553 standard; peptide; 15 AA.
XX
AC ADL21553;
XX
DT 20-MAY-2004 (first entry)
XX
DE 125P5C8 protein-related peptide #2801.
XX
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
XX
PD 27-NOV-2003.
XX
PF 13-MAR-2002; 2002US-00099460.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PI (PARI/) PARIS M.
XX
PI (CHAL/) CHALLITA-BID P M.
XX
PA (HUBE/) HUBERT R S.
XX
PA (AFAR/) AFAR D B H.
XX
PA (RAIT/) RAITANO A B.
XX
PA (GEWW/) GE W.
XX
PA (MORR/) MORRISON R K.
XX
PA (MORR/) MORRISON K J M.
XX
PA (JAKO/) JAKOBOVITS A.
XX
PI Farie M, Challita-Bid PM, Hubert RS, Afar DBH, Raitano AB, Ge W,
PI Morrison RK, Morrison KM, Jakobovits A;
PI MPI, 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
PS Example 51, Page 123, 183pp; English.
XX
CC The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
SQ Sequence 15 AA;
Query Match 35.4%; Score 34; DB 8; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTTAAVSPGK 18
DB 3 GHILNSGTNPGK 14
RESULT 15
ADL21974
XX ADL21974 standard; peptide; 15 AA.

XX ADL21974;
AC 20-MAY-2004 (first entry)
XX
DE 125P5C8 protein-related peptide #3222.
XX
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
XX
PD 27-NOV-2003.
XX
PF 13-MAR-2002; 2002US-00099460.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (FARI/) FARIS M.
PA (CHAL/) CHALLITA-BID P M.
PA (HUBE/) HUBERT R S.
PA (AFAR/) AFAR D E H.
PA (RAIT/) RAITANO A B.
PA (GEWW/) GE W.
PA (MORR/) MORRISON R K.
PA (MORR/) MORRISON R J M.
PA (JAKO/) JAKOBOVITS A.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,
PI Morrison RK, Morrison KM, Jakobovits A;
XX
DR MPI; 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
PS Example 51; Page 127; 183pp; English.
XX
CC The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 35.4%; Score 34; DB 8; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTRAAVSPGK 18
|:|:|:|
Db 1 GHLSNGTNPGR 12
|:|:|:|
RESULT 16
ADL22093
ID ADL22093 standard; peptide; 15 AA.
XX
AC ADL22093;
XX
DT 20-MAY-2004 (first entry)
XX
DE 125P5C8 protein-related peptide #3341.
XX
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
PI

XX 27-NOV-2003.
PD
XX
PF 13-MAR-2002; 2002US-00099460.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
PA (FARI/) FARIS M.
PA (CHAL/) CHALLITA-BID P M.
PA (HUBE/) HUBERT R S.
PA (AFAR/) AFAR D E H.
PA (RAIT/) RAITANO A B.
PA (GEWW/) GE W.
PA (MORR/) MORRISON R K.
PA (MORR/) MORRISON R J M.
PA (JAKO/) JAKOBOVITS A.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,
PI Morrison RK, Morrison KM, Jakobovits A;
XX
DR MPI; 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
PS Example 51; Page 129; 183pp; English.
XX
CC The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 35.4%; Score 34; DB 8; Length 15;
Best Local Similarity 41.7%; Pred. No. 95;
Matches 5; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLTRAAVSPGK 18
|:|:|:|
Db 2 GHLSNGTNPGR 13
|:|:|:|
RESULT 17
ADO37897
ID ADO37897 standard; peptide; 6 AA.
XX
AC ADO37897;
XX
DT 29-JUL-2004 (first entry)
XX
DE Binding partner polypeptide of the invention SEQ ID NO:957.
XX
KM polypeptide-tagged collection; capture system; tagged polypeptide;
KM pharmaceutical; diagnostic.
XX
OS Synthetic.
XX
PN WO2004039962-A2.
XX
PD 13-MAY-2004.
XX
PF 30-OCT-2003; 2003WO-US034821.
XX
PR 30-OCT-2002; 2002US-042923P.
PR 30-OCT-2002; 2002US-0423018P.
XX
PA (POIN-) POINTILLISTE INC.
XX
PI Aulic-Riche D, Ackinson B, Geyzen MH;

CC describes apparatus useful for monitoring an interaction of an exogenous
 CC molecule with a capture agent, the array both in the presence and
 CC absence of candidate compounds, identifying molecules that modulate
 CC trafficking in biological particles or modulate activity, functional or
 CC structural properties of the biological particle. As such, it can be used
 CC for elucidating biological pathways and their reactions that occur either
 CC simultaneously or sequentially, disease processes, inhibitors and
 CC enhancers of a molecular system or for understanding receptor-signal
 CC recognition. In particular, it enables assaying one or more biological
 CC samples having one or more targets per sample on a single array, such
 CC that it is cost effective and specific. This peptide sequence is an
 CC exemplary 6-mer peptide epitope that provides a highly specific capture
 CC agent of the invention.

XX Sequence 6 AA;

Query Match 34.4%; Score 33; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 BPHGY 8
 |||||
 Db 1 BPHGY 5

RESULT 20
 ADS96242
 ID ADS96242 standard; peptide; 6 AA.

XX ADS96242;

XX 13-JAN-2005 (first entry)

XX Tagged polypeptide-associated peptide #736.

XX Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.

XX Synthetic.

XX US2004209282-A1.

XX 21-OCT-2004.

XX 30-OCT-2003; 2003US-00699088.

XX 30-OCT-2002; 2002US-04232923P.

XX 30-OCT-2002; 2002US-0423018P.

XX (AULT/) AULT-RICHE D.

XX (ATRI/) ATKINSON B.

XX Ault-Riche D, Atkinson B;

XX WPI, 2004-756625/74.

XX Evenly distributing tags among members of starting library by dividing
 PT starting library into sublibraries, attaching tag to members of
 PT sublibrary, mixing tagged sublibraries and splitting mixed library into
 PT array libraries.

XX Disclosure; SEQ ID NO 957; 293pp; English.

XX The invention relates to evenly distributing tags (e.g. epitopes) or
 CC nucleic acid molecules encoding polypeptide tags among members of a
 CC starting library, involving optionally adjusting the diversity of a
 CC starting library so that the diversity is within an order of magnitude of
 CC the number of molecules in the library, dividing the starting library
 CC into n sublibraries designated 1-n, where n is equal to or less than the
 CC number of unique tags (where each unique tag specifically binds to a
 CC different capture agent), attaching a tag to several members of each
 CC sublibrary to produce n tagged sublibraries containing tagged members
 CC (where each member has the same tag, and the tag is unique to each
 CC sublibrary), mixing some or all of the tagged sublibraries to produce a

CC mixed library (where the number of tagged molecules added from each
 CC sublibrary is the same), and splitting the mixed library into q arrays.
 CC libraries, where q is from 1 up to a predetermined number of arrays. Also
 CC included are a collection of tagged molecules produced by the method, a
 CC capture system comprising the tagged polypeptides and an addressable
 CC collection of capture agent (where each locus in the collection contains
 CC capture agents that specifically bind to the same tag, and the tagged
 CC molecules are specifically bound to capture agents), capturing molecules
 CC (involving contacting a capture system with molecules under conditions,
 CC where molecules bind to the capture system, and the capture system
 CC comprises several of addressed loci with an addressed collection of
 CC polypeptide-tagged molecules bound to addressed capture agents at each
 CC locus, the capture agents at each locus bind to the same polypeptide tag,
 CC the polypeptide tag to which the capture agent binds is different among
 CC the loci, each locus in capture system contains a several of different
 CC molecules, each with the same tag bound to the capture agents, and the
 CC polypeptide tags are evenly distributed among the tagged molecules such
 CC that the diversity of tagged molecules at each locus in the capture
 CC system is within one order of magnitude), sorting molecules or reducing
 CC their diversity, and reducing the diversity of a collection of molecules.
 CC The starting library encodes antibodies (or their fragments or single-
 CC chain antibody fragments (scFvs)) or is comprised of antibodies (or their
 CC fragment), where the antibodies or their fragments specifically bind to
 CC antigens. The methods are useful for evenly distributing tags among
 CC members of starting library, for identifying modulators of interactions
 CC between capture systems and molecules (which involves adding/exposing a
 CC test compound to the capture system to a condition before, during or
 CC after contacting the capture system with molecules or before, during or
 CC after contacting the capture agents with the tagged molecules, and
 CC identifying a change in an interaction of the molecules with the capture
 CC system or tagged molecules with the capture agents to identify a test
 CC compound that modulates the interaction between the molecules and the
 CC capture system or between tagged molecules and capture agents. The change
 CC is assessed by detecting a change in binding pattern or a physical or
 CC chemical change in the bound molecules or a conformational change in the
 CC bound molecules and/or tagged molecules). The present sequence is a
 CC peptide included in the sequence listing but not mentioned anywhere else
 CC in the specification.

XX Sequence 6 AA;

Query Match 34.4%; Score 33; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 BPHGY 8
 |||||
 Db 1 BPHGY 5

RESULT 21

AD245691
 ID AD245691 standard; peptide; 6 AA.

XX AD245691;

XX 14-JUL-2005 (first entry)

XX Antigenic peptide, SEQ ID NO: 9.

XX Antigen; protein purification.

XX Synthetic.

XX US2005095648-A1.

XX 05-MAY-2005.

XX 22-MAR-2004; 2004US-00806924.

XX 30-OCT-2003; 2003US-00699088.

XX 30-OCT-2003; 2003WO-US034821.

PA (GEYS/) GEYSEN M.
 XX (AULT/) AULT-RICHE D.
 PI Geyzen M, Ault-Riche D;
 XX
 DR WPI, 2005-345019/35.
 XX
 PT Collection of antigenic polypeptides useful as binding partners for use
 PT with capture agents, comprises three antigenic polypeptides that comprise
 PT unique residues and include critical residues occupying N and C terminal
 PT positions.
 XX
 PS Claim 22; SEQ ID NO 9, 196pp; English.
 XX
 CC The present invention relates to a collection (I) of antigenic
 CC polypeptides (AD245683 - AD246593), which comprises at least three
 CC antigenic polypeptides that comprise five to eight unique residues and
 CC include at least four residues, designated critical residues, chosen from
 CC Glu, Pro, Gln, Asn, Phe, His, Thr, Lys, Ieu, Asp, where the critical
 CC residues occupy the N and C terminal positions in each polypeptide, and
 CC no more than three polypeptides in the collection contain the same four
 CC critical residues. (I) is useful as binding partners for use with capture
 CC agents which recognize the highly antigenic, highly specific
 CC polypeptides.
 CC
 SQ Sequence 6 AA;
 XX
 Query Match 34.4%; Score 33; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EPHGY 8
 Db 1 EPHGY 5
 XX
 RESULT 22
 ID AEB29801 standard; peptide; 6 AA.
 XX
 AC AEB29801;
 XX
 DT 06-OCT-2005 (first entry)
 XX
 DE Therapeutic complex associated antigenic peptide SEQ ID NO 9.
 XX
 KW immunomodulatory; cytostatic; antiinflammatory; antimicrobial;
 KW neuroprotective; nootropic; ophthalmological; antirheumatic;
 KW antiarthritic; vitruclide; dermatological; immunomodulator; therapeutic;
 KW pharmaceutical; cancer; autoimmune disease; immunosuppressive; infection;
 KW neurodegenerative disease; neuroprotective; neurological disease;
 KW ophthalmological disease; ocular disease; non-hodgkin lymphoma;
 KW hematological disease; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; musculoskeletal disease; multiple sclerosis;
 KW neuroprotective; immune disorder; neurological disease; melanoma;
 KW cytostatic; neoplasm; inflammation; viral infection; vitruclide; infection;
 KW antigen.
 XX
 OS Synthetic.
 XX
 PN WO2005067980-A2.
 XX
 PD 28-UTL-2005.
 XX
 PP 10-JAN-2005; 2005WO-US000816.
 XX
 PR 12-JAN-2004; 2004US-0536184P.
 PR 29-MAR-2004; 2004US-0557591P.
 XX
 PA (POIN-) POINTILLISTE INC.
 XX
 PI Ault-Riche D, Levy R;
 XX

DR WPI, 2005-533851/54.
 XX
 CC Complex for treating e.g. cancer, comprises a targeting domain
 PT specifically binding to a subject-specific target and an effector
 PT molecule rendering the complex biologically effective.
 XX
 PS Disclosure; SEQ ID NO 9, 403pp; English.
 XX
 CC The invention describes a therapeutic complex comprising a targeting
 CC domain that specifically binds to a subject-specific target and an
 CC effector molecule that renders the resulting therapeutic complex
 CC biologically effective, where the targeting domain and effector molecule
 CC are linked by a specific interaction of a binding partner and a capture
 CC agent. Also described are: preparing (M1) (I) by contacting a targeting
 CC domain and an effector molecule to form a complex; rendering an antibody
 CC or fragment therapeutically effective; rendering a target-specific
 CC polypeptide therapeutically effective; screening test molecules to
 CC identify effectors for use in (I); and screening test molecules to
 CC identify targeting domains for use in (I). (I) is used to render an
 CC antibody or its fragment or target specific polypeptide therapeutically
 CC effective. (II) is used to treat a disease or condition, by administering
 CC (II) which comprises a therapeutic complex designed for personalized
 CC treatment. The disease is chosen from B cell-mediated disease, autoimmune
 CC disease and T cell-mediated disease, cancers, inflammatory disease,
 CC autoimmune disease, infectious disease, neurodegenerative disease and
 CC ophthalmic disease, preferably non-Hodgkin's lymphoma, rheumatoid
 CC arthritis, lupus, multiple sclerosis, melanoma, posterior intraocular
 CC inflammation, pathogen and virus infection. The targeting domain and the
 CC effector are administered as a complex, or administered sequentially,
 CC simultaneously or intermittently. The targeting domain and effector are
 CC administered separately and either one or more doses of the targeting
 CC domain is(are) administered prior to administration of a therapeutic
 CC complex also comprising the targeting domain, or one or more doses of the
 CC effector prior is(are) administered prior to administration of a
 CC therapeutic complex comprising the effector. This is the amino acid
 CC sequence of an antigenic peptide used in the creation of a therapeutic
 CC complex of the invention.
 CC
 SQ Sequence 6 AA;
 XX
 Query Match 34.4%; Score 33; DB 9; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EPHGY 8
 Db 1 EPHGY 5
 XX
 RESULT 23
 ID AAE26394 standard; peptide; 12 AA.
 XX
 AC AAE26394;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human GPR10 mutant C-terminal peptide, V266A.
 XX
 KW Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
 KW PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
 KW insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
 KW anticonvulsant; mutant; mutein.
 XX
 OS Homo sapiens.
 XX
 PN Synthetic.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 8
 FT /note= "Wild-type Val substituted with Ala; This position
 FT corresponds to position 366 of the wild-type protein"
 XX
 PN US2002037533-A1.

```
XX 28-MAR-2002.
PD 17-AUG-2001; 2001US-00932161.
XX 28-APR-2000; 2000US-00560915.
XX (CIVE/) CIVELLI O.
XX (LINS/) LIN S.
XX CIVELLI O, Lin S;
XX WPI; 2002-403931/43.
XX Screening for compounds useful for promoting wakefulness or sleep, and
PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
PT apnea, comprises administering a prolactin releasing peptide agonist or
PT antagonist.
XX Example 2; Page 23; 35pp; English.
XX The present invention relates to a method of screening for compounds for
CC promoting wakefulness or sleep in a mammal. The method involves
CC administering a prolactin releasing peptide (PrP) receptor (GPR10)
CC agonist or antagonist respectively and determining the ability of the
CC compound to promote wakefulness or sleep. The compounds identified from
CC the method are used in the therapy of epilepsy and other diseases
CC associated with absence seizures and in promoting wakefulness and sleep
CC in individuals having sleep disorders such as insomnia and narcolepsy.
CC PrP receptor agonists may be used to treat common disorders which lead
CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and
CC psychogenic hypersomnia. PrP receptor antagonists are useful for
CC promoting sleep and for treating insomnia such as adjustment sleep
CC disorder and psychophysiologic insomnia. The present sequence is human
CC GPR10 mutant C-terminal peptide
XX
SQ Sequence 12 AA;
XX
XX Query Match 34.4%; Score 33; DB 5; Length 12;
XX Best Local Similarity 60.0%; Pred. No. 1.1e+02;
XX Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
OY 5 PHGYLLTAAV 14
DB 1 PHGQNMNTASV 10
XX
RESULT 24
XX AAM97665
XX ID AAM97665 standard; peptide; 14 AA.
XX
XX AAM97665;
XX
XX 24-JAN-2002 (first entry)
XX Human peptide #940 encoded by a SNP oligonucleotide.
XX
XX Immunosuppressive; immunostimulatory; antiinflammatory; cytostatic;
XX neuroprotective; antimicrobial; gene therapy; vaccine; amylose; cancer;
XX amyloid protein; angiotensin; apoptosis related protein; cadherin;
XX cyclin; polymerase; oncogene; histone; kinase; colony stimulating factor;
XX complement related protein; cyclochrome; kinesin; cytokine; interferon;
XX interleukin; G-protein coupled receptor; thioesterase; inflammation;
XX multifactorial disease; autoimmune disease; infection;
XX nervous system disease.
XX
XX Homo sapiens.
XX
XX WO200147944-A2.
XX
XX 05-JUL-2001.
XX
XX 28-DEC-2000; 2000WO-US035498.
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XX 28-DEC-1999; 99US-0173419P.
XX 27-DEC-2000; 2000US-00173419.
XX (CURA-) CURAGEN CORP.
XX
XX Shinketsu RA, Leach M;
XX
XX WPI; 2001-465210/50.
XX Polymorphic nucleic acids encoding e.g. amylases, cyclins, polymerases,
XX oncogenes and histones, useful for diagnosing and treating, e.g. cancer,
XX autoimmune diseases and infections.
XX
XX Disclosure; Page 3873; 4143pp; English.
XX
XX The present invention relates to oligonucleotides (see AAL26793-AAL34659)
XX encoding polymorphic variants of proteins related to amylases, amyloid
XX proteins, angiotensin, apoptosis related proteins, cadherin, cyclin,
XX polymerase, oncogene, histones, kinases, colony stimulating factors,
XX complement related proteins, cyclochromes, kinesins, cytokines,
XX interferons, interleukins, G-protein coupled receptors and thioesterases.
XX The present sequence is a peptide encoded by one such oligonucleotide.
XX The oligonucleotides and the peptides encoded by them may be used in the
XX prevention, diagnosis and treatment of diseases associated with
XX inappropriate expression of the proteins listed above. Disorders that may
XX be prevented, diagnosed and/or treated include multifactorial diseases
XX with a genetic component, such as autoimmune diseases (e.g. rheumatoid
XX arthritis, multiple sclerosis, diabetes, systemic lupus erythematosus
XX and Grave's disease), inflammation, cancer (e.g. cancers of the bladder,
XX brain, breast, colon and kidney, leukaemia), diseases of the nervous
XX system and an infection of pathogenic organisms
XX
XX Sequence 14 AA;
XX
XX Query Match 34.4%; Score 33; DB 4; Length 14;
XX Best Local Similarity 71.4%; Pred. No. 1.3e+02;
XX Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 5 PHGYLLT 11
DB 5 PHGYRMT 11
XX
RESULT 25
XX ABG67141
XX ID ABG67141 standard; peptide; 17 AA.
XX
XX ABG67141;
XX
XX 24-SEP-2002 (first entry)
XX HCV peptide FRI having reactivity with human monoclonal antibodies.
XX
XX Hepatitis C virus vaccine; HCV; hypervariable region 1; HVRI;
XX envelope protein E2; antibody; helper T-lymphocyte;
XX cytotoxic T-lymphocyte; HCV infection; virucide.
XX
XX Hepatitis C virus.
XX
XX WO200245743-A2.
XX
XX 13-JUN-2002.
XX
XX 07-DEC-2001; 2001WO-GB005421.
XX
XX 09-DEC-2000; 2000GB-00030102.
XX 18-DEC-2000; 2000GB-00030789.
XX (ALLA/) ALLAIN J.
XX
XX Allain J, Li C, Piccolella B;
XX
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DR WPI, 2002-508540/54.
 XX Hepatitis C virus (HCV) vaccines able to raise antibodies, helper T
 PT lymphocytes and/or cytotoxic T lymphocytes able to bind to the
 PT hypervariable 1 region of the infecting HCV strain.
 XX
 PS Example 4, Page 27, 52pp; English.
 XX
 CC The present invention relates to a hepatitis C virus (HCV) vaccine
 CC comprising different groups of peptides each group being capable of
 CC raising, in an infected individual, an antibody able to bind to the
 CC hypervariable 1 (HVR1) region of the envelope protein E2 of the infecting
 CC HCV strain. The different groups of peptides are administered
 CC sequentially to raise antibodies, helper T-lymphocytes, and cytotoxic T-
 CC lymphocytes which are cross-reactive to the HVR1 region of the infecting
 CC HCV. The vaccines are useful for preventing and treating chronic HCV
 CC infections. ABG67139-ABG67169 represent HCV peptides having reactivity
 CC with human monoclonal antibodies
 XX
 SQ Sequence 17 AA;
 Query Match 34.4%; Score 33; DB 5; Length 17;
 Best Local Similarity 70.0%; Pred. No. 1.7e+02;
 Matches 7; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
 QY 8 YLTLAAVSPG 17
 DB 4 YGLTALUSPG 13
 RESULT 26
 AAW45412
 ID AAW45412 standard; peptide; 18 AA.
 AC AAW45412;
 DT 14-MAY-1998 (first entry)
 DE N-terminal amino acid sequence of (R)-specific acylase, large subunit.
 KM Biocatalyst; K1/1 acylase activity; acylamide; stereoselective; racemic;
 KM amine acylase; stereoisomolomer.
 XX
 OS Archaeobacter aureescens.
 OS
 PH Key Location/Qualifiers
 FT Misc-difference 4 /note= "the identity of this Arg is not certain"
 FT Misc-difference 6 /note= "the identity of this Arg is not certain"
 FT Misc-difference 9 /note= "amino acid residue unknown"
 FT
 XX
 PN WO9741214-A1.
 PD 06-NOV-1997.
 XX
 PP 14-APR-1997, 97WO-EP001866.
 XX
 PR 25-APR-1996, 96BP-00810266.
 XX
 PA (NOVS) NOVARTIS AG.
 XX
 PI Ghisalba O, Kiltelmann M, Laumen K, Walservolken P,
 DR WPI, 1997-549719/50.
 XX
 PT Bio:catalyst which exhibits amine cyclase enzymatic activity - is
 PT obtained from Rhodococcus globerulus, Rhodococcus equi or Arthrobacter
 PT aureescens.
 XX
 PS Claim 30; Page 48; 67pp; English.
 XX

CC This is the N-terminal amino acid sequence of the (R)-specific acylase of
 CC Arthrobacter aureescens Acs5b (large subunit) which acts as a biocatalyst
 CC exhibiting amine acylase enzymatic activity without added lipase or
 CC esterase activity. It is capable of stereoselectively hydrolysing a
 CC racemic acylamide which has an aliphatic acyl residue and which is not a
 CC derivative of a natural amino acid. The biocatalyst is especially used
 CC for the stereoselective hydrolysis of N-acetyl-1-phenylethylamine or N-
 CC acetyl-2-amino-1-phenyl-4-pentene, giving one enantiomer of the
 CC corresponding phenylamine and leaving the other enantiomer of the
 CC starting amide. No end uses are given for the separated enantiomers,
 CC although reference is made to the need for enantiomerically pure
 CC pharmaceutical and agrochemical drugs
 XX
 SQ Sequence 18 AA;
 Query Match 34.4%; Score 33; DB 2; Length 18;
 Best Local Similarity 41.2%; Pred. No. 1.8e+02;
 Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
 QY 2 AFEPHGVLTLAAVSPGK 18
 DB 2 AIRIRGYXDTPSVAPGS 18
 RESULT 27
 AAE26395
 ID AAE26395 standard; peptide; 12 AA.
 AC AAE26395;
 DT 13-DEC-2002 (first entry)
 DE Human GPR10 mutant C-terminal peptide, S367A.
 XX
 KM Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
 KM PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
 KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
 KM anticonvulsant; mutant; mutcin.
 XX
 OS Homo sapiens.
 OS
 OS Synthetic.
 PH Key Location/Qualifiers
 FT Misc-difference 9 /note= "Wild-type Ser substituted with Ala; This position
 FT corresponds to position 367 of the wild-type protein"
 FT
 XX
 PN US2002037533-A1.
 PD 28-MAR-2002.
 XX
 PP 17-AUG-2001, 2001US-00932161.
 XX
 PR 28-APR-2000, 2000US-00560915.
 XX
 PA (CIVE/) CIVELLI O.
 PA (LINS/) LIN S.
 XX
 PI Civelli O, Lin S;
 XX
 DR WPI, 2002-403931/43.
 XX
 PT Screening for compounds useful for promoting wakefulness or sleep, and
 PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
 PT apnea, comprises administering a prolactin releasing peptide agonist or
 PT antagonist.
 XX
 PS Example 2, Page 23; 35pp; English.
 XX
 CC The present invention relates to a method of screening for compounds for
 CC promoting wakefulness or sleep in a mammal. The method involves
 CC administering a prolactin releasing peptide (PRP) receptor (GPR10)
 CC agonist or antagonist respectively and determining the ability of the

CC compound to promote wakefulness or sleep. The compounds identified from
 CC the method are used in the therapy of epilepsy and other diseases
 CC associated with absence seizures and in promoting wakefulness and sleep
 CC in individuals having sleep disorders such as insomnia and narcolepsy.
 CC PRP receptor agonists may be used to treat common disorders which lead
 CC to sleepiness, e.g., sleep apnoea, narcolepsy, idiopathic hypersomnia and
 CC psychogenic hypersomnia. PRP receptor antagonists are useful for
 CC promoting sleep and for treating insomnia such as adjustment sleep
 CC disorder and psychophysiological insomnia. The present sequence is human
 CC GPR10 mutant C-terminal peptide

XX Sequence 12 AA;

QY Query Match 33.3%; Score 32; DB 5; Length 12;

Best Local Similarity 60.0%; Pred. No. 1.6e+02; Mismatches 0; Gaps 0;

Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Db 5 PHGYLLTAAV 14
 1 PHGONMTVAV 10

RESULT 28

AAW45125 standard; peptide; 16 AA.

AC AAW45125;

DT 28-APR-1998 (first entry)

DE Human cartilage glycoprotein 39 derived peptide #26.

KM Articular cartilage; immunosuppressive therapy; antigen; autoantigen;

KM immunological tolerance; T-cell; human cartilage glycoprotein 39;

KM HC gp-39; rheumatoid arthritis; epitope.

OS Synthetic.

OS Homo sapiens.

PN WO9740068-A1.

PD 30-OCT-1997.

PF 22-APR-1997; 97WO-EP002051.

PR 24-APR-1996; 96EP-00201106.

PA (ALKU) AKZO NOBEL NV.

PI Boehr AMH, Verheijden GFW;

PT WPI; 1997-535775/49.

PS Disclosure; Page 16; 82pp; English.

XX The present sequence represents a peptide which resembles or mimics an
 CC epitope present on human cartilage glycoprotein 39 (HC gp-39), an
 CC autoantigen in rheumatoid arthritis. The invention relates to peptides
 CC consisting of 16-55 amino acid residues comprising at least one of the
 CC following 19 sequences: LVCYVTSMS; FLCHYIYS; IISPNIS; LKTLISVG;
 CC FKSYPPPT; PDGDLML; LYSRRKQ; YDIKISQ; LDFISMT; FISTMTDP;
 CC FKGGDAS; VAVGDMRL; MLRGAPAS; LAYELCDF; LRGATVHT; YLKORLAG;
 CC LAGAVWAL; VWALDLDF; or LDLDFFQS. They can be used medicinally in antigen
 CC specific immunosuppressive therapy, particularly the treatment of T-cell
 CC mediated destruction of articular cartilage in autoimmune diseases (e.g.
 CC rheumatoid arthritis). They can also be used to detect activated
 CC autoreactive T cells in an individual. The peptides have a specific
 CC effect on the autoreactive T cells, thus leaving the other components of
 CC the immune system intact, unlike the non-specific suppressive effect of

CC immunosuppressive drugs, and do not cause toxic side effects. The
 CC peptides are predominantly recognised by autoreactive T cells from
 CC rheumatoid arthritis patients, but rarely by those from healthy donors

XX Sequence 16 AA;

QY Query Match 33.3%; Score 32; DB 2; Length 16;

Best Local Similarity 70.0%; Pred. No. 2.3e+02; Mismatches 1; Gaps 0;

Matches 7; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Db 9 LITAAVSPK 18
 2 LLSAALSAK 11

RESULT 29

AAU74686 standard; peptide; 9 AA.

AC AAU74686;

DT 09-APR-2002 (first entry)

DE Human cancer antigen ATP4/CREB-2 natural immunogenic ligand.

KM Human; cancer antigen; ATP4; CREB-2; vaccine; cytostatic;

KM immunogenic ligand; gene therapy; MHC; major histocompatibility complex;

KM adoptive immunotherapy; cancer; ovarian cancer.

OS Homo sapiens.

PN WO200192306-A2.

PD 06-DEC-2001.

PF 30-MAY-2001; 2001WO-US017454.

PR 31-MAY-2000; 2000US-0209388P.

PR 20-DEC-2000; 2000US-0257007P.

PA (GENZ) GENZYME CORP.

PI Nicolette CA;

PT WPI; 2002-097764/13.

PS Claim 6; Page 56; 68pp; English.

XX The invention relates to compounds comprising an immunogenic ligand whose
 CC sequence is based in part on residues 42-50 of human cancer antigen
 CC ATP4/CREB-2 (not defined) and the polynucleotides encoding them. Also
 CC included are an antibody that specifically recognises and binds the
 CC compound, a method for inducing an immune response in a subject by
 CC delivering the compound, a method of immunotherapy comprising
 CC administering to a subject the antibody, an immune effector cell that has
 CC been raised in vitro or in vivo in the presence and at the expense of an
 CC antigen presenting cell that presents the immunogenic compound in the
 CC context of an MHC (major histocompatibility complex) molecule and a
 CC method of adoptive immunotherapy comprising administering the immune
 CC effector cell. The compounds are useful for modulating an immune response
 CC to the synthetic and naturally occurring compounds. The compounds are
 CC especially useful in gene therapy or as components of anti-cancer
 CC vaccines. The compounds are useful for treating cancer, particularly
 CC ovarian cancer. The compounds are also useful for generating antibodies
 CC that specifically recognise and bind to these molecules. These antibodies
 CC are further useful for immunotherapy when administered to a subject. The
 CC peptides, polypeptides and polynucleotides are useful in diagnostic
 CC methods, for the detection and purification of antibodies, or as
 CC immunogens for the production of antibodies. The present sequence

CC represent a human cancer antigen ATP4/CREB-2 based immunogenic ligand of
 CC the invention. Note: Immunogenic ligands AAU74681-AAU74686 are stated to
 CC be encoded by the degenerate DNA sequences AAS20120-AAS20125 respectively
 CC but have not been cross-referenced or CDS features put in due to the
 CC degeneracy of the DNA sequences

XX
 SO Sequence 9 AA;

Query Match 32.3%; Score 31; DB 5; Length 9;
 Best Local Similarity 66.7%; Pred. No. 2e+06;
 Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 PEPHGY 8
 |||||
 Db 3 FKPHGP 8

RESULT 30

ABR82211
 ID ABR82211 standard; peptide; 9 AA.

XX
 AC ABR82211;

XX
 DT 13-OCT-2003 (first entry)

XX
 DE Human cancer antigen ATP4/CREB-2 epitope.

XX
 KM ATP4/CREB-2; neoplasia; cytosolic; cancer; antigen; human.

XX
 OS Homo sapiens.

XX
 PN WO2003050307-A1.

XX
 PD 19-JUN-2003.

XX
 PF 05-DEC-2001; 2001WO-US048123.

XX
 PR 05-DEC-2001; 2001WO-US048123.

XX
 PA (GENZ) GENZYME CORP.

XX
 PI Nicotinic CA;

XX
 DR WPI, 2003-532922/50.

XX
 DR N-PSDB; ACCB5028.

XX
 PT Aiding in the diagnosis of a neoplastic condition or susceptibility to a
 PT neoplastic condition of an animal cell or tissue comprises determining an
 PT amount of expression of an ATP4/CREB-2 protein in a test sample from the
 PT cell or tissue.

XX
 PS Claim 6; Page 31; 81pp; English.

XX
 CC The invention relates to aiding in the diagnosis of a neoplastic

CC condition or susceptibility to a neoplastic condition of an animal cell

CC or tissue. The method involves determining an amount of expression of an

CC ATP4/CREB-2 protein in a test sample isolated from the cell or tissue,

CC and diagnosing a neoplastic condition or susceptibility to the neoplastic

CC condition based on the amount of expression of the ATP4/CREB-2 protein.

CC The method and kit are useful in detecting, diagnosing, prognosing, and

CC treating and monitoring the progress of ATP4/CREB-2-related cancers and

CC malignancies. The method may also be used in screening agonists and

CC antagonists of cancer antigens associated with ATP4/CREB-2-related

CC cancers and malignancies. The present sequence represents a human cancer

XX
 XX Sequence 9 AA;

Db |||||
 3 FKPHGP 8

RESULT 31

AAV13274
 ID AAV13274 standard; peptide; 15 AA.

XX
 AC AAV13274;

XX
 DT 21-JUN-1999 (first entry)

XX
 DE Naturally occurring variant of the glutenin epitope Y13221.

XX
 KW Gluten; variant; gliadin; glutenin; gluten-sensitive T-cell; vaccine;

XX
 KM gluten tolerance; gluten-sensitivity; celiac disease; CD; celiac sprue;

XX
 OS Synthetic.

XX
 PN EP905518-A1.

XX
 PD 31-MAR-1999.

XX
 PF 23-SEP-1997; 97EP-00202909.

XX
 PR 23-SEP-1997; 97EP-00202909.

XX
 PA (ZIEK-) ACAD ZIEKENHUIS LEIDEN.

XX
 PU (UYLE-) RIJDSUNTIV LEIDEN.

XX
 PI Konig F, Van De Wal Y, Drijfhout JW, Kooy-Winkeljaer EMC;

XX
 DR WPI; 1999-192792/17;

XX
 PT New antigenic peptides of gluten and methods for isolating them, useful

XX
 PT as diagnostic agents and for treatment of gluten sensitivity i.e. Celiac

XX
 PT disease (CD).

XX
 PS Disclosure; Page 28; 58pp; English.

XX
 CC Peptides AAV13220-13343 represents gluten derived peptides, and their

XX
 CC variants. The specification describes a method to find and characterize

XX
 CC peptides that are recognized by an intestinally derived gluten-sensitive

XX
 CC T-cells. The method comprises establishing and contacting at least one

XX
 CC gluten-sensitive T-cell clone with a mixture of gluten-derived peptides,

XX
 CC and fractionating the mixture to select peptides that stimulate the

XX
 CC clonal cells from bioactive fractions. Peptides AAV13220 (gliadin derived

XX
 CC peptide) and AAV13221 (glutenin derived peptide) were identified using

XX
 CC these methods, and can be used in pharmaceuticals/medicines (vaccines)

XX
 CC for inducing tolerance to gluten, or to treat gluten-sensitive (i.e.

XX
 CC celiac disease (CD) or celiac sprue, tropical sprue, childhood food

XX
 CC allergies and dermatitis herpetiformis (DH). The peptides are also useful

XX
 CC for elimination of a group of gluten-sensitive T-cells, and for

XX
 CC generating antibodies, T-cell receptors, anti-idiotypic B- or T-cells by

XX
 XX immunization of a mammal with the peptide

SO Sequence 15 AA;

Query Match 32.3%; Score 31; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 3.2e+02;
 Matches 6; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

OY 7 GYLTLTAVSPGX 18
 |||||
 Db 4 GYPTSAQPRQ 15

RESULT 32

ADK40482
 ID ADK40482 standard; peptide; 18 AA.

XX
 AC ADK40482;

XX 06-MAY-2004 (first entry)
 DT KDR & VEGF/KDR complex binding peptide of the TN12 peptide library ID133.
 XX
 DE endotheelial cell; vascular endothelial growth factor; VEGF;
 XX receptor tyrosine kinase; VEGF-2; kinase domain region; KDR;
 KM foetal liver kinase-1; flk-1; VEGF/KDR complex; angiogenesis;
 KM neoplastic tumour; radiotherapeutic; malaria; HIV; SIV infection;
 KM simian haemorrhagic fever virus;
 KM enterohaemorrhagic Escherichia coli infection; protozoacidal; anti-HIV;
 KM virucidal; antibacterial; cytostatic.
 XX
 OS Synthetic.
 XX
 PN WO2003074005-A2.
 XX
 PD 12-SEP-2003.
 XX
 PP 03-MAR-2003; 2003WO-US006731.
 XX
 PR 01-MAR-2002; 2002US-0360851P.
 XX
 PR 15-JAN-2003; 2003US-0440411P.
 XX
 PA (DYAX-) DYAX CORP.
 XX (BRAC) BRACCO INT BV.
 XX
 PI Sato AK, Sexton DJ, Ladhner RC, Dransfield DT, Swenson RE;
 PI Martineili ER, Ramalingam K, Nunn AD, Von Wronski MA, Shrivastava A;
 PI Pochon S, Bussat P, Arbogast C, Pillai R, Fan H, Linder KE, Song B;
 PI Nanjappan P;
 XX
 DR WPI; 2003-779009/73.
 PT New polypeptide that binds to vascular endothelial growth factor receptor
 PT -2, useful for diagnosis and treatment of e.g. tumors, and its conjugates
 PT with therapeutic or imaging agents.
 XX
 PS Claim 79; SEQ ID NO 133; 350pp; English.
 XX
 CC This invention relates to novel peptides useful for detecting and
 CC targeting primary receptors on endothelial cells that bind vascular
 CC endothelial growth factor (VEGF). Specifically, it refers to detecting
 CC the receptor tyrosine kinase identified as VEGF-2, which is also known as
 CC kinase domain region (KDR) and foetal liver kinase-1 (flk-1). The present
 CC invention describes the involvement of the VEGF/KDR complex as important
 CC in angiogenesis, and that VEGF/KDR complex binding or KDR binding
 CC polypeptides can be used for imaging neoplastic tumours. Furthermore,
 CC these compositions are useful for targeting radiotherapeutics to specific
 CC sites for treating diseases associated with KDR activation, which include
 CC malaria, HIV, SIV infection, simian haemorrhagic fever virus and
 CC enterohaemorrhagic Escherichia coli infection. Accordingly, these
 CC compositions exhibit various activities including protozoacidal, anti-
 CC HIV, virucidal, antibacterial and cytostatic. This peptide sequence is a
 CC high affinity binding peptide of KDR and the VEGF/KDR complex, part of
 CC the TN12 peptide library of the invention.
 XX
 SQ Sequence 18 AA;
 QY
 Db 3 FEBHYLLT 11
 :|:|:|
 6 YEDHTYMLT 14
 RESULT 33
 ADR40700
 ID ADR40700 standard; peptide; 18 AA.
 XX
 AC ADR40700;

XX 21-OCT-2004 (first entry)
 DT Cyclic KDR/ VEGF binding peptide of the secondary TN12 library Seq 133.
 XX
 DE kinase domain region; KDR; vascular endothelial growth factor; VEGF;
 XX VEGF receptor 2; VEGFR2; foetal liver kinase 1; flk-1; angiogenesis;
 KM neoplastic tumour; malaria; HIV infection; SIV infection;
 KM simian haemorrhagic fever virus infection;
 KM enterohaemorrhagic Escherichia coli infection; cytostatic;
 KM antiangiogenic; antimarial; anti-HIV; virucidal; antibacterial;
 KM TN12 library; cyclic.
 XX
 OS Synthetic.
 XX
 PN Key Location/Qualifiers
 FT Disulfide-bond 4..15
 XX
 PN WO2004065621-A1.
 XX
 PD 05-AUG-2004.
 XX
 PP 11-SEP-2003; 2003WO-US028787.
 XX
 PR 15-JAN-2003; 2003US-0440411P.
 XX
 PR 03-MAR-2003; 2003US-00382082.
 XX
 PR 03-MAR-2003; 2003WO-US006731.
 XX
 PA (DYAX-) DYAX CORP.
 XX (BRAC) BRACCO INT BV.
 XX
 PI Sato AK, Sexton DJ, Dransfield DT, Ladhner RC, Arbogast C;
 PI Bussat P, Fan H, Kurnara S, Linder KE, Martineili ER, Nanjappan P;
 PI Nunn A, Pillai R, Pochon S, Ramalingam K, Shrivastava A, Song B;
 PI Swenson RE, Von Wronski MA;
 XX
 DR WPI; 2004-580734/56.
 PT Novel isolated polypeptide having ability to bind to kinase domain region
 PT or vascular endothelial growth factor/kinase domain region complex,
 PT useful in inhibiting vascular endothelial growth factor activation of
 PT kinase domain region.
 XX
 PS Claim 11; SEQ ID NO 133; 470pp; English.
 XX
 CC This invention relates to novel isolated peptides that can bind to a
 CC kinase domain region (KDR) or vascular endothelial growth factor
 CC (VEGF)/KDR complex. Specifically, it refers to polypeptides, peptide
 CC dimers and multimeric complexes that bind with high affinity to KDR (also
 CC known as the VEGF receptor 2 (VEGFR2) and foetal liver kinase 1 (flk-1))
 CC or the VEGF/KDR complex, and as such due to the involvement of VEGF and
 CC KDR in angiogenesis these binding peptides can be used for imaging
 CC important sites of angiogenesis, as well as in targeting therapeutics to
 CC such sites. The present invention describes these peptides as useful for
 CC promoting or inhibiting angiogenesis and pathogenic conditions associated
 CC thereof such as neoplastic tumours. Furthermore, these binding peptides
 CC are useful for treating malaria, HIV infection, SIV infection, simian
 CC haemorrhagic fever virus infection and enterohaemorrhagic Escherichia
 CC coli infection. Accordingly, they exhibit cytostatic, antiangiogenic,
 CC antimarial, anti-HIV, virucidal and antibacterial activities. In
 CC particular, they inhibit VEGF activation of its receptor (i.e. KDR), and
 CC enable efficient detection, imaging and localisation of activated
 CC endothelial cells exhibiting upregulated KDR expression. This peptide
 CC sequence is a high affinity KDR and VEGF/KDR cyclic binding peptide
 CC belonging to the secondary TN12 library of the invention.
 XX
 SQ Sequence 18 AA;
 QY
 Db 3 FEBHYLLT 11
 :|:|:|
 6 YEDHTYMLT 14
 Query Match 32.3%; Score 31; DB 8; Length 18;
 Best Local Similarity 55.6%; Pred. No. 4e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 RESULT 33
 ADR40700
 ID ADR40700 standard; peptide; 18 AA.
 XX
 AC ADR40700;

Db :|:|:|
6 YEDHTYMLT 14

RESULT 34
ADK57606

ID ADK57606 standard; peptide; 18 AA.

AC ADK57606,

DT 05-MAY-2005 (first entry)

DE HLA-DR associated peptide antigen SEQ ID NO 31.

XX major histocompatibility complex; immunogenicity; rheumatoid arthritis;
KM Antirheumatic; Antiarthritic; Vaccine; Immune disorder; Inflammation;
KW musculoskeletal disease.

XX Homo sapiens.

PN WO2005014622-A2.

PD 17-FEB-2005.

PF 30-JUL-2004; 2004WO-EP008609.

PR 07-AUG-2003; 2003EP-00017551.

PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

PI Berentse N, Buurman G, Kropshofer H, Mueller BC;

PI Spindelreher ST, Vogt A, Zolg W;

DR WPI; 2005-202334/21.

XX Novel naturally processed major histocompatibility complex (MHC) class II

PT antigenic peptides, useful as vaccine for treating or preventing

PT rheumatoid arthritis (RA) and for diagnosing RA.

PS Claim 1; SEQ ID NO 31; 192bp; English.

XX The invention relates to a major histocompatibility complex (MHC) class

CC II antigenic peptide. The peptide is a marker for erosive and/or non-

CC erosive rheumatoid arthritis. The peptide is useful as anti-rheumatoid

CC arthritis vaccine for treating rheumatoid arthritis. The peptide is also

CC useful for diagnosing rheumatoid arthritis. The present sequence

CC represents a HLA-DR associated peptide antigen.

XX Sequence 18 AA;

Query Match

Best Local Similarity 32.3%; Score 31; DB 9; Length 18;

Matches 7; Conservative 2; Mismatches 4; Indels 4; Gaps 1;

DT 12-MAR-2002 (first entry)

DE Human protective DNA sequence CNI-00742 open reading frame #15.

XX Human, protective sequence; cell death; central nervous system; stroke;

KW ischaemia; open reading frame; ORF; cerebral herniation; septic embolism;

KM cerebral oedema; meningitis; protozoal infection; malaria; CNI-00733;

XX metazoal infection; vascular disease; eye; macular degeneration; trauma;

KW diabetic retinopathy; epidural haematoma; tumour; degenerative disease;

XX nutritional condition; environmental condition; metabolic condition;

PN CNI-00736; CNI-00738; CNI-00742; CNI-00748; cancer; gene therapy.

XX Homo sapiens.

PN WO200181361-A1.

PD 01-NOV-2001.

PF 09-APR-2001; 2001WO-US011501.

PR 11-APR-2000; 2000US-00547938.

PA (COGE-) COGENT NEUROSCIENCE INC.

PI Portbury SD, Puranam K, Katz LC, Lo DC, Barney S, Thomas MB;

PI WPI; 2002-066433/09.

DR N-PSDB; AAS98509.

XX Polypeptides and polynucleotides comprising protective sequences useful

PT for preventing, delaying or rescuing a cell from death in disease,

PT condition or disorders such as Alzheimer's disease, stroke, tumours,

PT trauma.

XX Claim 17; Fig 7B; 228bp; English.

XX The invention relates to an isolated polypeptide encoded by a protective

CC sequence, which is a polynucleotide comprising sequences which, when

CC introduced into a cell either predisposed to undergo cell death or in the

CC process of undergoing cell death, prevent, delay, or rescue the cell from

CC death, relative to a corresponding cell into which exogenous nucleic

CC acids have been introduced. The sequences of the invention are useful for

CC diagnosing a protective sequence-mediated condition, disorder or disease

CC in an individual. The treatable disorders are preferably of the central

CC nervous system of humans including ischaemia-related conditions such as

CC stroke, cerebral herniation, septic embolism, cerebral oedema, infections

CC such as meningitis, protozoal infections such as malaria, metastatic

CC infections such as echinococcosis, vascular diseases such as ischaemic

CC encephalopathy, conditions involving the eye such as macular

CC degeneration, diabetic retinopathy, trauma such as epidural haematoma,

CC tumours such as primary intracranial tumours, degenerative diseases such

CC as Alzheimer's disease and nutritional, environmental and metabolic

CC conditions. Sequences AAU7325-AAU7378 represent open reading frames of

CC the human protective sequence polynucleotides

XX Sequence 20 AA;

Query Match

Best Local Similarity 32.3%; Score 31; DB 5; Length 20;

Matches 5; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

DT 30-JUN-2005 (first entry)

DE Pig 3-alpha hydroxysteroid dehydrogenase peptide, SEQ ID NO:63.

XX Affinity tag; analyte detection; protein purification; diagnosis;

KW 3-alpha hydroxysteroid dehydrogenase.

XX Sus scrofa.

PN US2005085630-A1.
XX
PD 21-APR-2005.
XX
PF 16-OCT-2003; 2003US-00687297.
XX
PR 16-OCT-2003; 2003US-00687297.
XX
PA (AMBE-) AMBERGEN INC.
XX
PI Olejnik J, Rothschild KJ;
XX
DR WPI; 2005-314004/32.
XX
DR PIR; A42912.
PT Photocleavable compound useful to detect and isolate component e.g.
PT Protein from biological sample comprises affinity moiety attached via
PT linker to photoreactive group, which in turn attached via second linker
PT to protein reactive group.
XX
XX Disclosure; SEQ ID NO 63; 86pp; English.
XX
XX The invention relates to photocleavable isotope-coded affinity tags which
CC can be used to detect and isolate target proteins and protein fragments
CC from biological samples. The photocleavable isotope-coded affinity tags
CC comprise an affinity capable of binding to a capture reagent attached via
CC a first linker to a photoreactive group, which is in turn attached via a
CC second linker labeled with one or more stable isotopes to a protein-
CC reactive group which reacts with functional groups on polypeptides. The
CC invention also relates to methods of preparing the photocleavable
CC affinity tags, and to a method of providing information about a mixture
CC of proteins. This method comprises conjugating photocleavable affinity
CC tags to the proteins, subjecting these protein conjugates to proteolysis
CC to yield affinity tagged peptides, capturing these affinity tagged
CC peptides on a solid support, and releasing the peptides by exposing the
CC photocleavable group of the tag. The method optionally further involves
CC analyzing the released peptides using mass spectrometry. The
CC photocleavable affinity tags of the invention can be used to detect and
CC isolate target components, especially polypeptides, from heterogeneous
CC mixtures such as biological samples, proteinaceous compositions, nucleic
CC acids, biomass, cell cultures, cellular extracts, vesicles or in vivo
CC sources. The target components that can be isolated include immune system
CC modulators, cytokines, agents of the hematopoietic system, proteins,
CC nucleic acid, hormones, gene products, antigens, cells, toxins, bacteria,
CC membrane vesicles, virus particles or combinations of the above. The tags
CC may be used to screen for changes in the expression or state
CC of enzymatic activity of specific proteins, or to implement a variety of
CC clinical and diagnostic analyses to detect the presence, absence,
CC deficiency or excess of a given protein or protein function in a
CC biological fluid (e.g. blood) or in cells or tissues. For example, they
CC can be used for the detection of disorders such as bacterial, viral or
CC parasitic infections, genetic disorders (e.g., enzyme overproduction or
CC deficiency), or neoplasias (e.g., tumors) in a sample from a patient.
CC Additionally, the photocleavable tags are envisaged for use in the
CC controlled release of a therapeutic agent at a selected site for the
CC treatment of the above disorders. Use of the photocleavable affinity tag
CC in protein analysis is rapid and efficient, and proteins can be isolated
CC and identified without the interference of steric hindrance and other
CC prior art problems before down-stream analysis and processing. Sequences
CC AD225576-AD225580 represent peptide sequences identified from database searches as
CC the top 5 matches for a peptide AD225581 whose mass spectrum was
CC determined in an illustration of the invention.
XX
XX Sequence 20 AA;
SQ

Query Match 32.3%; Score 31; DB 9; Length 20;
Best Local Similarity 54.5%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFEPHGVLIT 11
DB 8 DAFEPHGQFVT 18

RESULT 37
AD268008
ID AD268008 standard; peptide; 20 AA.
XX
XX AD268008;
XX
DT 14-JUL-2005 (first entry)
XX
DE Peptide fragment.
XX
KM Protein purification.
XX
OS Unidentified.
XX
PN WO2005037210-A2.
XX
PD 28-APR-2005.
XX
PF 14-OCT-2004; 2004WO-US033819.
XX
PR 16-OCT-2003; 2003US-00687297.
XX
PA (AMBE-) AMBERGEN INC.
XX
PI Olejnik J, Rothschild KJ;
XX
DR WPI; 2005-333195/34.
XX
XX New photocleavable isotope-coded tag used to detect and isolate target
PT components from complex mixtures e.g. cells.
PT
XX Disclosure; SEQ ID NO 63; 241pp; English.
XX
XX The invention relates to agents and conjugates that can be used to detect
CC and isolate target components from complex mixtures such as proteins and
CC protein fragments from biological samples from in vivo and in vitro
CC sources. The agents comprise a detectable group bound to a photoreactive
CC group. The conjugates comprise agents coupled to substrates by covalent
CC bonds which can be selectively cleaved with the administration of
CC electromagnetic radiation. Target substances labeled with detectable
CC molecules can be easily identified and separated from a heterogeneous
CC mixture of substances. Exposure of the conjugate to radiation releases
CC the target in a functional form and completely unaltered. Using
CC photocleavable molecular precursors as the conjugates, labels can be
CC incorporated into macromolecules, the nascent macromolecules isolated and
CC the label completely removed. The invention also relates to targets
CC isolated with these conjugates which may be useful as pharmaceutical
CC agents or compositions that can be administered to humans and other
CC mammals. The present sequence is of a peptide fragment that was used to
CC identify a glyceraldehyde-3-phosphate dehydrogenase peptide fragment
CC AD268005 identified by the method of the invention.
XX
XX Sequence 20 AA;
SQ

Query Match 32.3%; Score 31; DB 9; Length 20;
Best Local Similarity 54.5%; Pred. No. 4.6e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFEPHGVLIT 11
DB 8 DAFEPHGQFVT 18

RESULT 38
AAG62667
ID AAG62667 standard; peptide; 11 AA.
XX
XX AAG62667;
XX
AC 17-SBP-2001 (first entry)
XX
DT
XX

DE	Beta-sheet breaker peptide inhibitor assay related peptide #2.
XX	
KM	Beta-sheet breaker peptide; protein conformational disease; amyloid;
KM	Alzheimer's disease; PAF; Down's syndrome; amyloidosis disorder;
KM	prion disease; prion associated neurodegenerative disease.
XX	
OS	Synthetic.
XX	
PN	WO200134631-A2.
XX	
PD	17-MAY-2001.
XX	
PE	04-NOV-2000; 2000WO-US030416.
XX	
FR	05-NOV-1999; 99US-0163911P.
XX	
PA	(AXON-) AXONYX INC.
XX	
PI	Soto-Jara C;
XX	
DR	WPI; 2001-408068/43.
XX	
PT	New peptide analogues and mimetics, useful by oral administration for the
PT	treatment of Alzheimer's and prion disease by stabilization of the
PT	conformation of amyloidogenic peptide.
XX	
PS	Example; Page 28; 48pp; English.
XX	
CC	The present invention relates to beta-sheet breaker peptide analogues
CC	capable of inhibiting beta-pleated sheet formation in amyloid beta-
CC	peptide. These are obtained by modification of a beta-sheet breaker
CC	peptide. They can be used to reduce the formation of amyloid or amyloid-
CC	like deposits involving abnormal folding into beta-sheet structures or
CC	conformational change in prion Pr protein. They are thus useful in the
CC	treatment of Alzheimer's disease, PAF, Down's syndrome, other amyloidosis
CC	disorders, prion diseases such as kuru, Creutzfeldt-Jakob disease,
CC	Gerstmann-Strussler-Scheinker syndrome, prion associated human
CC	neurodegenerative diseases, scrapie, spongiform encephalopathy,
CC	transmissible mink encephalopathy and chronic wasting disease of mule
CC	deer and elk. The present sequence is a peptide described in the
CC	exemplification of the invention
XX	
SQ	Sequence 11 AA;
	Query Match 31.2%; Score 30; DB 4; Length 11;
	Best Local Similarity 63.6%; Pred. No. 3.3e+02;
	Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0.
OY	7 GYLTLTAVSPG 17
DB	1 GYLTVAAVFRG 11
	RESULT 39
ID	ABU79065
XX	ABU79065 standard; peptide; 11 AA.
XX	
AC	ABU79065;
XX	
DT	17-JUN-2003 (first entry)
XX	
DE	Amyloid formation control peptide #2.
XX	
KM	Amyloid formation; amyloid-like deposit; Alzheimer's disease;
KM	pathological beta-sheet-rich conformation; Down's syndrome;
KM	amyloidosis disorder; human prion disease; kuru; CJD;
KM	Creutzfeldt-Jakob disease; Gerstmann-Strussler-Scheinker syndrome; GSS;
KM	prion associated human neurodegenerative disease; animal prion disease;
KM	scrapie; spongiform encephalopathy; transmissible mink encephalopathy;
XX	chronic wasting disease.
XX	
OS	Synthetic.
XX	

PN	US6462171-B1.
XX	
PD	08-OCT-2002.
XX	
PF	12-DEC-1996; 96US-00766596.
XX	
PR	07-JUN-1995; 95US-00478326.
XX	
PR	10-APR-1996; 96US-00630645.
XX	
PA	(UWNY) UNIV NEW YORK STATE.
XX	
PI	Soto-Jara C, Baumann MH, Frangione B;
XX	
DR	WPI, 2003-379012/36.
XX	
PT	Novel inhibitory peptides which inhibit and structurally block abnormal
PT	folding of protein into amyloid or amyloid-like deposit and into
PT	pathological beta-sheet rich conformation, useful for treating
PT	Alzheimer's disease.
XX	
PS	Example 1; Col 53-54; 51pp; English.
XX	
CC	The invention describes an isolated inhibitory peptide (I) which
CC	interacts with a hydrophobic beta-sheet forming cluster of amino acid
CC	residues on a protein or peptide for amyloid or amyloid-like deposit
CC	formation, and inhibits or structurally blocks the abnormal folding of
CC	proteins and peptides into amyloid or amyloid-like deposits and into
CC	pathological beta-sheet-rich conformation. (I) is useful for disorders or
CC	diseases associated with abnormal protein folding into amyloid or amyloid
CC	-like deposits or into pathological beta-sheet-rich precursors of such
CC	deposits, such as Alzheimer's disease, Down's syndrome, other amyloidosis
CC	disorders, human prion diseases, such as kuru, Creutzfeldt-Jakob disease
CC	(CJD), Gerstmann-Strausler-Scheinker syndrome (GSS), prion associated
CC	human neurodegenerative diseases as well as animal prion diseases such as
CC	scrapie, spongiform encephalopathy, transmissible mink encephalopathy and
CC	chronic wasting disease of mule deer and elk. (I) is also useful for
CC	detecting and diagnosing the presence or absence of amyloid or amyloid-
CC	like deposits in vivo and its precursors. This is the amino acid sequence
CC	of peptide associated with the inhibition of amyloid or amyloid like
CC	deposits
XX	
SQ	Sequence 11 AA;
XX	
Query Match	31.2%; Score 30; DB 6; Length 11;
Best Local Similarity	63.6%; Pred. No. 3.3e+02;
Matches	7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
QY	7 GYLTTAAVSPG 17
DB	1 GYLTTAAVFRG 11
XX	
RESULT 40	
ID	ABW00199 standard; peptide; 11 AA.
XX	ABW00199;
AC	
DT	15-JAN-2004 (first entry)
XX	
DE	Control peptide #2 used in the invention.
XX	
KW	Amyloid-like fibril deposit; prion related encephalopathy; gene therapy;
XX	Alzheimer's disease.
OS	Unidentified.
XX	
PN	US2003087407-A1.
XX	
PD	08-MAY-2003.
XX	
PF	06-SEP-2002; 2002US-00235483.
XX	

PR 07-JUN-1995; 95US-00478326.
 PR 10-APR-1996; 96US-00630645.
 PR 12-DEC-1996; 96US-00766596.
 XX
 PA (UNYNY) UNIV NEW YORK STATE.
 PI Soto-Jara C, Baumann MH, Frangione B;
 XX WPI; 2003-616149/58.
 DR
 XX
 PT New inhibitory peptide, useful for preparing a composition for
 PT diagnosing, preventing or treating disorders associated with amyloid-1-like
 PT fibril deposits, e.g. Alzheimer's disease, or prion related
 PT encephalopathies.
 XX
 PS Example 1; Page 28; 52pp; English.
 XX
 CC The invention relates to inhibitory peptide comprising a portion of at
 CC least three amino acid residues and a sequence predicted not to adopt a
 CC beta-sheet structure that associates with a hydrophobic beta-sheet
 CC cluster on a protein or peptide involved in the abnormal folding into a
 CC beta-sheet structure, to structurally block the abnormal folding of the
 CC protein or peptide. The inhibitory peptide is useful for preparing a
 CC composition for preventing, treating or detecting disorders or diseases
 CC associated with amyloid-like fibril deposits e.g. Alzheimer's disease and
 CC prion related encephalopathies. The invention is also useful in gene
 CC therapy. The present sequence is a control peptide used in the invention
 CC
 SQ Sequence 11 AA;
 Query Match 31.2%; Score 30; DB 7; Length 11;
 Best Local Similarity 63.6%; Pred. No. 3.3e+02;
 Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 7 GYLTAAVSPG 17
 DB 1 GYLTAAVFRG 11
 RESULT 41
 AAE26397
 ID AAE26397 standard; peptide; 12 AA.
 XX
 AC AAE26397;
 XX
 DT 13-DEC-2002 (first entry)
 XX
 DE Human GPR10 mutant C-terminal peptide, V369A.
 XX
 KM Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
 KM P-PRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
 KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
 KM anticonvulsant; mutant; mutain.
 XX
 OS Homo sapiens.
 OS Synthetic.
 OS
 FH Key Location/Qualifiers
 FT Misc-difference 11 /note= "Wild-type Val substituted with Ala; this position
 FT corresponds to position 369 of the wild-type protein"
 XX
 PN US2002037533-A1.
 XX
 PD 28-MAR-2002.
 XX
 PF 17-AUG-2001; 2001US-00932161.
 XX
 PR 28-APR-2000; 2000US-00560915.
 XX
 PA (CIVE/) CIVELLI O.
 PA (LINS/) LIN S.
 XX

PI Civeilli O, Lin S;
 XX WPI; 2002-403931/43.
 DR
 XX
 PT Screening for compounds useful for promoting wakefulness or sleep, and
 PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
 PT apnea, comprises administering a prolactin releasing peptide agonist or
 PT antagonist.
 XX
 PS Example 2; Page 23; 35pp; English.
 XX
 CC The present invention relates to a method of screening for compounds for
 CC promoting wakefulness or sleep in a mammal. The method involves
 CC administering a prolactin releasing peptide (PrRP) receptor (GPR10)
 CC agonist or antagonist respectively and determining the ability of the
 CC compound to promote wakefulness or sleep. The compounds identified from
 CC the method are used in the therapy of epilepsy and other diseases
 CC associated with absence seizures and in promoting wakefulness and sleep
 CC in individuals having sleep disorders such as insomnia and narcolepsy.
 CC PrRP receptor agonists may be used to treat common disorders which lead
 CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and
 CC psychogenic hypersomnia. PrRP receptor antagonists are useful for
 CC promoting sleep and for treating insomnia such as adjustment sleep
 CC disorder and psychophysilogic insomnia. The present sequence is human
 CC GPR10 mutant C-terminal peptide
 CC
 SQ Sequence 12 AA;
 Query Match 31.2%; Score 30; DB 5; Length 12;
 Best Local Similarity 45.5%; Pred. No. 3.7e+02;
 Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 QY 5 PHGYLTAAVS 15
 DB 1 PHGQNMVSVV 11
 RESULT 42
 ADU04328
 ID ADU04328 standard; peptide; 14 AA.
 XX
 AC ADU04328;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human immunoglobulin light chain (IgVL) FRI peptide 12.
 XX
 KM viral infection; virucide; autoimmune disease;
 KM lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin;
 KM antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO2004090544-A2.
 XX
 PD 21-OCT-2004.
 XX
 PF 13-APR-2004; 2004WO-CA000544.
 XX
 PR 09-APR-2003; 2003US-0461137P.
 PR 30-SEP-2003; 2003US-0506779P.
 XX
 PA (CABL-) CANADIAN BLOOD SERVICES.
 XX
 PI Hu Y, Brown E;
 XX
 DR WPI; 2004-766498/75.
 XX
 PT Characterizing a viral infection in a host, for developing treatment for
 PT severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining
 PT homology profile of a viral-based sequence element with an endogenous
 PT host element.
 XX

PS Example 1, Fig 5A, 16pp; English.

XX The invention relates to a novel method for characterising a viral

CC infection in a host. The method comprises identifying at least one viral-

CC based sequence element in a biological sample obtained from the host,

CC determining a homology profile of the viral-based sequence element with

CC at least one endogenous host element and characterising the viral

CC infection based on the homology profile, where the homology profile is

CC indicative of a viral behaviour of the viral infection in the host. The

CC method of the invention demonstrates virucide applications and may be

CC useful for preparing a medicament for detecting and/or treating a viral

CC infection or related condition, such as an autoimmune disease e.g. type

CC I cryoglobulinemia, or lymphoproliferative disorder. The viral

CC infection may be due to HCV (Hepatitis C virus), HIV or a member of a

CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or

CC Coronaviridae virus family. Treatment of the infection may utilise

CC vaccine or gene therapy. The target compound of the invention may be

CC useful for detecting the presence of a virus in a biological sample or

CC for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)

CC and/or Human T-lymphotropic virus 1 (HTLV-I) infection. The methods are

CC further useful for developing treatment regimes to target genotype-

CC specific viral variants. The current sequence is that of a human

CC immunoglobulin light chain (IgVL) FR peptide of the invention.

CC

XX Sequence 14 AA;

SO

Query March 31.2%; Score 30; DB 8; Length 14;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;

Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LTTAASPQK 18

DB 6 LTTATSPQK 14

RESULT 43

AA04059

ID AAR04059 standard; peptide; 19 AA.

AC AAR04059;

XX

DT 17-MAR-1993 (first entry)

XX

DE Reagent of GTP-binding protein (14).

XX

KM G-protein; signal transducing protein; cell proliferation; cancer;

KW dementia; receptor; transduction.

XX

OS Synthetic.

XX

PN JP02069665-A.

XX

PD 08-MAR-1990.

XX

PF 06-SEP-1988; 88JP-00221446.

XX

PR 06-SEP-1988; 88JP-00221446.

XX

PA (NISHI/) NISHIMOTO I.

XX

DR WPI, 1990-119771/16.

XX

PT Reagent of GTP-binding protein - consists of polypeptide of less than 33

PT aminoacid residues where 4 are basic aminoacid residues, etc.

XX

PS Disclosure; Fig 1; 4pp; Japanese.

XX

CC A reagent for activating GTP-binding protein (G-protein) consists of a

CC polypeptide of less than 33 amino acids, of which more than 4 are basic,

CC and more than 20% are hydrophobic. The reagent is useful for the

CC purification, identification, functional examination, etc. of G-protein,

CC a signal transducing protein. It will be possible to study the mechanism

CC of cell proliferation, anticancer action, prevention of dementia, by

CC activating/inhibiting the G-protein, using the reagent. The peptides

CC given in AAR04048-59, AAR05848, AAR09313 and indicated in the Features

CC table bind selectively, activating the G-protein. The peptides have the

CC same config. as the part of the receptor which binds to G-protein and is

CC effective for the transmission of signal information into the cell. The

CC reagent can be used in the form of powder or soln. Affinity purification

CC can be simply carried out by using ion-exchange resin beads such as

CC Sepharose. For example, the reagent is stuck onto the beads and

CC homogenate is passed through a column packed with the beads to obtain a

CC given G-binding protein

CC

XX Sequence 19 AA;

SO

Query March 31.2%; Score 30; DB 2; Length 19;

Best Local Similarity 54.5%; Pred. No. 6.4e+02;

Matches 6; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HGVLTTAASP 16

DB 2 HGVEDAAATP 12

RESULT 44

AA29388

ID AAY29388 standard; peptide; 20 AA.

AC AAY29388;

XX

DT 01-OCT-1999 (first entry)

XX

DE Final 3D profile with myoglobin backbone structure peptide #22.

XX

KM Myoglobin; Mb; sperm whale; protein design; function; property;

KW stereo structure; globular protein; detection.

XX

OS Synthetic.

OS Physeter sp.

XX

PN JP11193297-A.

XX

PD 21-JUL-1999.

XX

PF 06-OCT-1998; 98JP-00283852.

XX

PR 06-OCT-1997; 97JP-00272431.

XX

PA (RIKA) RIKAGAKU KENKYUSHO.

XX

DR WPI, 1999-462430/39.

XX

PT Method for designing artificial protein - useful for producing proteins

PT with required functions.

XX

PS Example; Page 4; 10pp; Japanese.

XX

CC The present invention describes a method for producing an ideal amino

CC acid sequence. The method comprises: (1) preparation of one initial amino

CC acid sequence corresponding to the structure of a protein; (2) selecting

CC the amino acid residues optimal to each site; (3) repeating the steps of

CC selecting the amino acid residues optimum to each sites of the total

CC amino acid residues constituting the N-order amino acid sequence

CC integer not less than 2) to give an N+1-order amino acid sequence

CC consisting of the selected amino acid residues until the N-order amino

CC acid sequence comes to be same as the N+1-order amino acid sequence; and

CC (4) selecting the resultant N-order amino acid sequence as the optimum

CC amino acid sequence of said protein. The method can design a protein with

CC desired functions and properties. AAY29343 to AAY29367 represent peptides

CC used in an example from the present invention where the stereo structure

CC of sperm whale myoglobin was targeted as a globular protein to detect an

CC amino acid sequence best fit to the structure of the main chain of the

CC sperm whale myoglobin

XX

SO Sequence 20 AA;

Query Match 31.2%; Score 30; DB 2; Length 20;
 Best Local Similarity 80.0%; Pred. No. 6.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGYL 9
 |||||
 10 PHGYM 14

RESULT 45
 ADU04264
 ID ADU04264 standard; peptide; 20 AA.
 XX
 AC ADU04264;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Human immunoglobulin light chain (IgVL) FR1 peptide 3.
 XX
 KM viral infection; viraemia; autoimmune disease;
 KM lymphoproliferative disorder; vaccine; gene therapy; immunoglobulin,
 KM antibody.
 XX
 OS Homo sapiens.
 XX
 PN WO2004090544-A2.
 XX
 PD 21-OCT-2004.
 XX
 PF 13-APR-2004; 2004WO-CA000544.
 XX
 PR 09-APR-2003; 2003US-0461137P.
 PR 30-SEP-2003; 2003US-0506779P.
 XX
 PA (CABL-) CANADIAN BLOOD SERVICES.
 XX
 PI Hu Y, Brown E;
 XX
 DR WPI; 2004-766498/75.
 XX
 PT Characterizing a viral infection in a host, for developing treatment for
 PT severe acute respiratory syndrome-coronavirus (SARS-CoV), by determining
 PT homology profile of a viral-based sequence element with an endogenous
 PT host element.
 XX
 PS Example 1; Fig 1C; 166pp; English.
 XX
 CC The invention relates to a novel method for characterizing a viral
 CC infection in a host. The method comprises identifying at least one viral-
 CC based sequence element in a biological sample obtained from the host,
 CC determining a homology profile of the viral-based sequence element with
 CC at least one endogenous host element and characterizing the viral
 CC infection based on the homology profile, where the homology profile is
 CC indicative of a viral behaviour of the viral infection in the host. The
 CC method of the invention demonstrates viraemia applications and may be
 CC useful for preparing a medicament for detecting and/or treating a viral
 CC infection or related condition, such as an autoimmune disease e.g. type
 CC II cryoglobulinaemia, or lymphoproliferative disorder. The viral
 CC infection may be due to HCV (Hepatitis C virus), HIV or a member of a
 CC Retroviridae, Flaviviridae, Herpesviridae, Papillomaviridae or
 CC Coronaviridae virus family. Treatment of the infection may utilize
 CC vaccine or gene therapy. The target compound of the invention may be
 CC useful for detecting the presence of a virus in a biological sample or
 CC for manufacturing a medicament for treating SARS coronavirus (SARS-CoV)
 CC and/or Human T-lymphotropic virus 1 (HTLV-1) infection. The methods are
 CC further useful for developing treatment regimes to target genotype-
 CC specific viral variants. The current sequence is that of a human
 CC immunoglobulin light chain (IgVL) FR1 peptide of the invention.
 XX
 SQ Sequence 20 AA;

Query Match 31.2%; Score 30; DB 8; Length 20;

Best Local Similarity 66.7%; Pred. No. 6.8e+02;
 Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LTRAVSPGK 18
 |||||
 9 LTRATSPGQ 17

RESULT 46
 ADO37698
 ID ADO37698 standard; peptide; 6 AA.
 XX
 AC ADO37698;
 XX
 DT 29-JUL-2004 (first entry)
 XX
 DE Binding partner polypeptide of the invention SEQ ID NO: 758.
 XX
 KM polypeptide-tagged collection; capture system; tagged polypeptide;
 KM pharmaceutical; diagnostic.
 XX
 OS Synthetic.
 XX
 PN WO2004039962-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034821.
 XX
 PR 30-OCT-2002; 2002US-0422923P.
 PR 30-OCT-2002; 2002US-0423018P.
 XX
 PA (POIN-) POINTILLISTE INC.
 XX
 PI Aul-Riche D, Atkinson B, Geyssen MH;
 XX
 DR WPI; 2004-376185/35.
 XX
 PT Evenly distributing tags among members of a starting library, useful in
 PT developing pharmaceuticals and diagnostics, comprises dividing the
 PT starting library into sub libraries and attaching a tag to members of
 PT each sub library.
 XX
 PS Claim 14; SEQ ID NO 758; 510pp; English.
 XX
 CC The invention relates to novel methods for producing polypeptide-tagged
 CC collections and capture systems containing the tagged polypeptides. The
 CC method is useful for evenly distributing tags among members of a starting
 CC library. The system, collection, kits and methods are useful in
 CC developing pharmaceuticals and diagnostics. The present sequence is used
 CC in the exemplification of the invention.
 XX
 SQ Sequence 6 AA;

Query Match 30.2%; Score 29; DB 8; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
 |||||
 1 KPHGY 5

RESULT 47
 ADO28220
 ID ADO28220 standard; peptide; 6 AA.
 XX
 AC ADO28220;
 XX
 DT 12-AUG-2004 (first entry)
 XX
 DE Capture system related peptide, SEQ ID 758.
 XX

KM Capture system.
 OS Synthetic.
 PN WO2004042019-A2.
 PD 21-MAY-2004.
 PF 30-OCT-2003; 2003WO-US034693.
 PR 30-OCT-2002; 2002US-0422923P.
 PR 30-OCT-2002; 2002US-0423018P.
 PA (POIN-) POINTILLISTE INC.
 PI Ault-Riche D, Atkinson B, Jesaitis L, Kumble KD, Sperinde G;
 DR WPI; 2004-431543/40.
 XX
 PT Capturing biological particles, by contacting biological particles with
 PT capture system comprising addressed loci, addressed collection of
 PT polypeptide tagged molecules, capture agents, and polypeptide tag to
 PT which capture agent binds.
 PS Disclosure; SEQ ID NO 758; 505bp; English.
 XX
 CC The present invention relates to a method for the capture and analysis of
 CC biological particles using a capture system. The method is useful for
 CC capturing biological particles such as cells, portions of cells, cell
 CC membranes, viruses, viral capsids, viral particles, bacterial cells,
 CC eukaryotic cells, intracellular particles and nuclei, cell membranes, cell
 CC membrane fragments, nuclear membranes, nuclear membrane fragments, viral
 CC vectors or viral capsids with or without packaged nucleic acid, phage,
 CC phage vectors, phage capsids with or without encapsulated nucleotide
 CC acid, liposomes and other micellar agents. The biological particles are
 CC cells chosen from immune cells, neurons, cancer cells, bacterial cells
 CC or infected cells, subcellular compartment, organelles, viral particles
 CC or pathogens. The cells are dendritic cells, T cells, or B cells. The
 CC method is also useful for identifying molecules that interact with
 CC infectious agents, for profiling the surface of a biological particles,
 CC for identifying a modulator of an interaction among proteins in the
 CC biological particle, for identifying molecules that modulates the
 CC trafficking, activity or functional or structural property in the
 CC biological particle, and for mapping epitopes of molecules displayed on
 CC the surface of a biological particles. The method is also useful for
 CC sorting biological particles, for identifying a receptor on the surface
 CC of biological particle that transduces a signal from a polypeptide, and
 CC for identifying the molecule that interacts with an apically-localized
 CC molecule on a biological particle. The present sequence was used to
 CC illustrate the invention.
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 30.2%; Score 29; DB 8; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EPHGY 8
 :||||
 Db 1 KPHGY 5
 RESULT 48
 ADS96043 ID ADS96043 standard; peptide; 6 AA.
 AC ADS96043;
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE 6-mer peptide epitope works as a highly specific capture agent Seq 758.
 XX

KM self-assembly array; capture agent; epitope; binding partner.
 OS Synthetic.
 PN WO2004071641-A2.
 PD 26-AUG-2004.
 PF 30-OCT-2003; 2003WO-US034747.
 PR 10-FEB-2003; 2003US-0446687P.
 PR
 PA (POIN-) POINTILLISTE INC.
 PA (AULT/) AULT-RICHE D.
 PA (KOMB/) KUMBLE K D.
 PA (SCHU/) SCHULZ R.
 PA (SCHU/) SCHULZ K.
 XX
 PI Ault-Riche D, Kumble KD, Schulz R, Schulz K;
 DR WPI; 2004-635071/61.
 XX
 PT Self-assembled array for monitoring interaction of molecules, comprising
 PT addressable array of capture agents having predetermined binding partners
 PT and conjugates comprising biological particle and/or molecule linked to
 PT binding partners.
 PS Disclosure; SEQ ID NO 758; 443bp; English.
 XX
 CC This invention relates to novel self-assembly arrays that each comprises
 CC an addressable collection of capture agents that have predetermined
 CC binding partners, as well as reagents for the covalent conjugation of the
 CC binding partners to molecules for display in the array. Specifically, it
 CC refers to the production of a flexible experimental surface, which can be
 CC adapted for use with almost any analytical system. The present invention
 CC describes apparatus useful for monitoring an interaction of an exogenous
 CC molecule with a capture agent of the array both in the presence and
 CC absence of candidate compounds, identifying molecules that modulate
 CC trafficking in biological particles or modulate activity, functional or
 CC structural properties of the biological particle. As such, it can be used
 CC for elucidating biological pathways and their reactions that occur either
 CC simultaneously or sequentially, disease processes, inhibitors and
 CC enhancers of a molecular system or for understanding receptor-signal
 CC recognition. In particular, it enables assaying one or more biological
 CC samples having one or more targets per sample on a single array, such
 CC that it is cost effective and specific. This peptide sequence is an
 CC exemplary 6-mer peptide epitope that provides a highly specific capture
 CC agent of the invention.
 XX
 SQ Sequence 6 AA;
 XX
 Query Match 30.2%; Score 29; DB 8; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06; 0; Indels 0; Gaps 0;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 EPHGY 8
 :||||
 Db 1 KPHGY 5
 RESULT 49
 ADS96043 ID ADS96043 standard; peptide; 6 AA.
 AC ADS96043;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Tagged polypeptide-associated peptide #544.
 XX
 KM Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.
 OS Synthetic.
 XX

US2004209282-A1.

21-OCT-2004.

30-OCT-2003; 2003US-00699088.

30-OCT-2002; 2002US-0422923P.

30-OCT-2002; 2002US-0423018P.

(AULT/) AULT-RICHE D.

(ATKI/) ATKINSON B.

Ault-Riche D, Atkinson B;

WPI; 2004-756825/74.

Evenly distributing tags among members of starting library by dividing starting library into sublibraries, attaching tag to members of sublibrary, mixing tagged sublibraries and splitting mixed library into array libraries.

Disclosure; SEQ ID NO 758; 293pp; English.

The invention relates to evenly distributing tags (e.g. epitopes) or nucleic acid molecules encoding polypeptide tags among members of a starting library, involving optionally adjusting the diversity of a starting library so that the diversity is within an order of magnitude of the number of molecules in the library, dividing the starting library into n sublibraries designated 1-n, where n is equal to or less than the number of capture tags (where each unique tag specifically binds to a different capture agent), attaching a tag to several members of each sublibrary to produce n tagged sublibraries containing tagged members (where each member has the same tag, and the tag is unique to each sublibrary), mixing some or all of the tagged sublibraries to produce a mixed library (where the number of tagged molecules added from each sublibrary is the same), and splitting the mixed library into q array libraries, where q is from 1 up to a predetermined number of arrays. Also included are a collection of tagged molecules produced by the method, a capture system comprising the tagged polypeptides and an addressable collection of capture agent (where each locus in the collection contains capture agents that specifically bind to the same tag, and the tagged molecules are specifically bound to capture agents), capturing molecules (involving contacting a capture system with molecules under conditions, where molecules bind to the capture system, and the capture system comprises several of addressed loci with an addressed collection of polypeptide-tagged molecules bound to addressed capture agents at each locus, the capture agents at each locus bind to the same polypeptide tag, the polypeptide tag to which the capture agent binds is different among the loci, each locus in capture system contains a several of different molecules, each with the same tag bound to the capture agents, and the polypeptide tags are evenly distributed among the tagged molecules such that the diversity of tagged molecules at each locus in the capture system is within one order of magnitude), sorting molecules or reducing their diversity, and reducing the diversity of a collection of molecules.

The starting library encodes antibodies (or their fragments or single-chain antibody fragments (SCFvs)) or is comprised of antibodies (or their fragment), where the antibodies or their fragments specifically bind to antigens. The methods are useful for evenly distributing tags among members of starting library, for identifying modulators of interactions between capture systems and molecules (which involves adding/exposing a test compound to the capture system to a condition before, during or after contacting the capture system with molecules or before, during or after contacting the capture agents with the tagged molecules, and identifying a change in an interaction of the molecules with the capture system or tagged molecules with the capture agents to identify a test compound that modulates the interaction between the molecules and the capture system or between tagged molecules and capture agents. The change is assessed by detecting a change in binding pattern or a physical or chemical change in the bound molecules or a conformational change in the bound molecules and/or tagged molecules). The present sequence is a peptide included in the sequence listing but not mentioned anywhere else in the specification.

```
XX      SQ      Sequence 6 AA;
Query Match          30.2%; Score 29; DB 8; Length 6;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches         4; Conservative    1; Mismatches     0; Indels       0; Gaps        0;

QY              4 EPHGY 8
                :| | | |
Db               1 KPHGY 5

RESULT 50
ADZ46403
ID      ADZ46403 standard; peptide; 6 AA.
XX
AC      ADZ46403;
XX
DT      14-JUL-2005 (first entry)
XX
DE      Antigenic peptide, SEQ ID NO: 721.
XX
KW      Antigen; protein purification.
OS      Synthetic.
XX
PN      US2005095648-A1.
XX
PD      05-MAY-2005.
PF      22-MAR-2004; 2004US-00806924.
PR      30-OCT-2003; 2003US-00699088.
PP      30-OCT-2003; 2003WO-US034821.
XX
PA      (GEYS/) GEYSEN M.
PI      (AULT/) AULT-RICHE D.
PX      Geysen M, Ault-Riche D;
DR      WPI, 2005-345019/35.
XX
PT      Collection of antigenic polypeptides useful as binding partners for use
PR      with capture agents, comprises three antigenic polypeptides that comprise
PP      unique residues and include critical residues occupying N and C terminal
PT      positions.
XX
PS      Claim 22, SEQ ID NO 721; 196pp; English.
XX
CC      The present invention relates to a collection (I) of antigenic
CC      polypeptides (ADZ45683 - ADZ46593), which comprises at least three
CC      antigenic polypeptides that comprise five to eight unique residues and
CC      include at least four residues, designated critical residues, chosen from
CC      Glu, Pro, Gln, Asn, Phe, His, Thr, Lys, Leu, Asp, where the critical
CC      residues occupy the N and C terminal positions in each polypeptide, and
CC      no more than three polypeptides in the collection contain the same four
CC      critical residues. (II) is useful as binding partners for use with capture
CC      agents which recognize the highly antigenic, highly specific
CC      polypeptides.
CX      XX
SQ      Sequence 6 AA;

Query Match          30.2%; Score 29; DB 9; Length 6;
Best Local Similarity 80.0%; Pred. No. 2e+06;
Matches         4; Conservative    1; Mismatches     0; Indels       0; Gaps        0;

QY              4 EPHGY 8
                :| | | |
Db               1 KPHGY 5
```

ID ABB30513 standard; peptide; 6 AA.
 AC ABB30513;
 DT 06-OCT-2005 (first entry)
 XX
 DE Therapeutic complex associated antigenic peptide SEQ ID NO 721.
 KW immunomodulatory; cytostatic; antiinflammatory; antimicrobial;
 KW neuroprotective; nootropic; ophthalmological; antirheumatic;
 KW antiarthritic; virocidic; dermatological; immunomodulatory; therapeutic;
 KW pharmacocuticular; cancer; autoimmune disease; immunosuppressive; infection;
 KW neurodegenerative disease; neuroprotective; neurological disease;
 KW ophthalmological; ocular disease; non-hodgkin lymphoma;
 KW hematological disease; rheumatoid arthritis; antiarthritic;
 KW antirheumatic; musculoskeletal disease; multiple sclerosis;
 KW neuroprotective; immune disorder; neurological disease; melanoma;
 KW cytostatic; neoplasm; inflammation; viral infection; virocidic; infection;
 KW antigen.
 XX
 OS Synthetic.
 PN WO2005067980-A2.
 PD 28-JUL-2005.
 XX
 PF 10-JAN-2005; 2005WO-US000816.
 XX
 PR 12-JAN-2004; 2004US-0536184P.
 PR 23-MAR-2004; 2004US-0557591P.
 XX
 XX (POIN-) POINTILLISTE INC.
 PA Ault-Riche D, Levy R;
 PI WPI; 2005-533851/54.
 DR
 XX
 PT Complex for treating e.g. cancer, comprises a targeting domain
 PT specifically binding to a subject-specific target and an effector
 PT molecule rendering the complex biologically effective.
 PS Disclosure; SEQ ID NO 721; 403pp; English.
 XX
 CC The invention describes a therapeutic complex comprising a targeting
 CC domain that specifically binds to a subject-specific target and an
 CC effector molecule that renders the resulting therapeutic complex
 CC biologically effective, where the targeting domain and effector molecule
 CC are linked by a specific interaction of a binding partner and a capture
 CC agent. Also described are: preparing (M1) (I) by contacting a targeting
 CC domain and an effector molecule to form a complex; rendering an antibody
 CC or fragment therapeutically effective; rendering a target-specific
 CC polypeptide therapeutically effective; screening test molecules to
 CC identify effectors for use in (I); and screening test molecules to
 CC identify targeting domains for use in (I). (I) is used to render an
 CC antibody or its fragment or target specific polypeptide therapeutically
 CC effective. (II) is used to treat a disease or condition, by administering
 CC (II) which comprises a therapeutic complex designed for personalized
 CC treatment. The disease is chosen from B cell-mediated disease, autoimmune
 CC disease and T cell-mediated disease, cancers, inflammatory disease,
 CC autoimmune disease, infectious disease, neurodegenerative disease and
 CC ophthalmic disease, preferably non-Hodgkin's lymphoma, rheumatoid
 CC arthritis, lupus, multiple sclerosis, melanoma, posterior intraocular
 CC inflammation, pathogen and virus infection. The targeting domain and the
 CC effector are administered as a complex, or administered sequentially,
 CC simultaneously or intermittently. The targeting domain and effector are
 CC administered separately and either one or more doses of the targeting
 CC domain is(are) administered prior to administration of a therapeutic
 CC complex also comprising the targeting domain, or one or more doses of the
 CC effector prior is(are) administered prior to administration of a
 CC therapeutic complex comprising the effector. This is the amino acid
 CC sequence of an antigenic peptide used in the creation of a therapeutic
 CC complex of the invention.

SO Sequence 6 AA;
 Query Match 30.2%; Score 29; DB 9; Length 6;
 Best Local Similarity 80.0%; Pred. No. 2e+06;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 QY 4 BPHGY 8
 DB 1 KPHGY 5
 XX
 DE Therapeutic complex associated antigenic peptide; 11 AA.
 AC AAG80180;
 DT 21-JAN-2002 (first entry)
 XX
 DE HER-2 mimotope SEQ ID 5.
 KW Mimotope; HER-2; vaccine; cancer; antibody; tumor cell; cytostatic;
 KW adenocarcinoma; gastrointestinal tract; prostate; breast;
 KW multiple myeloma; B-lymphoproliferative post-transplant syndrome;
 KW B-cell malignoma; chronic lymphatic leukemia.
 XX
 OS Unidentified.
 PN WO200178766-A1.
 PD 25-OCT-2001.
 XX
 PF 12-APR-2001; 2001WO-EP004251.
 XX
 PR 13-APR-2000; 2000DE-01018403.
 PR 23-AUG-2000; 2000DE-01041342.
 XX
 XX (BIOL-) BIO LIFE SCI FORSCHUNGS & ENTWICKLUNGSGR.
 PA Zielinski C, Scheiner O, Jensen-Jarolim B, Breiteneder H;
 PI WPI; 2002-017563/02.
 DR
 XX
 PT Preparing vaccine against cancer, useful for treatment or prevention,
 PT comprising coupling antibody mimetopes, selected from a phage-display
 PT library, to macromolecular carrier.
 PS Example 2B; Page 27; 36pp; German.
 XX
 CC This invention describes a novel method for preparing a vaccine (A)
 CC against cancer, comprising conjugating one or more mimetopes of an
 CC antibody (Ab) to a macromolecular carrier (I). The mimetopes are selected
 CC from a phage-display library using one or more autogenous or synthetic
 CC antibodies that are directed against one or more Ag expressed
 CC specifically on tumor cells. The products of the invention have
 CC cytostatic activity. (A) is used to prevent, or treat, cancers,
 CC particularly (adeno)carcinoma of the gastrointestinal tract, prostate or
 CC breast, multiple myeloma; B-lymphoproliferative post-transplant syndrome,
 CC B-cell malignoma, and chronic lymphatic leukemia. (A) can be produced
 CC even when the nature of Ag is not known; are free of phages and
 CC endotoxins (so well suited for use in humans) and provide active
 CC immunization before tumors have developed. AAG80176-AAG80182 represent
 CC peptide mimetopes used to illustrate the method of the invention
 CC
 SO Sequence 11 AA;
 Query Match 30.2%; Score 29; DB 5; Length 11;
 Best Local Similarity 71.4%; Pred. No. 4.9e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 QY 1 DAFPHG 7
 DB 4 DPHPHG 10

```

RESULT 53
ADJ67980 standard; peptide; 11 AA.
XX
AC ADJ67980;
XX
DT 20-MAY-2004 (first entry)
XX
DE T. thermophilus holB primer peptide #4.
XX
KM DNA polymerase; DNA sequencing; DNA amplification.
XX
OS Thermus thermophilus.
XX
PN US2004038289-A1.
XX
PD 26-FEB-2004.
XX
PF 25-SEP-2003; 2003US-00671403.
XX
PR 08-APR-1997; 97US-0043202P.
PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
PI O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,
PI Kuriyan J;
XX
DR WPI; 2004-203218/19.
DR N-PSDB; ADJ67979.
XX
PT Isolated DNA molecule from Bacillus stearothermophilus encoding a delta
PT subunit of a DNA polymerase I mul-type, useful for producing DNA
PT polymerases for use in DNA sequencing and DNA amplification methods.
XX
PS Example 14; SEQ ID NO 210; 245pp; English.
XX
CC The invention relates to an isolated DNA molecule from Bacillus
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The
CC subunits are useful for producing DNA polymerases for use in DNA
CC sequencing and DNA amplification methods. The present sequence is used in
CC the exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match          30.2%; Score 29; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTYL 10
   |||||
Db 7 HGTYL 11

RESULT 54
ADJ68192 standard; peptide; 11 AA.
XX
AC ADJ68192;
XX
DT 20-MAY-2004 (first entry)
XX
DE T. thermophilus holB primer peptide #4.
XX

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```

KM DNA polymerase; DNA sequencing; DNA amplification.
XX
OS Thermus thermophilus.
XX
PN US2004038290-A1.
XX
PD 26-FEB-2004.
XX
PF 25-SEP-2003; 2003US-00671419.
XX
PR 08-APR-1997; 97US-0043202P.
PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
PI O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,
PI Kuriyan J;
XX
DR WPI; 2004-203219/19.
DR N-PSDB; ADJ68191.
XX
PT Novel DNA molecule from Thermotoga species encoding delta prime subunit
PT of DNA polymerase III-type enzyme, useful for producing the enzyme by
PT recombinant techniques.
XX
PS Example 14; SEQ ID NO 210; 245pp; English.
XX
CC The invention relates to an isolated DNA molecule from Bacillus
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The
CC subunits are useful for producing DNA polymerases for use in DNA
CC sequencing and DNA amplification methods. The present sequence is used in
CC the exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match          30.2%; Score 29; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTYL 10
   |||||
Db 7 HGTYL 11

RESULT 55
ADK01270 standard; peptide; 11 AA.
XX
AC ADK01270;
XX
DT 20-MAY-2004 (first entry)
XX
DE DNA polymerase III-type enzyme subunit peptide fragment #25.
XX
KM DNA polymerase III delta subunit; chromosomal replicase;
KM DNA polymerase III; enzyme.
XX
OS Synthetic.
XX
PN US2004043415-A1.
XX
PD 04-MAR-2004.
XX
PF 25-SEP-2003; 2003US-00671134.
PR 08-APR-1997; 97US-0043202P.
XX

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PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
PI O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
PI Kuriyan J;
XX
DR WPI; 2004-225698/21.
XX
PT New holB DNA molecule derived from an Aquifex species, encoding a delta
PT prime subunit of a DNA polymerase III-type enzyme, useful for amplifying
PT or sequencing nucleic acid molecules.
XX
PS Example 14; SEQ ID NO 210; 245bp; English.
XX
CC The invention relates to an isolated DNA molecule from an Aquifex species
CC encoding a delta subunit of a DNA polymerase III-type enzyme. The delta
CC subunit encoded by the DNA molecule is useful as part of a thermostable
CC DNA polymerase III enzyme complex useful in amplifying or sequencing a
CC nucleic acid molecule. The polymerase is especially useful as a
CC chromosomal replicase. This sequence represents a DNA polymerase III-type
CC enzyme subunit peptide fragment of the invention.
XX
SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 HGYYL 10
Db 7 HGYYL 11

RESULT 56
ADJ79489
ID ADJ79489 standard; peptide; 11 AA.
XX
AC ADJ79489;
XX
DT 20-MAY-2004 (first entry)
XX
DE T. thermophilus holB primer peptide #4.
XX
KW DNA polymerase; DNA sequencing; DNA amplification.
XX
OS Thermus thermophilus.
XX
PN US2004043414-A1.
XX
PD 04-MAR-2004.
XX
PF 25-SEP-2003; 2003US-00670844.
XX
PR 08-APR-1997; 97US-0043202P.
PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX

PI O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
PI Kuriyan J;
XX
DR WPI; 2004-225698/21.
DR N-PSDB; ADJ79488.
XX
PT Novel isolated DNA molecule from Bacillus stearothermophilus, encoding
PT tau subunit of DNA polymerase III-type enzyme, useful in amplification
PT and sequencing reactions.
XX
PS Example 14; SEQ ID NO 210; 245bp; English.
XX
CC The invention relates to an isolated DNA molecule from Bacillus
CC stearothermophilus encoding a delta subunit of a DNA polymerase I. The
CC subunits are useful for producing DNA polymerases for use in DNA
CC sequencing and DNA amplification methods. The present sequence is used in
CC the exemplification of the present invention.
XX
SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 6 HGYYL 10
Db 7 HGYYL 11

RESULT 57
ADJ84929
ID ADJ84929 standard; peptide; 11 AA.
XX
AC ADJ84929;
XX
DT 03-JUN-2004 (first entry)
XX
DE Bacterial DNA polymerase III-associated peptide #5.
XX
KW DNA polymerase III; DNA pol III; thermophilic bacteria;
KW polymerase chain reaction; PCR; thermostable polymerase; DNA sequencing;
KW dnaX; holA; holB; dnaB; dnaN; dnaQ; dnaB; ssb.
XX
OS Unidentified.
XX
PN US2004048309-A1.
XX
PD 11-MAR-2004.
XX
PF 26-SEP-2003; 2003US-00673098.
XX
PR 08-APR-1997; 97US-0043202P.
PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
PA (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
PI O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
PI Kuriyan J;
XX
DR WPI; 2004-228491/22.
XX
PT Novel isolated Thermotoga delta primer subunit of DNA polymerase III-type
PT enzyme, useful for amplifying and sequencing DNA molecule by polymerase
PT chain reaction.
XX
PS Disclosure; SEQ ID NO 210; 235bp; English.

XX The invention relates to an isolated Thermotoga delta' (prime) subunit of
CC a DNA polymerase III-type (polIII) enzyme appearing as AB084867, encoded
CC by a nucleic acid molecule hybridizing to the complement of AB084866. The
CC DNA and protein are two of a number of DNAs and proteins from
CC thermotable bacteria polIII subunits disclosed in the specification
CC (e.g. the dnaX, holA, holB, dnaN, dnaQ, dnaE, ssb genes). Also
CC included are a clamp loader complex comprising polIII delta', a DNA
CC polymerase III-type enzyme comprising the clamp loader and a kit
CC comprising a container that contains either a deoxynucleoside
CC triphosphate or a dideoxynucleoside triphosphate and a container
CC containing a DNA polymerase III-type enzyme complex. The polIII delta'
CC subunits are useful for amplifying and sequencing a DNA molecule by PCR.
CC The present sequence is a bacterial polIII subunit-associated peptide
CC included in the sequence listing but not mentioned anywhere else in the
CC specification.

XX Sequence 11 AA;
SQ

Query Match 30.2%; Score 29; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTL 10
|||||
DB 7 HGTL 11

RESULT 58
ADM77717
ID ADM77717 standard; peptide; 11 AA.
XX ADM77717;
DT 15-JUL-2004 (first entry)
XX
XX DNA polymerase III-type enzyme related peptide #35.
DE
XX
XX Bacillus PolC subunit; DNA polymerase III; dnaX; dnaN; holB;
KM thermophilic bacterium; enzyme.
XX
XX Thermus thermophilus.
OS
XX
XX US2004077012-A1.
PN
XX
XX 22-APR-2004.
PD
XX
XX 26-SEP-2003; 2003US-00672638.
PF
XX
XX 08-APR-1997; 97US-0043202P.
PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
XX (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
XX O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
PI Kuriyan J;
PI
XX
XX WPI; 2004-340000/31.
DR
XX
XX Novel isolated Bacillus PolC subunit of DNA polymerase III-type enzyme,
PT useful for amplifying and sequencing DNA molecules by polymerase chain
PT reaction.
XX
XX Example 14; SEQ ID NO 210; 245pp; English.
PS
XX The invention relates to an isolated Bacillus PolC subunit of a DNA

CC polymerase III-type enzyme. The invention also relates to a method of
CC preparing DNA polymerase III enzymes, DNA molecules obtained by
CC amplifying and sequencing using the DNA polymerase III enzymes, DNA
CC probes constructed from the DNA sequences coding for dnaX, dnaN and holB
CC genes, DNA molecules encoding the DNA polymerase III enzymes, a method of
CC producing a recombinant thermotable DNA polymerase III enzyme from
CC thermophilic bacterium and a method of isolating a target DNA fragment
CC consisting essentially of DNA encoding a DNA polymerase III enzyme. The
CC Bacillus PolC subunit is useful for amplifying and sequencing a DNA
CC molecule by PCR. This sequence represents a DNA polymerase III-type
CC enzyme related peptide of the invention.

XX Sequence 11 AA;
SQ

Query Match 30.2%; Score 29; DB 8; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTL 10
|||||
DB 7 HGTL 11

RESULT 59
ADM66384
ID ADM66384 standard; peptide; 11 AA.
XX ADM66384;
AC
XX
XX 15-JUL-2004 (first entry)
DT
XX
XX T. thermophilus holB primer peptide #4.
DE
XX
XX DNA polymerase; DNA sequencing; DNA amplification.
KM
XX
XX Thermus thermophilus.
OS
XX
XX US2004081995-A1.
PN
XX
XX 29-APR-2004.
PD
XX
XX 26-SEP-2003; 2003US-00673127.
PF
XX
XX 08-APR-1997; 97US-0043202P.
PR 08-APR-1998; 98US-00057416.
PR 18-AUG-2000; 2000US-00642218.
PR 21-NOV-2000; 2000US-00716964.
XX
XX (ODON/) O'DONNELL M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
XX O'donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
PI Kuriyan J;
PI
XX
XX WPI; 2004-340140/31.
DR N-PSDB; ADM66383.
DR
XX
XX Novel isolated Bacillus beta subunit of DNA polymerase III-type enzyme,
PT useful for amplifying and sequencing DNA molecule by polymerase chain
PT reaction.
XX
XX Example 14; SEQ ID NO 210; 245pp; English.
PS
XX The invention relates to an isolated DNA molecule from Bacillus
CC steatothermophilus encoding a delta subunit of a DNA polymerase I. The
CC subunits are useful for producing DNA polymerases for use in DNA
CC sequencing and DNA amplification methods. The present sequence is used in
CC the exemplification of the present invention.

SQ Sequence 11 AA;
 Query Match 30.2%; Score 29; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 HGVL 10
 |||||
 Db 7 HGVL 11
 RESULT 60
 ADO04437
 ID ADO04437 standard; peptide; 11 AA.
 AC ADO04437;
 DT 26-AUG-2004 (first entry)
 DE Conserved DNA polymerase III delta' subunit peptide #2.
 DE
 XX
 XX DNA polymerase III; single-stranded DNA binding protein; ssb;
 KM chromosomal replicase; secondary structure element; replication.
 OS Bacteria.
 XX
 PN US2004106137-A1.
 XX
 PD 03-JUN-2004.
 XX
 PF 25-SEP-2003; 2003US-00670817.
 XX
 PR 08-APR-1997; 97US-0043202P.
 PR 08-APR-1998; 98US-00057416.
 PR 18-AUG-2000; 2000US-00642218.
 PR 21-NOV-2000; 2000US-00716964.
 XX
 PA (ODON/) O'DONNELL M E.
 PA (YUZH/) YUZHAKOV A.
 PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 PI O'Donnell ME, Yuzhakov A, Yurleva O, Jeruzalmi D, Bruck I,
 PI Kuriyan J;
 DR WPI; 2004-419457/39.
 XX
 PT Novel isolated DNA derived from *Bacillus stearothermophilus*, encoding
 PT single-strand DNA binding protein, useful in removing secondary structure
 PT element from single-stranded DNA during DNA replication.
 XX
 PS Example 14; SEQ ID NO 210; 245bp; English.
 XX
 CC The invention relates to an isolated DNA molecule from *Bacillus* sp.
 CC encoding a single-strand DNA binding protein (ssb) appearing as ADO04402
 CC encoding the protein appearing as ADO04403, and DNAs hybridizing to
 CC complementary sequence of ADO04402 under hybridization conditions. Also
 CC included are an expression system comprising an expression vector into
 CC which the ssb gene is inserted and a host cell comprising a heterologous
 CC ssb gene. The following are disclosed as new, a kit (comprising a
 CC container that contains either a deoxynucleoside triphosphate or a
 CC dideoxynucleoside triphosphate, and a container containing DNA polymerase
 CC III-type complex), methods and products (for identifying, isolating and
 CC cloning DNA molecules encoding subunits encoded by genes of DNA
 CC polymerase III-type enzyme from thermophilic bacteria); preparing DNA
 CC polymerase III enzymes, DNA molecules obtained by amplifying and
 CC sequencing using the DNA polymerase III enzymes, recombinant alpha, beta,
 CC epsilon, tau, gamma, delta and delta' DNA polymerase III subunits, genes
 CC encoding bacterial chromosomal replicases, and producing a recombinant
 CC thermostable DNA polymerase III enzyme from a thermophilic bacterium. The
 CC ssb protein and gene, derived from *Bacillus stearothermophilus*, are

CC useful in producing a recombinant thermostable single-strand binding
 CC protein useful in removing secondary structure element from ssDNA during
 CC replication. The present sequence is a bacterial DNA polymerase III
 CC subunit derived peptide (or consensus motif) used to design PCR primers
 CC for isolation of the DNA polIII genes.
 XX
 SQ Sequence 11 AA;
 Query Match 30.2%; Score 29; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 6 HGVL 10
 |||||
 Db 7 HGVL 11
 RESULT 61
 ADP82514
 ID ADP82514 standard; peptide; 11 AA.
 AC ADP82514;
 DT 26-AUG-2004 (first entry)
 DE
 DE
 XX
 XX DNA polymerase III delta' subunit peptide seqd 210.
 XX
 KM single-strand binding protein; SSB; DNA-protein complex;
 KM DNA polymerase III-type enzyme complex; thermostable DNA polymerase III;
 KM secondary structure element; replication; holB; DNA polymerase III;
 KM delta' subunit.
 XX
 OS *Thermus thermophilus*.
 XX
 PN US2004110210-A1.
 XX
 PD 10-JUN-2004.
 XX
 PF 26-SEP-2003; 2003US-00673119.
 XX
 PR 08-APR-1997; 97US-0043202P.
 PR 08-APR-1998; 98US-00057416.
 PR 18-AUG-2000; 2000US-00642218.
 PR 21-NOV-2000; 2000US-00716964.
 XX
 PA (ODON/) O'DONNELL M E.
 PA (YUZH/) YUZHAKOV A.
 PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 PI O'Donnell ME, Yuzhakov A, Yurleva O, Jeruzalmi D, Bruck I,
 PI Kuriyan J;
 DR WPI; 2004-440355/41.
 XX
 PT Novel isolated *Bacillus stearothermophilus* single-strand binding protein,
 PT useful in removing secondary structure element from single-stranded DNA
 PT during DNA replication.
 XX
 PS Example 14; SEQ ID NO 210; 245bp; English.
 XX
 CC The invention describes an isolated *Bacillus* sp. single-strand binding
 CC protein (II), comprising a fully defined sequence (S1) of 164 amino acids
 CC as given in specification or encoded by a nucleic acid molecule
 CC hybridizing to the complement of a fully defined sequence (S2) of 492
 CC base pairs as given in specification. Also described are: a DNA-protein
 CC complex (II) comprising a DNA molecule containing a single-stranded
 CC region and (I) that is bound to the single-stranded region of the DNA
 CC molecule; a kit comprising a container that contains either a
 CC deoxynucleoside triphosphate or a dideoxynucleoside triphosphate, and
 CC container that contains a DNA polymerase III-type enzyme complex, and

CC container that contains (1); methods and products for identifying,
 CC isolating and cloning DNA molecules encoding subunits encoded by genes of
 CC DNA polymerase III-type enzyme; kits for amplification and sequencing of
 CC DNA molecules; DNA polymerase III enzyme subunits; preparing DNA
 CC polymerase III enzyme; DNA molecules obtained by amplifying and
 CC sequencing using the DNA polymerase III enzymes; producing and isolating
 CC a recombinant thermostable DNA polymerase III enzyme or its subunit from
 CC thermophilic bacterium; DNA (III) encoding (I); an expression system
 CC comprising an expression vector into which (III) is inserted; and a host
 CC cell comprising a heterologous (III). (I) is useful in removing a
 CC secondary structure element from single-stranded DNA (ssDNA),
 CC particularly during replication. (I) binds to single stranded regions of
 CC DNA strands during DNA replication and prevents the rewinding of the DNA
 CC strands. This is the amino acid sequence of a DNA polymerase III delta
 CC subunit peptide used to create a primer for the isolation of *Thermus*
 CC thermophilus holB.

XX Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTYL 10
 |||||
 Db 7 HGTYL 11

RESULT 62

AD515721
 ID AD515721 standard; peptide; 11 AA.

XX AD515721;

XX 30-DEC-2004 (first entry)

XX Peptide for *T. thermophilus* DNA polymerase III delta PCR primer #2.

XX DNA polymerase III subunit; HolC; thermostable DNA polymerase;

XX thermophilic bacterium; gamma subunit; tau subunit; epsilon subunit;

XX alpha subunit; PolC; delta subunit; delta' subunit; beta subunit; SSB;

XX single stranded binding protein; long chain extension;

XX cognate sliding clamp; clamp loader; DNA stimulated ATPase.

XX Bacteria.

XX US2004197796-A1.

XX 07-OCT-2004.

XX 25-SEP-2003; 2003US-00671207.

XX 08-APR-1997; 97US-0043202P.

XX 08-APR-1998; 98US-00057416.

XX 18-AUG-2000; 2000US-00642218.

XX 21-NOV-2000; 2000US-00716964.

XX (ODON/) O'DONNELL M E.

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XX (YURI/) YURIEVA O.

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XX (KURI/) KURIYAN J.

XX O'Donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,

PI Kuriyan J;

XX WPI; 2004-718457/70.

XX Novel isolated DNA molecule from *Bacillus* species encoding beta subunit

PT of DNA polymerase III-type enzyme, useful for producing recombinant

XX thermostable beta subunit of DNA polymerase III-type enzyme.

PS Example 14; SEQ ID NO 210; 245bp; English.

XX The invention relates to an isolated DNA molecule from a *Bacillus* sp.
 CC encoding a beta subunit of a DNA polymerase III-type enzyme (appearing as
 CC AD515684 and encoding the protein appearing as AD515685), or hybridizing
 CC to the complement of AD515684 under hybridization conditions comprising
 CC at most about 0.9 M sodium citrate buffer at least 37C. Also included are
 CC an expression system comprising an expression vector into which AD515684
 CC is inserted and a host cell comprising AD515684. Also disclosed are
 CC methods and products for identifying, isolating and cloning DNA molecules
 CC which encode accessory subunits of a DNA polymerase III-type enzyme
 CC (gamma, tau, epsilon, alpha, PolC, delta, delta', and beta as well as SSB
 CC (single stranded binding protein)), methods for identifying polymerase
 CC III-type enzymes, isolated and purified DNA polymerase III from *Thermus*
 CC thermophilus and *B. stearothermophilus*, methods for preparing DNA
 CC polymerase III-type enzyme and kits for amplification and sequencing of
 CC DNA molecules that can achieve long chain extension of primed DNA. DNA
 CC polymerase III beta DNA is useful for producing a recombinant
 CC thermostable beta subunit of a DNA polymerase III-type enzyme from
 CC *Bacillus* sp., which involves transforming a host cell with DNA polymerase
 CC III beta DNA under conditions suitable for expression of the beta
 CC subunit, and isolating the beta subunit. DNA polymerase III beta DNA
 CC enables the investigator to obtain a thermostable polymerase III-type
 CC enzyme from a thermophilic bacterium that exhibits the ability to extend a
 CC primer over a long stretch (greater than 5 kb) of single-stranded (ss) DNA
 CC at elevated temperature, the ability to be stimulated by a cognate
 CC sliding clamp (e.g., beta) of the type that is assembled on DNA by
 CC 'clamp' loader (e.g., gamma complex), and have a clamp loading subunit
 CC that shows DNA stimulated ATPase activity at elevated temperatures and/or
 CC ionic strength. The *Thermus thermophilus* HolC gene was isolated by
 CC designing PCR primers from the peptide sequences of the genes immediately
 CC 5' and 3' to it (nearest neighbours), relying on the presumption that the
 CC gene arrangement would be preserved in closely related species. The
 CC present sequence is a nearest neighbour peptide from a related species,
 CC used to design primers for the amplification of *T. thermophilus* HolC
 CC gene.

XX Sequence 11 AA;

Query Match 30.2%; Score 29; DB 8; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02; Mismatches 0; Indels 0; Gaps 0;

Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTYL 10
 |||||
 Db 7 HGTYL 11

RESULT 63

AD55212
 ID AD55212 standard; peptide; 11 AA.

XX AD55212;

XX 19-MAY-2005 (first entry)

XX *T. thermophilus* holB downstream peptide, SEQ ID 210.

XX DNA polymerase; DNA amplification; primer extension.

XX Synthetic.

XX US2005048510-A1.

XX 03-MAR-2005.

XX 26-SEP-2003; 2003US-0067120.

XX 08-APR-1997; 97US-0043202P.

XX 08-APR-1998; 98US-00057416.

XX 18-AUG-2000; 2000US-00642218.

XX 21-NOV-2000; 2000US-00716964.

PA (ODON/) O'DONNELL M E.
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 PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 XX
 PI O'Donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,
 PI Kuriyan J,
 DR WPI, 2005-202083/21.
 DR N-PSDB; ADY55211.
 XX
 PT New isolated Aquifex delta prime subunit of DNA polymerase III-type
 PT enzyme, useful for amplifying and sequencing DNA molecule.
 XX
 PS Disclosure; SEQ ID NO 210; 245bp; English.
 XX
 CC The invention relates to a novel isolated Aquifex delta prime subunit of
 CC a DNA polymerase III-type enzyme. The subunit comprises a fully defined
 CC 305 amino acid (ADY55128) sequence given in the specification, and
 CC encoded by a nucleic acid molecule hybridizing to the complement of a
 CC fully defined 1051 nucleotide (ADY55127) sequence given in the
 CC specification. The invention further comprises: a clamp loader complex
 CC comprising the Aquifex delta prime subunit; a DNA polymerase III-type
 CC enzyme complex comprising the clamp loader complex; and a kit comprising
 CC a container containing either a deoxynucleoside triphosphate or a
 CC dideoxynucleoside triphosphate, and a container having a DNA polymerase
 CC III-type enzyme complex. The Aquifex delta prime subunit is useful for
 CC extending a primer over a long stretch of single-stranded DNA at an
 CC elevated temperature. The Aquifex delta prime subunit or DNA polymerase
 CC III-type enzyme complex is useful for amplifying and sequencing a DNA
 CC molecule. This sequence represents a T. thermophilus holB downstream
 CC peptide of the invention.
 XX
 SQ Sequence 11 AA;
 XX

Query Match 30.2%; Score 29; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTYL 10
 |||||
 Db 7 HGTYL 11

RESULT 64
 ADZ76788
 ID ADZ76788 standard; peptide; 11 AA.
 XX
 AC ADZ76788;
 XX
 DT 14-JUL-2005 (first entry)
 XX
 DE T. thermophilus holB gene primer derived peptide, SEQ ID 210.
 XX
 KW recombinant DNA; thermostable; PolC; DNA polymerase; PCR.
 XX
 OS Synthetic.
 XX
 PN US200510920-A1.
 PD 12-MAY-2005.
 XX
 PP 25-SEP-2003; 2003US-00671412.
 XX
 PR 08-APR-1997; 97US-0043302P.
 PR 08-APR-1998; 98US-00057416.
 PR 18-AUG-2000; 2000US-00642218.
 PR 21-NOV-2000; 2000US-00716964.
 XX
 PA (ODON/) O'DONNELL M E.
 PA (YUZH/) YUZHAKOV A.

PA (YURI/) YURIEVA O.
 PA (JERU/) JERUZALMI D.
 PA (BRUC/) BRUCK I.
 PA (KURI/) KURIYAN J.
 XX
 PI O'Donnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I,
 PI Kuriyan J,
 DR WPI, 2005-354712/36.
 DR N-PSDB; ADZ76787.
 XX
 PT New isolated DNA molecule from a Bacillus species encoding a PolC subunit
 PT of a DNA polymerase III-type enzyme, useful in producing thermostable DNA
 PT polymerases for use as chromosomal replicases.
 XX
 PS Example 14; SEQ ID NO 210; 245bp; English.
 XX
 CC The invention relates to a novel isolated DNA molecule from a Bacillus
 CC species encoding a PolC subunit of a DNA polymerase III-type enzyme
 CC comprising a sequence of 4301 base pairs (ADZ76761), encoding a sequence
 CC of 1433 amino acids (ADZ76762), or hybridizing to the complement of
 CC ADZ76761, where the sequences are given in the specification. The
 CC invention further comprises: an expression system comprising an
 CC expression vector into which is inserted the heterologous DNA molecule;
 CC a host cell comprising the heterologous DNA molecule; a method for
 CC producing a recombinant thermostable PolC subunit of a DNA polymerase III
 CC -type enzyme from a Bacillus species; and an isolated DNA molecule from
 CC Bacillus stearothermophilus encoding a PolC subunit of a DNA polymerase
 CC III enzyme, where the PolC subunit can co-operate with a clamp loader to
 CC form a DNA polymerase III-like particle. The methods and compositions of
 CC the present invention are useful in producing thermostable DNA
 CC polymerases for use as chromosomal replicases. The thermostable DNA
 CC polymerases, for use as chromosomal replicases, provide a faster and
 CC longer chain production in PCR, and a higher quality of DNA sequencing
 CC ladders. This sequence represents a T. thermophilus holB gene primer
 CC derived peptide of the invention.
 XX
 SQ Sequence 11 AA;
 XX

Query Match 30.2%; Score 29; DB 9; Length 11;
 Best Local Similarity 100.0%; Pred. No. 4.9e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGTYL 10
 |||||
 Db 7 HGTYL 11

RESULT 65
 ABA24796
 ID ABA24796 standard; peptide; 11 AA.
 XX
 AC ABA24796;
 XX
 DT 28-JUL-2005 (first entry)
 XX
 DE Thermus thermophilus holB peptide for downstream PCR primer.
 XX
 KW cloning; DNA polymerase; thermostability; DNA replication.
 XX
 OS Thermus thermophilus.
 XX
 PN US2005112580-A1.
 PD 26-MAY-2005.
 XX
 PP 26-SEP-2003; 2003US-00671859.
 XX
 PR 08-APR-1997; 97US-0043202P.
 PR 08-APR-1998; 98US-00057416.
 PR 18-AUG-2000; 2000US-00642218.
 PR 21-NOV-2000; 2000US-00716964.
 XX

PA (ODON/) O'DONNELL, M E.
PA (YUZH/) YUZHAKOV A.
PA (YURI/) YURIEVA O.
PA (JERU/) JERUZALMI D.
PA (BRUC/) BRUCK I.
PA (KURI/) KURIYAN J.
XX
XX
PI Odonnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
PI Kuriyan J;
XX
DR WPI; 2005-371651/38.
XX
XX
PT New isolated Bacillus delta or delta prime or tau subunit of DNA
PT polymerase III-type enzymes, useful as thermostable DNA polymerases and
PT chromosomal replicases, and in providing high-fidelity amplified copies
PT of nucleic acid molecules.
XX
PS Example 14; SEQ ID NO 210; 245pp; English.
XX
XX
CC The invention relates to an isolated Bacillus delta or delta prime or tau
CC subunit of a DNA polymerase III-type enzyme, the isolated subunit
CC comprising a fully defined sequence of 348, 252 or 559 amino acids
CC (AEA24764, AEA24766 or AEA24768), or being encoded by a nucleic acid
CC molecule hybridizing to the complement of a fully defined sequence of
CC 1044, 757 or 1677 bp (AEA24763, AEA24765 or AEA24767) at 0.9 M sodium
CC citrate buffer and at least 37 deg C. The methods and compositions of the
CC present invention are useful in thermostable DNA polymerases,
CC particularly to polymerases as chromosomal replicases derived from
CC thermophilic bacteria, and for providing high-fidelity amplified copies
CC of a nucleic acid molecule. This sequence represents a peptide from a DNA
CC polymerase III subunit of the invention
XX
SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYLE 10
|||||
DB 7 HGYLE 11

RESULT 66
AEA34219
ID AEA34219 standard; peptide; 11 AA.
XX
XX
AC AEA34219;
XX
XX

DT 28-JUL-2005 (first entry)
XX

DE Thermus thermophilus HolB peptide for downstream PCR primer.
XX

KW cloning; DNA polymerase; thermostability; DNA replication.
XX

OS Thermus thermophilus.
XX

PN US6897053-B1.
XX

PD 24-MAY-2005.
XX

PF 21-NOV-2000; 2000US-00716964.
XX

PR 08-APR-1997; 97US-0043202P.
XX

PR 08-APR-1998; 98US-00057416.
XX

PR 18-AUG-2000; 2000US-00642218.
XX

PA (UYRQ) UNIV ROCKEFELLER.
XX

PI Odonnell ME, Yurieva O;
XX

DR WPI; 2005-370754/38.
XX

PT New isolated DNA molecules encoding the delta subunit of DNA polymerase
PT III-type enzymes that function as chromosomal replicase, useful for
PT amplifying or sequencing DNA molecules.
XX
XX
XX

PS Example 14; SEQ ID NO 210; 236pp; English.
XX

CC The invention relates to an isolated Bacillus delta or delta prime or tau
CC subunit of a DNA polymerase III-type enzyme, the isolated subunit
CC comprising a fully defined sequence of 348, 252 or 559 amino acids
CC (AEA34187, AEA34189 or AEA34191), or being encoded by a nucleic acid
CC molecule hybridizing to the complement of a fully defined sequence of
CC 1044, 757 or 1677 bp (AEA34186, AEA34188 or AEA34190) at 0.9 M sodium
CC citrate buffer and at least 37 deg C. The methods and compositions of the
CC present invention are useful in thermostable DNA polymerases,
CC particularly to polymerases as chromosomal replicases derived from
CC thermophilic bacteria, and for providing high-fidelity amplified copies
CC of a nucleic acid molecule. This sequence represents a peptide from a DNA
CC polymerase III subunit of the invention
XX

SQ Sequence 11 AA;

Query Match 30.2%; Score 29; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYLE 10
|||||
DB 7 HGYLE 11

RESULT 67
AEB51623
ID AEB51623 standard; peptide; 11 AA.
XX
XX
AC AEB51623;
XX
XX

DT 22-SEP-2005 (first entry)
XX

DE DNA polymerase III-type enzyme holB peptide, SEQ ID 210.
XX

KW DNA polymerase.
XX

OS Thermus thermophilus.
XX

PN US2005153299-A1.
XX

PD 14-JUL-2005.
XX

PF 25-SEP-2003; 2003US-00671106.
XX

PR 08-APR-1997; 97US-0043202P.
XX

PR 08-APR-1998; 98US-00057416.
XX

PR 18-AUG-2000; 2000US-00642218.
XX

PR 21-NOV-2000; 2000US-00716964.
XX

PA (ODON/) O'DONNELL, M E.
XX

PA (YUZH/) YUZHAKOV A.
XX

PA (YURI/) YURIEVA O.
XX

PA (JERU/) JERUZALMI D.
XX

PA (BRUC/) BRUCK I.
XX

PA (KURI/) KURIYAN J.
XX

PI Odonnell ME, Yuzhakov A, Yurieva O, Jeruzalmi D, Bruck I;
XX

DR WPI; 2005-496822/50.
XX

PT New isolated DNA molecule from Bacillus stearothermophilus encoding a
PT delta prime subunit of a DNA polymerase III-type enzyme, useful producing
PT recombinant thermostable delta prime subunit of a DNA polymerase III-type
PT enzyme.
XX
XX

PS Example 14; SEQ ID NO 210; 246pp; English.

XX The present invention relates to a DNA polymerase III-type enzyme
CC subunits and their coding sequences. The coding sequence for a *Bacillus*
CC *stereothermophilus* delta prime subunit of DNA polymerase III-type enzyme
CC is specifically claimed (AB51592). Also disclosed are: preparation
CC methods for DNA Polymerase III-type enzymes; methods for amplifying and
CC sequencing the DNA molecule; and DNA amplification kits. The present
CC sequence was used to illustrate the invention.
XX
SQ Sequence 11 AA;
QY
Db 6 HGVL 10
7 HGVL 11
Query Match 30.2%; Score 29; DB 9; Length 11;
Best Local Similarity 100.0%; Pred. No. 4.9e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
RESULT 68
AAE26390
ID AAE26390 standard; peptide; 12 AA.
XX
AC AAE26390;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human wild-type GPR10 C-terminal peptide #1.
XX
KM Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
KM PRRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
KM anticonvulsant.
XX
OS Homo sapiens.
XX
PN US2002037533-A1.
XX
PD 28-MAR-2002.
XX
PF 17-AUG-2001; 2001US-00932161.
XX
PR 28-APR-2000; 2000US-00560915.
XX
PA (CIYE/) CIVELLI O.
XX (LINS/) LIN S.
XX
PI Cive111 O, Lin S;
XX
DR WPI; 2002-403931/43.
XX
PT Screening for compounds useful for promoting wakefulness or sleep, and
PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
PT apnea, comprises administering a prolactin releasing peptide agonist or
PT antagonist.
XX
PS Example 2; Page 22; 35pp; English.
XX
CC The present invention relates to a method of screening for compounds for
CC promoting wakefulness or sleep in a mammal. The method involves
CC administering a prolactin releasing peptide (PRP) receptor (GPR10)
CC agonist or antagonist respectively and determining the ability of the
CC compound to promote wakefulness or sleep. The compounds identified from
CC the method are used in the therapy of epilepsy and other diseases
CC associated with absence seizures and in promoting wakefulness and sleep
CC in individuals having sleep disorders such as insomnia and narcolepsy.
CC PRRP receptor agonists may be used to treat common disorders which lead
CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and
CC psychogenic hypersomnia. PRRP receptor antagonists are useful for
CC promoting sleep and for treating insomnia such as adjustment sleep
CC disorder and psychophysiological insomnia. The present sequence is human
CC wild-type GPR10 C-terminal peptide

XX
SQ Sequence 12 AA;
QY
Db 5 PHGVLITAAV 14
1 PHGQNMIVSV 10
Query Match 30.2%; Score 29; DB 5; Length 12;
Best Local Similarity 50.0%; Pred. No. 5.5e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
RESULT 69
AAE26398
ID AAE26398 standard; peptide; 12 AA.
XX
AC AAE26398;
XX
DT 13-DEC-2002 (first entry)
XX
DE Human GPR10 mutant C-terminal peptide, I370A.
XX
KM Human; wakefulness; sleep disorder; prolactin releasing peptide receptor;
KM PRRP; GPR10; therapy; epilepsy; narcolepsy; sleepiness; sleep apnoea;
KM insomnia; idiopathic hypersomnia; psychogenic hypersomnia; seizure;
KM anticonvulsant; mutant; mutein.
XX
OS Homo sapiens.
XX
OS Synthetic.
FH Key Location/Qualifiers
FT Misc-difference 12 /note="wild-type Ile substituted with Ala; This position
FT corresponds to position 370 of the wild-type protein"
XX
PN US2002037533-A1.
XX
PD 28-MAR-2002.
XX
PF 17-AUG-2001; 2001US-00932161.
XX
PR 28-APR-2000; 2000US-00560915.
XX
PA (CIYE/) CIVELLI O.
XX (LINS/) LIN S.
XX
PI Cive111 O, Lin S;
XX
DR WPI; 2002-403931/43.
XX
PT Screening for compounds useful for promoting wakefulness or sleep, and
PT for treating sleeping disorders, e.g. insomnia, hypersomnia or sleep
PT apnea, comprises administering a prolactin releasing peptide agonist or
PT antagonist.
XX
PS Example 2; Page 23; 35pp; English.
XX
CC The present invention relates to a method of screening for compounds for
CC promoting wakefulness or sleep in a mammal. The method involves
CC administering a prolactin releasing peptide (PRP) receptor (GPR10)
CC agonist or antagonist respectively and determining the ability of the
CC compound to promote wakefulness or sleep. The compounds identified from
CC the method are used in the therapy of epilepsy and other diseases
CC associated with absence seizures and in promoting wakefulness and sleep
CC in individuals having sleep disorders such as insomnia and narcolepsy.
CC PRRP receptor agonists may be used to treat common disorders which lead
CC to sleepiness, e.g. sleep apnoea, narcolepsy, idiopathic hypersomnia and
CC psychogenic hypersomnia. PRRP receptor antagonists are useful for
CC promoting sleep and for treating insomnia such as adjustment sleep
CC disorder and psychophysiological insomnia. The present sequence is human
CC GPR10 mutant C-terminal peptide
SQ Sequence 12 AA;

AC ADM344479,
 XX 10-MAR-2005 (first entry)
 XX HLA binding epitope #5229.
 DE
 XX
 KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;
 KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX
 OS Unidentified.
 OS
 XX WO2003040165-A2.
 PN
 XX
 PD 15-MAY-2003.
 PD
 XX 18-OCT-2001; 2001WO-US051650.
 PF
 XX 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S;
 PI
 XX WPI; 2003-441519/41.
 DR
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 PS
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 30.2%; Score 29; DB 7; Length 13;
 Best Local Similarity 41.7%; Pred. No. 6e+02;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 AFEPPHGYLTAA 13
 DB 1 AYZAVAYTLKAA 12
 ID
 ID ADM35712 standard; peptide; 13 AA.
 XX
 XX ADM35712;
 AC
 XX
 DT 10-MAR-2005 (first entry)
 XX
 DE HLA binding epitope #6462.
 XX
 KM Virucide; cytostatic; gene therapy; vaccine; epitope; cytotoxic T cell;

KM MHC class I; CTL; HTL; A2-restricted cytotoxic lymphocyte; HLA;
 KM viral disease; cancer.
 XX
 OS Unidentified.
 OS
 XX WO2003040165-A2.
 PN
 XX
 PD 15-MAY-2003.
 PD
 XX 18-OCT-2001; 2001WO-US051650.
 PF
 XX 19-OCT-2000; 2000US-0242350P.
 PR 20-APR-2001; 2001US-0285624P.
 XX
 XX (EPIM-) EPIMMUNE INC.
 PA
 XX Sette A, Sidney J, Southwood S;
 PI
 XX WPI; 2003-441519/41.
 DR
 XX
 PT New composition comprising at least one peptide having allele-specific
 PT binding motifs for HLA, useful for preventing, treating or diagnosing
 PT viral diseases and cancer.
 PS
 XX
 PS Claim 1; Page 52-379; 382pp; English.
 CC The invention relates to a composition comprising at least one peptide
 CC having an isolated, prepared epitope selected from any of the sequences
 CC from 30 lists given in the specification. Also disclosed is a method for
 CC inducing a cytotoxic T cell response against a pre-selected antigen in a
 CC patient expressing a specific MHC class I allele by contacting cytotoxic
 CC T cells from the patient with the composition cited above. The
 CC composition comprises an epitope that is joined by an amino acid linker.
 CC The epitope is admixed or joined to a CTL or HTL epitope. The epitope is
 CC bound to an HLA molecule on the antigen-presenting cell, where when an A2
 CC -restricted cytotoxic lymphocyte (CTL) is present, a receptor of the CTL
 CC binds to a complex of the HLA molecule and the epitope. Specifically
 CC claimed are peptides having allele-specific binding motifs for HLA. The
 CC compositions and methods are useful for preventing, treating or
 CC diagnosing viral diseases and cancer. The peptide epitopes are useful as
 CC diagnostic agents for evaluating immune responses, for making antibodies
 CC and for evaluating efficacy of a vaccine. Sequences given in ADM29251-
 CC ADM37745 represent epitopes of the invention as given in Tables 2-31.
 XX
 XX Sequence 13 AA;
 SQ
 Query Match 30.2%; Score 29; DB 7; Length 13;
 Best Local Similarity 41.7%; Pred. No. 6e+02;
 Matches 5; Conservative 3; Mismatches 4; Indels 0; Gaps 0;
 QY 2 AFEPPHGYLTAA 13
 DB 1 AYZAVAYTLKAA 12
 ID
 ID ADM30473 standard; peptide; 13 AA.
 XX
 XX ADM30473;
 AC
 XX
 DT 18-NOV-2004 (first entry)
 XX
 DE Kinase peptide K063D104.
 DE
 XX
 KM Cardiant; Vasotropic; Antiarteriosclerotic; Vulnery; Cytostatic;
 KM Ophthalmological; Antidiabetic; Antirheumatic; Antiarthritic;
 KM Antipsoriatic; Anorectic; Anti-HIV; Angiogenesis modulator; angiogenesis;
 KM Kinase; cardiovascular disease; cancer; rheumatoid arthritis; psoriasis;
 KM obesity; haemangioma; AIDS; Kaposi sarcoma; arteriosclerosis; restenosis.
 XX
 OS Unidentified.
 XX

XX 19-SEP-2002.
PD 13-MAR-2002; 2002WO-US007855.
PF 14-MAR-2001; 2001US-00809638.
PR (AGEN-) AGENSYS INC.
PA Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX WPI; 2002-713510/77.
DR
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 206; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 30.2%; Score 29; DB 5; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY 7 GYLLTAVSPG 17
DB 5 GHILNGTNP 15
XX
RESULT 77
ABJ14367
ID ABJ14367 standard; peptide; 15 AA.
XX
AC ABJ14367;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #2993.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX WPI; 2002-713510/77.
DR
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX

XX Disclosure; Page 200; 274pp; English.
PS
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 30.2%; Score 29; DB 5; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
OY 7 GYLLTAVSPG 17
DB 5 GHILNGTNP 15
XX
RESULT 78
ABJ14669
ID ABJ14669 standard; peptide; 15 AA.
XX
AC ABJ14669;
XX
DT 10-DEC-2002 (first entry)
XX
DE Human 125P5C8 epitope #3295.
XX
KW Human; 125P5C8; cancer; cytostatic; breast cancer; prostate cancer;
KW bladder cancer; kidney cancer; colon cancer; ovarian cancer; epitope.
XX
OS Homo sapiens.
XX
PN WO200272785-A2.
XX
PD 19-SEP-2002.
XX
PF 13-MAR-2002; 2002WO-US007855.
PR 14-MAR-2001; 2001US-00809638.
XX
PA (AGEN-) AGENSYS INC.
XX
PI Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison K, Jakobovits A;
XX WPI; 2002-713510/77.
DR
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT treating or preventing cancer that expresses or over expresses 125P5C8.
XX
PS Disclosure; Page 207; 274pp; English.
XX
CC The present invention relates to compositions comprising a substance that
CC modulates the status of 125P5C8 or a molecule that is modulated by
CC 125P5C8. The status of a cell that expresses 125P5C8 is modulated. The
CC composition is useful for treating cancer, particularly prostate,
CC bladder, kidney, colon, ovary or breast cancer. The 125P5C8 protein
CC and/or a nucleotide sequence encoding the protein is useful for
CC immunising a mammal against cancer. The present sequence is a 125P5C8
CC epitope shown in the exemplification of the invention
XX
SQ Sequence 15 AA;
XX
Query Match 30.2%; Score 29; DB 5; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

XX 20-MAY-2004 (first entry)
DT
XX 125P5C8 protein-related peptide #3154.
DE
XX 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
XX
PD 27-NOV-2003.
XX
PF 13-MAR-2002; 2002US-00099460.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
XX (PARI/) PARIS M.
PA (CHAL/) CHALLITA-BID P M.
PA (HUBE/) HUBERT R S.
PA (AFAR/) AFAR D E H.
PA (RAIT/) RAITANO A B.
PA (GEMW/) GE W.
PA (MORR/) MORRISON R K.
PA (MORR/) MORRISON K J M.
PA (JAKO/) JAKOBOVITS A.
XX
XX Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison KJM, Jakobovits A;
XX
XX WPI; 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
PS Example 51; Page 127; 183pp; English.
XX
XX The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 30.2%; Score 29; DB 8; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
QY 7 GYLLTAAVSPG 17
|:|:|:|:
Db 5 GHILSGTNGP 15
XX
RESULT 82
ADL21870
ID ADL21870 standard; peptide; 15 AA.
XX
AC ADL21870;
XX
DT 20-MAY-2004 (first entry)
XX
DE 125P5C8 protein-related peptide #3118.
XX
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
XX
PD 27-NOV-2003.

XX 13-MAR-2002; 2002US-00099460.
PF
XX 14-MAR-2001; 2001US-00809638.
PR
XX
XX (PARI/) PARIS M.
PA (CHAL/) CHALLITA-BID P M.
PA (HUBE/) HUBERT R S.
PA (AFAR/) AFAR D E H.
PA (RAIT/) RAITANO A B.
PA (GEMW/) GE W.
PA (MORR/) MORRISON R K.
PA (MORR/) MORRISON K J M.
PA (JAKO/) JAKOBOVITS A.
XX
XX Faris M, Challita-Bid PM, Hubert RS, Afar DEH, Raitano AB, Ge W;
PI Morrison RK, Morrison KJM, Jakobovits A;
XX
XX WPI; 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
PS Example 51; Page 126; 183pp; English.
XX
XX The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
SQ Sequence 15 AA;
XX
Query Match 30.2%; Score 29; DB 8; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
XX
QY 7 GYLLTAAVSPG 17
|:|:|:|:
Db 5 GHILSGTNGP 15
XX
RESULT 83
ADL21604
ID ADL21604 standard; peptide; 15 AA.
XX
AC ADL21604;
XX
DT 20-MAY-2004 (first entry)
XX
DE 125P5C8 protein-related peptide #2852.
XX
KM 125P5C8; cancer-associated gene; cancer-associated protein; cancer.
XX
OS Unidentified.
XX
PN US2003219444-A1.
XX
PD 27-NOV-2003.
XX
PF 13-MAR-2002; 2002US-00099460.
XX
PR 14-MAR-2001; 2001US-00809638.
XX
XX (PARI/) PARIS M.
PA (CHAL/) CHALLITA-BID P M.
PA (HUBE/) HUBERT R S.
PA (AFAR/) AFAR D E H.
PA (RAIT/) RAITANO A B.
PA (GEMW/) GE W.
PA (MORR/) MORRISON R K.

PA (MORR/) MORRISON K J M.
PA (JAKO/) JAKOBOVITS A.
XX
PI Paris M, Challita-Eid PM, Hubert RS, Afar DEH, Raitano AB, Ge W,
PI Morrison RK, Morrison KDM, Jakobovits A;
XX
DR MPI; 2004-021932/02.
XX
PT New composition comprising a substance that modulates the status of
PT 125P5C8 gene or a molecule that is modulated by 125P5C8, useful for
PT diagnosing or treating cancer.
XX
XX Example 51; Page 124; 183pp; English.
XX
CC The invention comprises a composition which contains a substance that can
CC modulate the status of 125P5C8 (125P5C8 is a novel cancer-associated
CC gene/protein), or a molecule that is modulated by 125P5C8. The
CC composition of the invention is useful for diagnosing or treating cancer.
CC The present amino acid sequence represents a 125P5C8-related peptide
CC which was used in an example of the invention.
XX
XX Sequence 15 AA;
SQ
Query Match 30.2%; Score 29; DB 8; Length 15;
Best Local Similarity 36.4%; Pred. No. 7.2e+02;
Matches 4; Conservative 4; Mismatches 3; Indels 0; Gaps 0;
QY 7 GYLLTAAVSRG 17
Db 5 GHLLNGSTNPG 15
RESULT 84
ABBI4772
ID ABBI4772 standard; protein; 17 AA.
XX
AC ABBI4772;
XX
DT 23-JAN-2002 (first entry)
XX
DE Human nervous system related polypeptide SEQ ID NO 3429.
XX
XX Human; nootropic; neuroprotective; cytosolic; dermatological; virucide;
KW immunosuppressive; antiinflammatory; anti-HIV; antibacterial; vulnereary;
KW antiparasitosis; antiscikling; antiamebic; antiahrilic; cancer;
KW antirheumatic; hepatotropic; cerebroprotective; antiinflammatory;
KW antiallergic; antidiabetic; antituber; anticonvulsant; antifungal;
KW antiparasitic; cardiac; immune disorder; cardiovascular disorder;
KW neurological disease; infection; nephrotropic; gene therapy; vaccine.
XX
OS Homo sapiens.
XX
XX WO20015963-A2.
XX
PD 16-AUG-2001.
XX
PF 17-JAN-2001; 2001WO-US001334.
XX
PR 31-JAN-2000; 2000US-0179065P.
PR 04-FEB-2000; 2000US-0180628P.
PR 24-FEB-2000; 2000US-0184664P.
PR 02-MAR-2000; 2000US-0186350P.
PR 16-MAR-2000; 2000US-0189874P.
PR 17-MAR-2000; 2000US-0190076P.
PR 18-APR-2000; 2000US-0198123P.
PR 19-MAY-2000; 2000US-020515P.
PR 07-JUN-2000; 2000US-0209467P.
PR 28-JUN-2000; 2000US-0214886P.
PR 30-JUN-2000; 2000US-0215135P.
PR 07-JUL-2000; 2000US-0216647P.
PR 07-JUL-2000; 2000US-0216880P.
PR 11-JUL-2000; 2000US-0217487P.
PR 11-JUL-2000; 2000US-0217496P.

PR 14-JUL-2000; 2000US-0218290P.
PR 26-JUL-2000; 2000US-0220963P.
PR 26-JUL-2000; 2000US-0220964P.
PR 14-AUG-2000; 2000US-0224518P.
PR 14-AUG-2000; 2000US-0224519P.
PR 14-AUG-2000; 2000US-0225213P.
PR 14-AUG-2000; 2000US-0225214P.
PR 14-AUG-2000; 2000US-0225267P.
PR 14-AUG-2000; 2000US-0225268P.
PR 14-AUG-2000; 2000US-0225270P.
PR 14-AUG-2000; 2000US-0225447P.
PR 14-AUG-2000; 2000US-0225477P.
PR 14-AUG-2000; 2000US-0225758P.
PR 14-AUG-2000; 2000US-0225759P.
PR 18-AUG-2000; 2000US-0226779P.
PR 22-AUG-2000; 2000US-0226681P.
PR 22-AUG-2000; 2000US-0226688P.
PR 22-AUG-2000; 2000US-0227182P.
PR 23-AUG-2000; 2000US-0227009P.
PR 30-AUG-2000; 2000US-0228924P.
PR 01-SEP-2000; 2000US-0229287P.
PR 01-SEP-2000; 2000US-0229343P.
PR 01-SEP-2000; 2000US-0229344P.
PR 01-SEP-2000; 2000US-0229345P.
PR 05-SEP-2000; 2000US-0229509P.
PR 05-SEP-2000; 2000US-0229513P.
PR 06-SEP-2000; 2000US-0230437P.
PR 06-SEP-2000; 2000US-0230438P.
PR 08-SEP-2000; 2000US-0231242P.
PR 08-SEP-2000; 2000US-0231243P.
PR 08-SEP-2000; 2000US-0231244P.
PR 08-SEP-2000; 2000US-0231413P.
PR 08-SEP-2000; 2000US-0231414P.
PR 08-SEP-2000; 2000US-0232080P.
PR 08-SEP-2000; 2000US-0232081P.
PR 12-SEP-2000; 2000US-0231968P.
PR 14-SEP-2000; 2000US-0232397P.
PR 14-SEP-2000; 2000US-0232398P.
PR 14-SEP-2000; 2000US-0232399P.
PR 14-SEP-2000; 2000US-0232400P.
PR 14-SEP-2000; 2000US-0232401P.
PR 14-SEP-2000; 2000US-0233063P.
PR 14-SEP-2000; 2000US-0233064P.
PR 14-SEP-2000; 2000US-0233065P.
PR 21-SEP-2000; 2000US-0234223P.
PR 21-SEP-2000; 2000US-0234274P.
PR 25-SEP-2000; 2000US-0234997P.
PR 25-SEP-2000; 2000US-0234998P.
PR 26-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235484P.
PR 27-SEP-2000; 2000US-0235836P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236327P.
PR 29-SEP-2000; 2000US-0236367P.
PR 29-SEP-2000; 2000US-0236368P.
PR 29-SEP-2000; 2000US-0236369P.
PR 29-SEP-2000; 2000US-0236370P.
PR 02-OCT-2000; 2000US-0236802P.
PR 02-OCT-2000; 2000US-0237037P.
PR 02-OCT-2000; 2000US-0237038P.
PR 02-OCT-2000; 2000US-0237039P.
PR 02-OCT-2000; 2000US-0237040P.
PR 13-OCT-2000; 2000US-0239352P.
PR 13-OCT-2000; 2000US-0239352P.
PR 13-OCT-2000; 2000US-0239377P.
PR 20-OCT-2000; 2000US-0240960P.
PR 20-OCT-2000; 2000US-0241785P.
PR 20-OCT-2000; 2000US-0241786P.
PR 20-OCT-2000; 2000US-0241787P.
PR 20-OCT-2000; 2000US-0241808P.
PR 20-OCT-2000; 2000US-0241809P.
PR 20-OCT-2000; 2000US-0241826P.
PR 20-OCT-2000; 2000US-0242221P.
PR 01-NOV-2000; 2000US-0244617P.

PR 08-NOV-2000; 2000US-0246474P.
 PR 08-NOV-2000; 2000US-0246475P.
 PR 08-NOV-2000; 2000US-0246476P.
 PR 08-NOV-2000; 2000US-0246477P.
 PR 08-NOV-2000; 2000US-0246478P.
 PR 08-NOV-2000; 2000US-0246523P.
 PR 08-NOV-2000; 2000US-0246524P.
 PR 08-NOV-2000; 2000US-0246525P.
 PR 08-NOV-2000; 2000US-0246526P.
 PR 08-NOV-2000; 2000US-0246527P.
 PR 08-NOV-2000; 2000US-0246528P.
 PR 08-NOV-2000; 2000US-0246532P.
 PR 08-NOV-2000; 2000US-0246609P.
 PR 08-NOV-2000; 2000US-0246610P.
 PR 08-NOV-2000; 2000US-0246611P.
 PR 08-NOV-2000; 2000US-0246613P.
 PR 17-NOV-2000; 2000US-0249207P.
 PR 17-NOV-2000; 2000US-0249208P.
 PR 17-NOV-2000; 2000US-0249209P.
 PR 17-NOV-2000; 2000US-0249210P.
 PR 17-NOV-2000; 2000US-0249211P.
 PR 17-NOV-2000; 2000US-0249212P.
 PR 17-NOV-2000; 2000US-0249213P.
 PR 17-NOV-2000; 2000US-0249215P.
 PR 17-NOV-2000; 2000US-0249216P.
 PR 17-NOV-2000; 2000US-0249217P.
 PR 17-NOV-2000; 2000US-0249218P.
 PR 17-NOV-2000; 2000US-0249244P.
 PR 17-NOV-2000; 2000US-0249245P.
 PR 17-NOV-2000; 2000US-0249264P.
 PR 17-NOV-2000; 2000US-0249265P.
 PR 17-NOV-2000; 2000US-0249267P.
 PR 17-NOV-2000; 2000US-0249299P.
 PR 17-NOV-2000; 2000US-0249300P.
 PR 01-DEC-2000; 2000US-0250391P.
 PR 01-DEC-2000; 2000US-0251160P.
 PR 05-DEC-2000; 2000US-0251030P.
 PR 05-DEC-2000; 2000US-0251988P.
 PR 06-DEC-2000; 2000US-0251719P.
 PR 06-DEC-2000; 2000US-0251856P.
 PR 08-DEC-2000; 2000US-0251868P.
 PR 08-DEC-2000; 2000US-0251869P.
 PR 08-DEC-2000; 2000US-0251989P.
 PR 08-DEC-2000; 2000US-0251990P.
 PR 11-DEC-2000; 2000US-0254097P.
 PR 05-JAN-2001; 2001US-0259678P.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PT Rosen CA, Baraesh SC, Ruben SM;
 PT
 DR WPI; 2001-541565/60.
 DR N-PSDB; ABA11098.
 XX
 PT Nucleic acids encoding 3224 human nervous system antigen polypeptides,
 PT useful for preventing, diagnosing and/or treating nervous system cancers
 PT and metastases.
 XX
 XX
 PS Claim 11; SEQ ID NO 3429; 1701pp + Sequence listing; English.
 XX
 CC The invention relates to novel genes (ABA11004-ABA21534) and proteins
 CC (ABBI4678-ABBI18001) useful for preventing, treating or ameliorating
 CC medical conditions e.g. by protein or gene therapy. The genes are
 CC isolated from a range of human tissues disclosed in the specification.
 CC The nucleic acids, proteins, antibodies and (anti)agonists are useful in
 CC the diagnosis, treatment and prevention of: (a) cancer, e.g. breast and
 CC ovarian cancer and other cancers of the adrenal gland, bone, bone marrow,
 CC breast, gastrointestinal tract, liver, lung, or urogenital; (b) immune
 CC disorders e.g. Addison's disease, allergies, autoimmune haemolytic
 CC anaemia, autoimmune thyroiditis, diabetes mellitus, Crohn's disease,
 CC multiple sclerosis, rheumatoid arthritis and ulcerative colitis; (c)

CC cardiovascular disorders such as myocardial ischaemias; (d) wound healing
 CC ; (e) neurological diseases e.g. cerebral anoxia and epilepsy; and (f)
 CC infectious diseases such as viral, bacterial, fungal and parasitic
 CC infections. Note: The sequence data for this patent did not form part of
 CC the printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX
 SQ Sequence 17 AA;
 Query Match 30.2%; Score 29; DB 4; Length 17;
 Best Local Similarity 54.5%; Pred. No. 8.4e+02;
 Matches 6; Conservative 3; Mismatches 2; Indels 0; Gaps 0;
 Db 3 PEPHYLTTAA 13
 1 WDPGLSLVTTAA 11
 RESULT 85
 ID AEB11968 standard; peptide; 17 AA.
 XX
 AC AEB11968;
 XX
 DT 25-AUG-2005 (first entry)
 XX
 DE Salmonella flagellin tryptic peptide.
 XX
 KM Flagellin; cytostatic; antidote; cancer; neoplasm; stress; tranquilizer.
 XX
 OS Salmonella typhimurium.
 XX
 PN WO2005056042-A2.
 XX
 PD 23-JUN-2005.
 XX
 PF 02-DEC-2004; 2004WO-US040753.
 XX
 PR 02-DEC-2003; 2003US-0526460P.
 PR 02-DEC-2003; 2003US-0526461P.
 PR 02-DEC-2003; 2003US-0526496P.
 PR 02-DEC-2003; 2003US-0526666P.
 XX
 PA (CLEV-) CLEVELAND CLINIC FOUND.
 XX
 PI Gudkov AV;
 XX
 DR WPI; 2005-458516/46.
 XX
 PT Protecting patient from effects of radiation treatment or treatment or
 PT condition that triggers apoptosis comprises administering flagellin.
 PT
 XX
 PS Example 3; Fig 3; 67pp; English.
 XX
 CC The invention provides a method of protecting a mammal from the effects
 CC of radiation by administering a composition comprising flagellin. The
 CC composition may be administered in combination with a radioprotectant,
 CC such as an antioxidant selected from amifostine and vitamin B, or a
 CC cytokine such as stem cell factor. The method may also be used to protect
 CC a patient from one or more treatments or conditions that trigger
 CC apoptosis, such as cancer treatment by chemotherapy or radiotherapy, or a
 CC stress resulting from radiation, wounding, poisoning, infection or
 CC temperature shock. Preferably the flagellin is derived from a Salmonella
 CC species. The present sequence is that of a tryptic peptide of a
 CC Salmonella flagellin, isolated in an example from the invention which
 CC showed that flagellin activates nuclear factor-kappa B.
 XX
 SQ Sequence 17 AA;
 Query Match 30.2%; Score 29; DB 9; Length 17;
 Best Local Similarity 50.0%; Pred. No. 8.4e+02;
 Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18
| : : | | : | |
DB 6 GAVVTDVAVPDK 17

RESULT 86
ID AEB11815 standard; peptide; 17 AA.
XX AEB11815;
XX

AC AEB11815;
XX
XX 25-AUG-2005 (first entry)
DT

XX Salmonella typhimurium flagellin tryptic peptide.
DE

XX
XX Nuclear factor kappa B inducer; flagellin; cytosolic; flagellin; cancer;
KM neoplasm; stress; tranquilizer.
XX

XX Salmonella typhimurium.
OS

XX MO2005056054-A2.
PN

XX 23-JUN-2005.
PD

XX 02-DEC-2004; 2004MO-US040749.
XX

XX 02-DEC-2003; 2003US-0526461P.
PR

XX 02-DEC-2003; 2003US-0526496P.
PR

XX 02-DEC-2004; 2004US-0526460P.
PR

XX (CLEV-) CLEVELAND CLINIC FOUND.
PA

XX Gudkov AV, Stark G, Lu T, Burdelya L;
PI

XX MPI; 2005-458520/46.
DR

XX Protection of a patient from at least one treatment e.g. cancer treatment
PT that trigger apoptosis involves administering a composition comprising an
PT agent, which induces NF-KB.

XX Example 3; Fig 3; 68pp; English.
PS

XX The present invention relates to a method of protecting a patient from
CC one or more treatments that trigger apoptosis by administering a
CC composition comprising an agent that induces nuclear factor kappa B (NF-
CC KB). The agent may be flagellin or transforming growth factor-beta. The
CC treatment may be cancer treatment such as chemotherapy or radiotherapy.
CC The agent may be administered prior to, together with, or after a
CC treatment for the cancer. The invention also provides methods of using
CC the NF-KB inducer agent to: treat a mammal suffering from a
CC constitutively active NF-KB cancer; treat a mammal suffering from damage
CC to normal tissue attributable to treatment of a cancer or to stress; and
CC to modulate cell aging in a mammal. Also provided is a method of
CC screening for an inducer of NF-KB. The cancer treatment includes
CC treatment for breast, colon, lung, kidney, liver cancer etc. The stress
CC includes wounding, poisoning, infection and temperature shock. The
CC treatment modulates cell aging and avoids side effects. In an example
CC from the invention, the NF-KB activating factor in a Salmonella culture
CC broth was identified as flagellin by mass spectrometry. The present
CC sequence is that of an isolated flagellin tryptic peptide.
XX

XX Sequence 17 AA;
SQ

Query Match 30.2%; Score 29; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18
| : : | | : | |
DB 6 GAVVTDVAVPDK 17

RESULT 87
ID AEA52660 standard; peptide; 17 AA.
XX AEA52660;
XX

XX 25-AUG-2005 (first entry)
DT

XX Peptide from Salmonella flagellin, peptide #11.
DE

XX Apoptosis modulation; flagellin; drug screening; p53 modulator;
KM cytosolic; antiemetic; tranquilizer; antimicrobial; antidote;
KM antidiabetic; cancer; stress; radiation sickness; poison intoxication;
XX infection; temperature disorder.
XX

XX Salmonella.
OS

XX MO2005057218-A2.
PN

XX 23-JUN-2005.
PD

XX 02-DEC-2004; 2004MO-US040579.
XX

XX 02-DEC-2003; 2003US-0526460P.
PR

XX 02-DEC-2003; 2003US-0526461P.
PR

XX 02-DEC-2003; 2003US-0526666P.
PR

XX (CLEV-) CLEVELAND CLINIC FOUND.
PA

XX Gudkov AV;
PI

XX MPI; 2005-445220/45.
DR

XX Screening for apoptosis modulator, involves adding suspected modulator to
PT cell-based apoptosis system, separately adding control to cell-based
PT apoptosis system, and comparing level of apoptosis of suspected modulator
PT and control.
XX

XX Disclosure; Fig 3; 68pp; English.
PS

XX The present invention relates to a method of protecting a patient from
CC treatments that trigger apoptosis by administering an agent that induces
CC nuclear factor-kappaB. The agent may be flagellin or TGFbeta. Claimed is
CC a method of screening (M1) for a modulator of apoptosis (I), by adding a
CC suspected modulator to a cell-based apoptosis system; separately adding a
CC control to a cell-based apoptosis system; and comparing the level of
CC apoptosis in steps (a) and (b). The suspected modulator is derived from a
CC mammalian parasite, such as Salmonella, Mycoplasma and Chlamydia. (M1)
CC preferably involves screening for a modulator of NF-kappaB. (M1)
CC transforming growth factor beta (TGFbeta), or modulator of p53.
CC Cytostatic; Antiemetic; Tranquillizer; Vulnerary; Antimicrobial; Antidote;
CC Vasotropic. Apoptosis modulator; NF-kappa B modulator; TGFbeta; modulator
CC ; p53 pathway modulator. (M1) is useful for screening a modulator of
CC apoptosis, preferably modulator of NF-kappaB, TGFbeta or p53. The
CC modulator is useful for treating cancer, which involves administering (I)
CC to a subject in need of treatment, where (I) enhances apoptosis. The
CC treatment is a cancer treatment such as chemotherapy or radiation
CC therapy. (I) is useful for treating a mammal suffering from damage to
CC normal tissue attributable to treatment of a cancer, modulating cell
CC aging in a mammal, and for protecting a patient from conditions that
CC trigger apoptosis, where the condition is stress, radiation, wounding,
CC poisoning, infection and temperature shock. The present sequence is a
CC peptide from flagellin, peptide #11.
XX

XX Sequence 17 AA;
SQ

Query Match 30.2%; Score 29; DB 9; Length 17;
Best Local Similarity 50.0%; Pred. No. 8.4e+02;
Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPGK 18
| : : | | : | |
DB 6 GAVVTDVAVPDK 17

Db 6 GAVVTDVADPK 17

RESULT 88

ABE53031 ID ABE53031 standard; peptide; 17 AA.

XX ABE53031;

AC XX

XX 22-SEP-2005 (first entry)

DT XX

XX Salmonella flagellin peptide #11.

DE XX

XX vulnerability; antimicrobial; cyostatic; tranquilizer; apoptosis inhibition;

KM therapeutic; chemotherapy; radiotherapy; infection; poison intoxication;

KM anticancer; toxicity and intoxication; wound healing; injury; stress;

KM psychiatric disorder; cancer neoplasm; flagellin.

XX

OS Salmonella.

XX

PN NO2005056055-A2.

XX

PD 23-JUN-2005.

XX

PF 02-DEC-2004; 2004MO-US040750.

XX

PR 02-DEC-2003; 2003US-0526460P.

PR 02-DEC-2003; 2003US-0526461P.

PR 02-DEC-2003; 2003US-0526466P.

PR 02-DEC-2003; 2003US-0526666P.

XX

PA (CLEV-) CLEVELAND CLINIC FOUND.

XX

PI Gudkov AV;

XX

DR WPI; 2005-458521/46.

XX

PT Use of a composition (A) comprising an agent which induces necrosis

PT factor (NF) kappa B for protection of mammal from the effects of

PT radiation and for the treatment or condition that trigger apoptosis.

XX

PS Example 3; Fig 3; 67pp; English.

XX

CC The invention describes a method of protecting a mammal from the effects

CC of radiation comprising administration of a composition (A) comprising an

CC agent which induces necrosis factor (NF)-kappa B. (1) is useful for the

CC treatment (such as cancer treatment, chemotherapy, radiation therapy or

CC stress e.g. radiation, wounding, poisoning, infection or temperature

CC shock) or conditions that trigger apoptosis. (1) is useful for the

CC protection of a mammal from the effects of radiation. This is the amino

CC acid sequence of a salmonella flagellin peptide identified from a cell

CC culture extract identifying flagellin as inducing NF-kB DNA binding

CC activity.

XX

XX

SO Sequence 17 AA;

Query Match 30.2%; Score 29; DB 9; Length 17;

Best Local Similarity 50.0%; Pred. No. 8.4e+02;

Matches 6; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAVSPGK 18

DB 6 GAVVTDVADPK 17

RESULT 89

ABU09114 ID ABU09114 standard; peptide; 18 AA.

XX

AC ABU09114;

XX

DT 16-JUN-2003 (first entry)

XX

DE C. elegans Mad peptide containing a SID domain.

XX

XX Mad; SID; msin3 interacting domain; bHLHZip; gene expression;

KM basic region-helix-loop-helix-leucine zipper protein;

KM transcriptional repressor; transcriptional regulator.

XX

OS Caenorhabditis elegans.

XX

XX US6528620-B1.

PN XX

XX

PD 04-MAR-2003.

XX

PF 08-NOV-2000; 2000US-00708906.

XX

PR 08-NOV-1999; 99US-0163960P.

XX

XX (UTAH) UNIV UTAH RES FOUND.

PA

XX

PI Ayer DE, Billin AN;

XX

DR WPI; 2003-370637/35.

XX

PT New chimeric transcriptional regulator useful for regulating

PT transcription of a selected gene in a cell and for gene therapy

PT applications, comprises DNA-binding domain and a msin3A interaction

PT domain.

XX

PS Example 2; Fig 2A; 25pp; English.

XX

CC The invention relates to a chimeric transcriptional regulator comprising

CC a DNA-binding domain and a msin3A interaction domain (SID) capable of

CC binding msin3A. The SID consists of amino acids 8-20 of the human basic

CC region-helix-loop-helix-leucine zipper (bHLHZip) protein, Mad1. The SID

CC appears as ABU09103). Also included are a fusion comprising a SID capable

CC of binding msin3A, where the SID is linked to a DNA-binding molecule and

CC creating a transcriptional regulator, by synthesizing a msin3A-binding

CC molecule and linking the msin3A-binding molecule to a heterologous DNA-

CC binding molecule. The chimeric regulator and fusion protein are useful

CC for repressing transcription of a selected gene in a cell and in the

CC field of functional genomics as analytical tools to modulate the

CC transcription of any gene being studied in either cell or tissue cultures

CC or in whole living organisms. The chimeric regulator, preferably a

CC chimeric repressor, is useful in gene therapy applications. The present

CC sequence is a SID domain containing peptide derived from a basic region-

CC helix-loop-helix-leucine zipper (bHLHZip) protein, used to determine a

CC minimal SID domain peptide sequence

XX

SO Sequence 18 AA;

Query Match 30.2%; Score 29; DB 6; Length 18;

Best Local Similarity 85.7%; Pred. No. 9e+02;

Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYLTAA 13

DB 3 GHULTAA 9

RESULT 90

ADE37053 ID ADE37053 standard; peptide; 19 AA.

XX

AC ADE37053;

XX

DT 29-JAN-2004 (first entry)

XX

XX Nylon suture binding peptide SEQ ID NO:114.

DE

XX interfacial biomaterial; binding agent; biological substrate; cyostatic;

KM T1e2 receptor antagonist; cell culture; biological array;

KM transplant cell; transplant tissue; T1e2 receptor modulation;

KM tumour angiogenesis.

XX

OS Synthetic.
 XX
 PN MO2003072542-A2.
 XX
 PD 04-SEP-2003.
 XX
 PF 20-NOV-2002; 2002MO-US037414.
 XX
 PR 20-NOV-2001; 2001US-0331843P.
 XX
 PA (UYDU-) UNIV DUKE.
 XX
 PI Grinstaff MW, Kenan DJ, Walsh EB, Middleton C;
 XX
 DR WPI; 2003-833266/77.
 XX
 PT New interfacial biomaterial having binding agents that binds a non-
 PT biological and biological substrate, useful in cell culture, in the
 PT preparation of biological arrays, and for diagnostic and therapeutic
 PT interface.
 XX
 PS Example 6; SEQ ID NO 114; 150bp; English.
 XX
 CC The present invention describes an interfacial biomaterial (I) comprising
 CC binding agents, each having a first ligand that specifically binds a
 CC target non-biological substrate and a second ligand that specifically
 CC binds a target biological substrate. The binding agents define an
 CC interface between the target non-biological substrate and the target
 CC biological substrate, or a non-binding domain substantially lacks binding
 CC to a target biological substrate. (I) has cyostatic activity, and can be
 CC used as a Tie2 receptor antagonist. The methods and compositions of the
 CC present invention can be used in cell culture of fibroblasts, endothelial
 CC cells, stem cells, embryonic and newborn tissue cells and osteoblasts, in
 CC the preparation of biological arrays, in the enhancement of an
 CC interaction between biological materials, for coating implants for in
 CC vivo use, for coating donor transplant cells or tissues, for diagnostic
 CC and therapeutic interface, and for modulating Tie2 receptors in tumour
 CC angiogenesis. The present sequence is used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 19 AA;
 XX
 QY
 Db 1 DAFPHGY 8
 3 DFFNRHGY 10
 XX
 RESULT 91
 AAW21835
 ID AAW21835 standard; peptide; 20 AA.
 XX
 AC AAW21835;
 XX
 DT 26-OCT-1997 (first entry)
 XX
 DE KHLN-containing peptide.
 XX
 KW Immunosuppression; major histocompatibility complex class II; MHC;
 KW mixed lymphocyte reaction; allorecognition; cytotoxic T cell;
 KW alloimmunity; autoimmune disease; organ transplant; multiple sclerosis;
 KW rheumatoid arthritis.
 XX
 OS Synthetic.
 XX
 PN WO9710711-A1.
 XX
 PD 27-MAR-1997.
 XX
 PF 23-SEP-1996; 96MO-US015662.

XX
 PR 21-SEP-1995; 95US-0004117P.
 XX
 PA (AUTO-) AUTOIMMUNE INC.
 XX
 PI Sayegh MH, Murphy BT, Carpenter CB;
 XX
 DR WPI; 1997-202534/18.
 XX
 PT Suppression of immune responses with major histocompatibility complex
 PT class II peptide(s) - useful in allo:immunity, e.g. organ
 PT transplantation, and auto:immunity, e.g. in multiple sclerosis or
 PT rheumatoid arthritis.
 XX
 PS Disclosure; Page 13; 55pp; English.
 XX
 CC KHLN-containing peptides (AAW21835-37) derived from the alpha chain of
 CC the class II MHC can be administered to an individual as a means of
 CC suppressing an immune response. The peptides can suppress at least one
 CC (preferably all) of the following: a mixed lymphocyte reaction or other T
 CC -cell allorecognition reaction; generation of cytotoxic T-cells
 CC recognising an alloantigen; lymphocyte proliferation against tissue
 CC antigen; and stimulatory cytokine production by lymphocytes. Immune
 CC responses that can be abated or suppressed include alloimmunity (e.g. in
 CC organ transplantation) and autoimmunity (e.g. in multiple sclerosis or
 CC rheumatoid arthritis). Immune responses can be down-regulated
 CC specifically without the adverse effects of conventional treatments
 XX
 SQ Sequence 20 AA;
 XX
 QY
 Db 3 FEPHGYLTRAAYS 15
 1 FDPQGLRMAYVA 13
 XX
 RESULT 92
 ADX83646
 ID ADX83646 standard; peptide; 16 AA.
 XX
 AC ADX83646;
 XX
 DT 05-MAY-2005 (first entry)
 XX
 DE Rat insulin receptor substrate -1 (449-664) phosphopeptide, seqid:15.
 XX
 KW Insulin receptor substrate protein kinase inhibitor; insulin receptor;
 KW agonist; pharmaceutical; protein kinase C zeta inhibitor;
 KW protein kinase C inhibitor; non-insulin dependent diabetes;
 KW endocrine disease; gastrointestinal disease; metabolic disorder;
 KW antidiabetic; phosphorylation.
 XX
 OS Rattus sp.
 XX
 PN EP1508806-A1.
 XX
 PD 23-FEB-2005.
 XX
 PF 16-AUG-2003; 2003EP-00018517.
 XX
 PR 16-AUG-2003; 2003EP-00018517.
 XX
 PA (AVER) AVENTIS PHARMA DEUT GMBH.
 XX
 PI Temagels N, Eckel J, Metzger S, Sommerfeld M;
 XX
 DR WPI; 2005-174505/19.
 XX
 PT Identifying insulin receptor substrate (IRS) protein kinase inhibitor, by
 PT contacting protein kinase C (PKC)-zeta with IRS peptide having PKC-zeta-

PT Ser-phosphorylation site and putative inhibitor, and measuring
 PT phosphorylation.
 XX
 PS Example 5, SEQ ID NO 15, 50pp; English.
 CC The present invention relates to a method for the identification of
 CC insulin receptor substrate (IRS) protein kinase inhibitors or agonists
 CC which involve contacting protein kinase C (PKC)-zeta with at least one
 CC IRS peptide comprising at least one putative inhibitor and measuring the
 CC the presence of at least one putative inhibitor and measuring the
 CC phosphorylation of the PKC-zeta-Ser-phosphorylation site. The IRS-1
 CC peptides of the invention are useful for producing antibodies against a
 CC PKC-zeta-Ser-phosphorylation site and for preparing a pharmaceutical
 CC composition for the treatment of diabetes type II. The invention also
 CC provides an automated and miniaturized method for screening IRS kinase
 CC protein inhibitors or agonist. The present sequence is rat insulin
 CC receptor substrate (IRS)-1 (449-664) phosphopeptide. This peptide is used
 CC in the identification and functional analysis of IRS-1 serine
 CC phosphorylation sites targeted by PKC.
 CC
 SQ Sequence 16 AA;
 Query Match 29.7%; Score 28.5; DB 9; Length 16;
 Best Local Similarity 40.0%; Pred. No. 9, Se+02;
 Matches 6; Conservative 5; Mismatches 1; Indels 3; Gaps 1;
 QY 4 EPHGYL--TAAVS 15
 DB 2 DPNGYMMSPSMAAS 16
 RESULT 93
 ADO37172
 ID ADO37172 standard; peptide; 6 AA.
 AC ADO37172;
 XX
 DT 29-JUL-2004 (first entry)
 DE Binding partner polypeptide of the invention SEQ ID NO.232.
 XX
 KM polypeptide-tagged collection; capture system; tagged polypeptide;
 KM pharmaceutical; diagnostic.
 OS Synthetic.
 XX
 PN WO2004039962-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034821.
 XX
 PR 30-OCT-2002; 2002US-0422923P.
 PR 30-OCT-2002; 2002US-0423018P.
 XX
 PA (POIN-) POINTILLISTE INC.
 XX
 PI Ault-Riche D, Atkinson B, Geyzen MH;
 XX
 DR WPI; 2004-376185/35.
 XX
 PT Evenly distributing tags among members of a starting library, useful in
 PT developing pharmaceuticals and diagnostics, comprises dividing the
 PT starting library into sub libraries and attaching a tag to members of
 PT each sub library.
 XX
 PS Claim 141; SEQ ID NO 232; 510pp; English.
 CC The invention relates to novel methods for producing polypeptide-tagged
 CC collections and capture systems containing the tagged polypeptides. The
 CC method is useful for evenly distributing tags among members of a starting
 CC library. The system, collection, kits and methods are useful in
 CC developing pharmaceuticals and diagnostics. The present sequence is used

CC in the exemplification of the invention.
 XX
 SQ Sequence 6 AA;
 Query Match 29.2%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PHGY 8
 DB 1 PHGY 4
 RESULT 94
 ADO37180
 ID ADO37180 standard; peptide; 6 AA.
 AC ADO37180;
 XX
 DT 29-JUL-2004 (first entry)
 DE Binding partner polypeptide of the invention SEQ ID NO.240.
 XX
 KM polypeptide-tagged collection; capture system; tagged polypeptide;
 KM pharmaceutical; diagnostic.
 OS Synthetic.
 XX
 PN WO2004039962-A2.
 XX
 PD 13-MAY-2004.
 XX
 PF 30-OCT-2003; 2003WO-US034821.
 XX
 PR 30-OCT-2002; 2002US-0422923P.
 PR 30-OCT-2002; 2002US-0423018P.
 XX
 PA (POIN-) POINTILLISTE INC.
 XX
 PI Ault-Riche D, Atkinson B, Geyzen MH;
 XX
 DR WPI; 2004-376185/35.
 XX
 PT Evenly distributing tags among members of a starting library, useful in
 PT developing pharmaceuticals and diagnostics, comprises dividing the
 PT starting library into sub libraries and attaching a tag to members of
 PT each sub library.
 XX
 PS Claim 141; SEQ ID NO 240; 510pp; English.
 CC The invention relates to novel methods for producing polypeptide-tagged
 CC collections and capture systems containing the tagged polypeptides. The
 CC method is useful for evenly distributing tags among members of a starting
 CC library. The system, collection, kits and methods are useful in
 CC developing pharmaceuticals and diagnostics. The present sequence is used
 CC in the exemplification of the invention.
 CC
 SQ Sequence 6 AA;
 Query Match 29.2%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PHGY 8
 DB 1 PHGY 4
 RESULT 95
 ADO27694
 ID ADO27694 standard; peptide; 6 AA.
 AC ADO27694;

```
XX 12-AUG-2004 (first entry)
DT
XX Capture system related peptide, SEQ ID 232.
DE
XX Capture system.
KW
XX Synthetic.
OS
XX MO2004042019-A2.
PN
XX 21-MAY-2004.
PD
XX 30-OCT-2003; 2003MO-US034693.
PF
XX 30-OCT-2002; 2002US-0422923P.
PR 30-OCT-2002; 2002US-0423018P.
XX
XX (POIN-) POINTILLISTE INC.
PA
XX Ault-Riche D, Atkinson B, Jeeatlis L, Kumble KD, Sperinde G;
PI MPI; 2004-431543/40.
DR
XX
XX Capturing biological particles, by contacting biological particles with
PT capture system comprising addressed loci, addressed collection of
PT polypeptide tagged molecules, capture agents, and polypeptide tag to
PT which capture agent binds.
XX
XX Disclosure; SEQ ID NO 232; 505pp; English.
XX
XX The present invention relates to a method for the capture and analysis of
CC biological particle using a capture system. The method is useful for
CC capturing biological particles such as cells, portions of cells, cell
CC membranes, viruses, viral capsids, viral particles, bacterial cells,
CC subcellular compartments, organelles and micelles, prokaryotic cells,
CC eukaryotic cells, intracellular particles, nuclei, cell membranes, cell
CC membrane fragments, nuclear membranes, nuclear membranes fragments, viral
CC vectors or viral capsids with or without packaged nucleic acid, phage,
CC phage vectors, phage capsids with or without encapsulated nucleotide
CC acid, liposomes and other micellar agents. The biological particles are
CC cells chosen from immune cells, neurons, cancer cells, bacterial cells
CC and infected cells, subcellular compartment, organelles, viral particles
CC or pathogens. The cells are dendritic cells, T cells, or B cells. The
CC method is also useful for identifying molecules that interact with
CC infectious agents, for profiling the surface of a biological particles,
CC for identifying a modulator of an interaction among proteins in the
CC biological particle, for identifying molecules that modulates the
CC trafficking, activity or functional or structural property in the
CC biological particle, and for mapping epitopes of molecules displayed on
CC the surface of a biological particles. The method is also useful for
CC sorting biological particles, for identifying a receptor on the surface
CC of biological particle that transduces a signal from a polypeptide, and
CC for identifying the molecule that interacts with an apically-localized
CC molecule on a biological particle. The present sequence was used to
CC illustrate the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 29.2%; Score 28; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PHGY 8
DB 1 PHGY 4
RESULT 96
AD027702
ID AD027702 standard; peptide; 6 AA.
XX
XX ADO27702;
```

```
XX 12-AUG-2004 (first entry)
DT
XX Capture system related peptide, SEQ ID 240.
DE
XX Capture system.
KW
XX Synthetic.
OS
XX MO2004042019-A2.
PN
XX 21-MAY-2004.
PD
XX 30-OCT-2003; 2003MO-US034693.
PF
XX 30-OCT-2002; 2002US-0422923P.
PR 30-OCT-2002; 2002US-0423018P.
XX
XX (POIN-) POINTILLISTE INC.
PA
XX Ault-Riche D, Atkinson B, Jeeatlis L, Kumble KD, Sperinde G;
PI MPI; 2004-431543/40.
DR
XX
XX Capturing biological particles, by contacting biological particles with
PT capture system comprising addressed loci, addressed collection of
PT polypeptide tagged molecules, capture agents, and polypeptide tag to
PT which capture agent binds.
XX
XX Disclosure; SEQ ID NO 240; 505pp; English.
XX
XX The present invention relates to a method for the capture and analysis of
CC biological particle using a capture system. The method is useful for
CC capturing biological particles such as cells, portions of cells, cell
CC membranes, viruses, viral capsids, viral particles, bacterial cells,
CC subcellular compartments, organelles and micelles, prokaryotic cells,
CC eukaryotic cells, intracellular particles, nuclei, cell membranes, cell
CC membrane fragments, nuclear membranes, nuclear membranes fragments, viral
CC vectors or viral capsids with or without packaged nucleic acid, phage,
CC phage vectors, phage capsids with or without encapsulated nucleotide
CC acid, liposomes and other micellar agents. The biological particles are
CC cells chosen from immune cells, neurons, cancer cells, bacterial cells
CC and infected cells, subcellular compartment, organelles, viral particles
CC or pathogens. The cells are dendritic cells, T cells, or B cells. The
CC method is also useful for identifying molecules that interact with
CC infectious agents, for profiling the surface of a biological particles,
CC for identifying a modulator of an interaction among proteins in the
CC biological particle, for identifying molecules that modulates the
CC trafficking, activity or functional or structural property in the
CC biological particle, and for mapping epitopes of molecules displayed on
CC the surface of a biological particles. The method is also useful for
CC sorting biological particles, for identifying a receptor on the surface
CC of biological particle that transduces a signal from a polypeptide, and
CC for identifying the molecule that interacts with an apically-localized
CC molecule on a biological particle. The present sequence was used to
CC illustrate the invention.
XX
XX Sequence 6 AA;
SQ
Query Match 29.2%; Score 28; DB 8; Length 6;
Best Local Similarity 100.0%; Pred. No. 2e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 PHGY 8
DB 1 PHGY 4
RESULT 97
ADR49879
ID ADR49879 standard; peptide; 6 AA.
XX
XX ADR49879;
```

XX 18-NOV-2004 (first entry)
 XX 6-mer peptide epitope works as a highly specific capture agent Seq 240.
 DE self-assembly array; capture agent; epitope; binding partner.
 XX Synthetic.
 OS
 XX WO2004071641-A2.
 PN
 XX 26-AUG-2004.
 PD
 XX 30-OCT-2003; 2003WO-US034747.
 PF
 XX 10-FEB-2003; 2003US-0446687P.
 PR
 XX (POIN-) POINTILLISTE INC.
 PA (AULT/) AULT-RICHE D.
 PA (KUMB/) KUMBLE K D.
 PA (SCHU/) SCHULZ R.
 PA (SCHU/) SCHULZ K.
 XX
 XX Ault-Riche D, Kumble KD, Schulz R, Schulz K;
 PI WPI; 2004-635071/61.
 DR
 XX Self-assembled array for monitoring interaction of molecules, comprising
 PT addressable array of capture agents having predetermined binding partners
 PT and conjugates comprising biological particle and/or molecule linked to
 PT binding partners.
 XX
 XX Disclosure; SEQ ID NO 240; 443pp; English.
 PS
 XX This invention relates to novel self-assembly arrays that each comprises
 CC an addressable collection of capture agents that have predetermined
 CC binding partners, as well as reagents for the covalent conjugation of the
 CC binding partners to molecules for display in the array. Specifically, it
 CC refers to the production of a flexible experimental surface, which can be
 CC adapted for use with almost any analytical system. The present invention
 CC describes apparatus useful for monitoring an interaction of an exogenous
 CC molecule with a capture agent of the array both in the presence and
 CC absence of candidate compounds, identifying molecules that modulate
 CC trafficking in biological particles or modulate activity, functional or
 CC structural properties of the biological particle. As such, it can be used
 CC for elucidating biological pathways and their reactions that occur either
 CC simultaneously or sequentially, disease processes, inhibitors and
 CC enhancers of a molecular system or for understanding receptor-signal
 CC recognition. In particular, it enables assaying one or more biological
 CC samples having one or more targets per sample on a single array, such
 CC that it is cost effective and specific. This peptide sequence is an
 CC exemplary 6-mer peptide epitope that provides a highly specific capture
 CC agent of the invention.
 CC
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 29.2%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PHGY 8
 DB 1 PHGY 4
 Db
 RESULT 98
 ADR49871
 ID ADR49871 standard; peptide; 6 AA.
 XX
 AC ADR49871;
 XX
 DT 18-NOV-2004 (first entry)
 XX

DE 6-mer peptide epitope works as a highly specific capture agent Seq 232.
 XX
 XX self-assembly array; capture agent; epitope; binding partner.
 KM
 XX Synthetic.
 OS
 XX WO2004071641-A2.
 PN
 XX 26-AUG-2004.
 PD
 XX 30-OCT-2003; 2003WO-US034747.
 PF
 XX 10-FEB-2003; 2003US-0446687P.
 PR
 XX (POIN-) POINTILLISTE INC.
 PA (AULT/) AULT-RICHE D.
 PA (KUMB/) KUMBLE K D.
 PA (SCHU/) SCHULZ R.
 PA (SCHU/) SCHULZ K.
 XX
 XX Ault-Riche D, Kumble KD, Schulz R, Schulz K;
 PI WPI; 2004-635071/61.
 DR
 XX Self-assembled array for monitoring interaction of molecules, comprising
 PT addressable array of capture agents having predetermined binding partners
 PT and conjugates comprising biological particle and/or molecule linked to
 PT binding partners.
 XX
 XX Disclosure; SEQ ID NO 232; 443pp; English.
 PS
 XX This invention relates to novel self-assembly arrays that each comprises
 CC an addressable collection of capture agents that have predetermined
 CC binding partners, as well as reagents for the covalent conjugation of the
 CC binding partners to molecules for display in the array. Specifically, it
 CC refers to the production of a flexible experimental surface, which can be
 CC adapted for use with almost any analytical system. The present invention
 CC describes apparatus useful for monitoring an interaction of an exogenous
 CC molecule with a capture agent of the array both in the presence and
 CC absence of candidate compounds, identifying molecules that modulate
 CC trafficking in biological particles or modulate activity, functional or
 CC structural properties of the biological particle. As such, it can be used
 CC for elucidating biological pathways and their reactions that occur either
 CC simultaneously or sequentially, disease processes, inhibitors and
 CC enhancers of a molecular system or for understanding receptor-signal
 CC recognition. In particular, it enables assaying one or more biological
 CC samples having one or more targets per sample on a single array, such
 CC that it is cost effective and specific. This peptide sequence is an
 CC exemplary 6-mer peptide epitope that provides a highly specific capture
 CC agent of the invention.
 CC
 XX
 XX Sequence 6 AA;
 SQ
 Query Match 29.2%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PHGY 8
 DB 1 PHGY 4
 Db
 RESULT 99
 ADS95517
 ID ADS95517 standard; peptide; 6 AA.
 XX
 AC ADS95517;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DB Tagged polypeptide-associated peptide #46.
 XX
 KM Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.

XX Synthetic.
 OS
 XX
 PN US2004209282-A1.
 PD
 XX 21-OCT-2004.
 PF 30-OCT-2003; 2003US-00699088.
 PR 30-OCT-2002; 2002US-0422923P.
 PR 30-OCT-2002; 2002US-0423018P.
 PA (AULT/) AULT-RICHE D.
 PA (ATKI/) ATKINSON B.
 PI Ault-Riche D, Atkinson B;
 DR WPI; 2004-756825/74.
 XX
 PT Evenly distributing tags among members of starting library by dividing
 PT starting library into sublibraries, attaching tag to members of
 PT sublibrary, mixing tagged sublibraries and splitting mixed library into
 PT array libraries.
 PS Disclosure; SEQ ID NO 232; 293pp; English.
 XX
 XX The invention relates to evenly distributing tags (e.g. epitopes) or
 CC nucleic acid molecules encoding polypeptide tags among members of a
 CC starting library, involving optionally adjusting the diversity of a
 CC starting library so that the diversity is within an order of magnitude of
 CC the number of molecules in the library, dividing the starting library
 CC into n sublibraries designated 1-n, where n is equal to or less than the
 CC number of unique tags (where each unique tag specifically binds to a
 CC different capture agent), attaching a tag to several members of each
 CC sublibrary to produce n tagged sublibraries containing tagged members
 CC (where each member has the same tag, and the tag is unique to each
 CC sublibrary), mixing some or all of the tagged sublibraries to produce a
 CC mixed library (where the number of tagged molecules added from each
 CC sublibrary is the same), and splitting the mixed library into q array
 CC libraries, where q is from 1 up to a predetermined number of arrays. Also
 CC included are a collection of tagged molecules produced by the method, a
 CC capture system comprising the tagged polypeptides and an addressable
 CC collection of capture agent (where each locus in the collection contains
 CC capture agents that specifically bind to the same tag, and the tagged
 CC molecules are specifically bound to capture agents), capturing molecules
 CC (involving contacting a capture system with molecules under conditions,
 CC where molecules bind to the capture system, and the capture system
 CC comprises several of addressed loci with an addressed collection of
 CC polypeptide-tagged molecules bound to addressed capture agents at each
 CC locus, the capture agents at each locus bind to the same polypeptide tag,
 CC the polypeptide tag to which the capture agent binds is different among
 CC the loci, each locus in capture system contains a several of different
 CC molecules, each with the same tag bound to the capture agents, and the
 CC polypeptide tags are evenly distributed among the tagged molecules such
 CC that the diversity of tagged molecules at each locus in the capture
 CC system is within one order of magnitude), sorting molecules or reducing
 CC their diversity, and reducing the diversity of a collection of molecules.
 CC The starting library encodes antibodies (or their fragments or single-
 CC chain antibody fragments (ScrVs)) or is comprised of antibodies (or their
 CC fragment), where the antibodies or their fragments specifically bind to
 CC antigens. The methods are useful for evenly distributing tags among
 CC members of starting library, for identifying modulators of interactions
 CC between capture systems and molecules (which involves adding/exposing a
 CC test compound to the capture system to a condition before, during or
 CC after contacting the capture system with molecules or before, during or
 CC after contacting the capture agents with the tagged molecules, and
 CC identifying a change in an interaction of the molecules with the capture
 CC system or tagged molecules with the capture agents to identify a test
 CC compound that modulates the interaction between the molecules and the
 CC capture system or between tagged molecules and capture agents. The change
 CC is assessed by detecting a change in binding pattern or a physical or
 CC chemical change in the bound molecules or a conformational change in the
 CC bound molecules and/or tagged molecules). The present sequence is a

CC peptide included in the sequence listing but not mentioned anywhere else
 CC in the specification.
 CC
 XX Sequence 6 AA;
 SQ
 Query Match 29.2%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 PHGY 8
 |||||
 DB 1 PHGY 4
 RESULT 100
 ADS95525
 ID ADS95525 standard; peptide; 6 AA.
 XX
 AC ADS95525;
 XX
 DT 13-JAN-2005 (first entry)
 XX
 DE Tagged polypeptide-associated peptide #54.
 XX
 KM Peptide tag; epitope; antibody; single-chain antibody fragment; ScFv.
 XX
 OS Synthetic.
 XX
 PN US2004209282-A1.
 PD
 XX 21-OCT-2004.
 PF 30-OCT-2003; 2003US-00699088.
 PR 30-OCT-2002; 2002US-0422923P.
 PR 30-OCT-2002; 2002US-0423018P.
 PA (AULT/) AULT-RICHE D.
 PA (ATKI/) ATKINSON B.
 PI Ault-Riche D, Atkinson B;
 DR WPI; 2004-756825/74.
 XX
 PT Evenly distributing tags among members of starting library by dividing
 PT starting library into sublibraries, attaching tag to members of
 PT sublibrary, mixing tagged sublibraries and splitting mixed library into
 PT array libraries.
 PS Disclosure; SEQ ID NO 240; 293pp; English.
 XX
 XX The invention relates to evenly distributing tags (e.g. epitopes) or
 CC nucleic acid molecules encoding polypeptide tags among members of a
 CC starting library, involving optionally adjusting the diversity of a
 CC starting library so that the diversity is within an order of magnitude of
 CC the number of molecules in the library, dividing the starting library
 CC into n sublibraries designated 1-n, where n is equal to or less than the
 CC number of unique tags (where each unique tag specifically binds to a
 CC different capture agent), attaching a tag to several members of each
 CC sublibrary to produce n tagged sublibraries containing tagged members
 CC (where each member has the same tag, and the tag is unique to each
 CC sublibrary), mixing some or all of the tagged sublibraries to produce a
 CC mixed library (where the number of tagged molecules added from each
 CC sublibrary is the same), and splitting the mixed library into q array
 CC libraries, where q is from 1 up to a predetermined number of arrays. Also
 CC included are a collection of tagged molecules produced by the method, a
 CC capture system comprising the tagged polypeptides and an addressable
 CC collection of capture agent (where each locus in the collection contains
 CC capture agents that specifically bind to the same tag, and the tagged
 CC molecules are specifically bound to capture agents), capturing molecules
 CC (involving contacting a capture system with molecules under conditions,
 CC where molecules bind to the capture system, and the capture system
 CC comprises several of addressed loci with an addressed collection of

CC polypeptide-tagged molecules bound to addressed capture agents at each
 CC locus, the capture agents at each locus bind to the same polypeptide tag,
 CC the polypeptide tag to which the capture agent binds is different among
 CC the loci, each locus in capture system contains a several of different
 CC molecules, each with the same tag bound to the capture agents, and the
 CC polypeptide tags are evenly distributed among the tagged molecules such
 CC that the diversity of tagged molecules at each locus in the capture
 CC system is within one order of magnitude), sorting molecules or reducing
 CC their diversity, and reducing the diversity of a collection of molecules.
 CC The starting library encodes antibodies (or their fragments or single-
 CC chain antibody fragments (ScFvs)) or is comprised of antibodies (or their
 CC fragments), where the antibodies or their fragments specifically bind to
 CC antigens. The methods are useful for evenly distributing tags among
 CC members of starting library, for identifying modulators of interactions
 CC between capture systems and molecules (which involves adding/exposing a
 CC test compound to the capture system to a condition before, during or
 CC after contacting the capture system with molecules or before, during or
 CC identifying a change in an interaction of the molecules with the capture
 CC system or tagged molecules with the capture agents to identify a test
 CC compound that modulates the interaction between the molecules and the
 CC capture system or between tagged molecules and capture agents. The change
 CC is assessed by detecting a change in binding pattern or a physical or
 CC chemical change in the bound molecules or a conformational change in the
 CC bound molecules and/or tagged molecules). The present sequence is a
 CC peptide included in the sequence listing but not mentioned anywhere else
 CC in the specification.

XX
 SQ Sequence 6 AA;

Query Match 29.2%; Score 28; DB 8; Length 6;
 Best Local Similarity 100.0%; Pred. No. 2e+06;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 PHGY 8
 ||||
 Db 1 PHGY 4

Search completed: January 20, 2006, 19:05:24
 Job time : 72.0192 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:58:05 ; Search time 18.8654 Seconds
(without alignments)
78.883 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DAFPHGYLTAAVSPK 18

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 223517

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Issued Patente AA: *
2: /cgn2_6/ptodata/1/1aa/5 COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6 COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/7 COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/8 COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfile1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	96	100.0	18	2	US-09-292-225-6	Sequence 6, Appl1
2	33	34.4	12	2	US-09-560-915-8	Sequence 8, Appl1
3	33	34.4	12	2	US-09-932-161-8	Sequence 8, Appl1
4	33	34.4	18	2	US-09-171-646-4	Sequence 4, Appl1
5	32	33.3	12	2	US-09-560-915-9	Sequence 9, Appl1
6	32	33.3	12	2	US-09-932-161-9	Sequence 9, Appl1
7	32	33.3	16	2	US-09-171-705-26	Sequence 26, Appl1
8	32	33.3	16	2	US-09-657-757-26	Sequence 26, Appl1
9	31	32.3	9	2	US-09-870-0898-13	Sequence 13, Appl1
10	31	32.3	19	2	US-08-885-707-17	Sequence 17, Appl1
11	31	32.3	19	2	US-09-383-062-63	Sequence 63, Appl1
12	31	32.3	19	2	US-09-839-884-63	Sequence 63, Appl1
13	30	31.2	10	2	US-08-822-586-11	Sequence 11, Appl1
14	30	31.2	11	2	US-08-766-596A-66	Sequence 66, Appl1
15	30	31.2	12	2	US-09-560-915-11	Sequence 11, Appl1
16	30	31.2	12	2	US-09-932-161-11	Sequence 11, Appl1
17	29	30.2	11	2	US-09-716-964B-210	Sequence 210, Appl1
18	29	30.2	12	2	US-09-560-915-4	Sequence 4, Appl1
19	29	30.2	12	2	US-09-560-915-12	Sequence 12, Appl1
20	29	30.2	12	2	US-09-932-161-4	Sequence 4, Appl1
21	29	30.2	12	2	US-09-932-161-12	Sequence 12, Appl1
22	29	30.2	16	2	US-09-747-287A-205	Sequence 205, Appl1
23	29	30.2	18	2	US-09-708-906-12	Sequence 12, Appl1
24	29	30.2	20	6	5258287-19	Patent No. 5258287
25	29	30.2	20	6	5258287-22	Patent No. 5258287
26	28	29.2	11	2	US-08-875-309-13	Sequence 13, Appl1
27	28	29.2	11	4	PCT-US96-00310-13	Sequence 13, Appl1

28	28	29.2	13	2	US-08-875-309-14	Sequence 14, App1
29	28	29.2	13	4	PCT-US96-00310-14	Sequence 14, App1
30	28	29.2	15	1	US-08-190-802A-17	Sequence 17, App1
31	28	29.2	15	2	US-08-875-309-17	Sequence 17, App1
32	28	29.2	15	2	US-08-477-346-17	Sequence 17, App1
33	28	29.2	15	2	US-08-473-089-17	Sequence 17, App1
34	28	29.2	15	2	US-09-009-953-176	Sequence 176, App
35	28	29.2	15	2	US-09-009-953-183	Sequence 183, App
36	28	29.2	15	2	US-08-487-072A-17	Sequence 17, App1
37	28	29.2	18	2	US-08-469-318-188	Sequence 188, App
38	28	29.2	18	2	US-08-469-318-189	Sequence 189, App
39	28	29.2	18	2	US-08-468-609A-188	Sequence 188, App
40	28	29.2	18	2	US-08-468-609A-189	Sequence 189, App
41	28	29.2	18	2	US-08-446-872A-188	Sequence 188, App
42	28	29.2	18	2	US-08-446-872A-189	Sequence 189, App
43	28	29.2	18	2	US-08-762-227A-188	Sequence 188, App
44	28	29.2	18	2	US-08-762-227A-189	Sequence 189, App
45	28	29.2	18	4	PCT-US95-01185-188	Sequence 188, App
46	28	29.2	18	4	PCT-US95-01185-189	Sequence 189, App
47	28	29.2	20	1	US-08-416-950-7	Sequence 7, App1
48	28	29.2	20	1	US-08-464-235-18	Sequence 18, App1
49	28	29.2	20	1	US-08-468-279-35	Sequence 35, App1
50	28	29.2	20	1	US-08-469-830-7	Sequence 7, App1
51	28	29.2	20	2	US-08-463-486-18	Sequence 18, App1
52	28	29.2	20	2	US-08-464-496-11	Sequence 11, App1
53	28	29.2	20	2	US-08-197-484-101	Sequence 101, App
54	28	29.2	20	2	US-08-591-502B-7	Sequence 7, App1
55	28	29.2	20	2	US-09-790-497A-446	Sequence 446, App
56	28	29.2	20	2	US-09-576-824A-446	Sequence 446, App
57	28	29.2	20	2	US-09-325-917A-4	Sequence 4, App1
58	28	29.2	20	2	US-09-863-054-18	Sequence 18, App1
59	28	29.2	20	4	PCT-US92-07218-11	Sequence 11, App1
60	28	29.2	20	4	PCT-US94-02195-11	Sequence 11, App1
61	28	29.2	20	4	PCT-US95-02121-101	Sequence 101, App
62	27.5	28.6	11	2	US-08-652-877-52	Sequence 52, App1
63	27.5	28.6	11	2	US-08-476-515A-52	Sequence 52, App1
64	27.5	28.6	17	4	US-08-408-604A-27	Sequence 27, App1
65	27.5	28.6	17	4	PCT-US93-09626-27	Sequence 27, App1
66	27.5	28.6	20	2	US-08-256-747C-15	Sequence 15, App1
67	27.5	28.6	20	2	US-08-834-130A-15	Sequence 15, App1
68	27.5	28.6	20	6	5164481-6	Patent No. 5164481
69	27	28.1	10	2	US-08-822-586-19	Sequence 19, App1
70	27	28.1	10	2	US-08-822-586-23	Sequence 23, App1
71	27	28.1	10	2	US-08-822-586-27	Sequence 27, App1
72	27	28.1	11	2	US-08-802-981-161	Sequence 161, App
73	27	28.1	11	2	US-09-747-287A-215	Sequence 215, App
74	27	28.1	11	2	US-09-394-019C-125	Sequence 125, App
75	27	28.1	12	2	US-08-802-981-162	Sequence 162, App
76	27	28.1	12	2	US-09-929-265-13	Sequence 13, App
77	27	28.1	12	2	US-09-747-287A-216	Sequence 216, App
78	27	28.1	12	2	US-09-394-019C-170	Sequence 170, App
79	27	28.1	13	2	US-08-802-981-42	Sequence 42, App1
80	27	28.1	13	2	US-08-802-981-46	Sequence 46, App1
81	27	28.1	13	2	US-08-802-981-45	Sequence 45, App1
82	27	28.1	13	2	US-08-802-981-51	Sequence 51, App1
83	27	28.1	13	2	US-08-802-981-170	Sequence 170, App
84	27	28.1	13	2	US-08-802-981-171	Sequence 171, App
85	27	28.1	13	2	US-08-802-981-175	Sequence 175, App
86	27	28.1	13	2	US-08-802-981-176	Sequence 176, App
87	27	28.1	13	2	US-09-747-287A-40	Sequence 40, App1
88	27	28.1	13	2	US-09-747-287A-41	Sequence 41, App1
89	27	28.1	13	2	US-09-747-287A-44	Sequence 44, App1
90	27	28.1	13	2	US-09-747-287A-50	Sequence 50, App1
91	27	28.1	13	2	US-09-747-287A-224	Sequence 224, App
92	27	28.1	13	2	US-09-747-287A-225	Sequence 225, App
93	27	28.1	13	2	US-09-747-287A-229	Sequence 229, App
94	27	28.1	13	2	US-09-747-287A-230	Sequence 230, App
95	27	28.1	13	2	US-09-394-019C-5	Sequence 5, App1
96	27	28.1	13	2	US-09-394-019C-6	Sequence 6, App1
97	27	28.1	13	2	US-09-394-019C-9	Sequence 9, App1
98	27	28.1	13	2	US-09-394-019C-15	Sequence 15, App1
99	27	28.1	13	2	US-09-394-019C-178	Sequence 178, App
100	27	28.1	13	2	US-09-394-019C-179	Sequence 179, App

ALIGNMENTS

RESULT 1

US-09-292-225-6
Sequence 6, Application US/09292225
Patent No. 6455686
GENERAL INFORMATION:
APPLICANT: McCall, Catherine A.
APPLICANT: Hunter, Shirley Wu
APPLICANT: Weber, Eric R.
TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
TITLE OF INVENTION: AND USUS THEROP
FILE REFERENCE: AL-2-C3
CURRENT APPLICATION NUMBER: US/09/292,225
CURRENT FILING DATE: 1999-04-15
EARLIER APPLICATION NUMBER: 60/098,909
EARLIER FILING DATE: 1998-09-02
EARLIER APPLICATION NUMBER: 60/085,295
EARLIER FILING DATE: 1998-05-13
EARLIER APPLICATION NUMBER: 60/098,565
EARLIER FILING DATE: 1998-04-17
EARLIER APPLICATION NUMBER: 09/062,013
EARLIER FILING DATE: 1998-04-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 6
LENGTH: 18
TYPE: PRT
ORGANISM: Dermatophagoides farinae
US-09-292-225-6

Query Match 100.0%; Score 96; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e-10;

Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 DAEPHGYLTAIVSPGK 18

DB 1 DAEPHGYLTAIVSPGK 18

RESULT 2

US-09-560-915-8
Sequence 8, Application US/09560915
Patent No. 6383764
GENERAL INFORMATION:
APPLICANT: Clivell, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (P-RP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/09/560,915
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human GPR10 variant
US-09-560-915-8

Query Match 34.4%; Score 33; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTAIV 14

DB 1 PHGYLTAIV 10

RESULT 3

US-09-932-161-8
Sequence 8, Application US/09932161
Patent No. 6884596
GENERAL INFORMATION:
APPLICANT: Clivell, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Promoting Wakefulness and Sleep
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 8
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human GPR10 variant
US-09-932-161-8

Query Match 34.4%; Score 33; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 28;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTAIV 14

DB 1 PHGYLTAIV 10

RESULT 4

US-09-171-646-4
Sequence 4, Application US/09171646A
Patent No. 6235516
GENERAL INFORMATION:
APPLICANT: Ghisalba, Oreste
APPLICANT: Kittelmann, Matthias
APPLICANT: Laumen, Kurt
APPLICANT: Walser-Volken, Paula
TITLE OF INVENTION: Biocatalysts With Amine Acylase Activity
FILE REFERENCE: 4-20825/A/PCT
CURRENT APPLICATION NUMBER: US/09/171,646A
CURRENT FILING DATE: 1998-11-12
EARLIER APPLICATION NUMBER: 96810266.5
EARLIER FILING DATE: 1996-04-25
NUMBER OF SEQ ID NOS: 4
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 18
TYPE: PRT
ORGANISM: Arthrobacter aureus
FEATURE:
NAME/KEY: UNSURE
LOCATION: (4...)
OTHER INFORMATION: amino acid is uncertain
NAME/KEY: UNSURE
LOCATION: (6...)
OTHER INFORMATION: amino acid is uncertain
FEATURE:
NAME/KEY: UNSURE
LOCATION: (9...)
OTHER INFORMATION: amino acid is unknown
US-09-171-646-4

Query Match 34.4%; Score 33; DB 2; Length 18;
Best Local Similarity 41.2%; Pred. No. 46;
Matches 7; Conservative 3; Mismatches 7; Indels 0; Gaps 0;


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QY      2 AFEPHGYLLTAAVSPGK 18
      |  ||  |  ::||:
Db      2 AIRIRGYXDTPSVAPGK 18

```

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RESULT 5
US-09-560-915-9
: Sequence 9, Application US/09560915
: Patent No. 6383764
: GENERAL INFORMATION:
: APPLICANT: Civeili, Oliver
: APPLICANT: Lin, Steven
: TITLE OF INVENTION: Therapeutic Compositions and Methods
: TITLE OF INVENTION: Relating to Prolactin Releasing Peptide (PRRP)
: FILE REFERENCE: P-UC 354
: CURRENT APPLICATION NUMBER: US/09/560,915
: CURRENT FILING DATE: 2000-04-28
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURE:
: OTHER INFORMATION: human GPR10 variant
US-09-560-915-9

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Query Match	33.3%	Score 32	DB 2	Length 12
Best Local Similarity	60.0%	Pred. No. 42		
Matches 6, Conservative	1	Mismatches 3	Indels 0	Gaps 0

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QY      5 PHGYLLTAAY 14
          ||| : |||
Db      1 PHGQNTVAAY 10

```

```

RESULT 6
US-09-932-161-9
: Sequence 9, Application US/09932161
: Patent No. 6884596
: GENERAL INFORMATION:
: APPLICANT: Civeili, Oliver
: APPLICANT: Lih, Steven
: TITLE OF INVENTION: Screening and Therapeutic Methods For
: TITLE OF INVENTION: Promoting Wakefulness and Sleep
: FILE REFERENCE: P-UC 4679
: CURRENT FILING DATE: 2001-08-17/932,161
: CURRENT FILING DATE: 2001-08-17/932,161
: PRIOR APPLICATION NUMBER: US 09/560,915
: PRIOR FILING DATE: 2000-04-28
: NUMBER OF SEQ ID NOS: 24
: SOFTWARE: FastSeq for Windows Version 4.0
: SEQ ID NO 9
: LENGTH: 12
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: human GFR10 variant
US-09-932-161-9

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Query Match	33.3%	Score 32;	DB 2;	Length 12;
Best Local Similarity	60.0%	Pred.No. 42;		
Matches	6;	Conservative	1;	Mismatches 3;
				Indels 0;
				Gaps 0;

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Qy      5 PHGYLLTAAY 14
         ||| : |||
Db      1 PHGQNTVAV 10

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RESULT 7
US-09-171-705-26
; Sequence 26, Application US/09171705
; Patent No. 6184204

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: GENERAL INFORMATION:
: APPLICANT: BOOTS, ANNA M.H.
: APPLICANT: VERHEIDEN, GILBERTUS F.M.
: TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
: TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
: PTL REFERENCE: O/96198 US
: CURRENT APPLICATION NUMBER: US/09/171,705
: CURRENT FILING DATE: 1999-02-09
: NUMBER OF SEQ ID NOS: 78
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 26
: LENGTH: 16
: TYPE: PRT
: ORGANISM: Artificial Sequence
: FEATURES:
: OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
: OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
US-09-171-705-26

```

Query Match	33.3%	Score 32;	DB 2;	Length 16;
Best Local Similarity	70.0%	Pred. No. 59;		
Matches 7;	Conservative 2;	Mismatches 1;	Indels 0;	Gaps 0

Qy	9 LITAAVSPCK 16
	: :
Db	2 LITSAALSACK 11

RESULT 8
 US-09-657-757-26
 : Sequence 26, Application US/09657757
 : Patent No. 6881824
 : GENERAL INFORMATION:
 : APPLICANT: BOOTS, ANNA M.H.
 : APPLICANT: VERHEIJDEN, GILBERTUS F.M.
 : TITLE OF INVENTION: NOVEL PEPTIDES SUITABLE FOR USE IN ANTIGEN SPECIFIC
 : TITLE OF INVENTION: IMMUNOSUPPRESSIVE THERAPY
 : FILE REFERENCE: C/96198 US
 : CURRENT APPLICATION NUMBER: US/09/657,757
 : CURRENT FILING DATE: 2000-09-08
 : PRIOR APPLICATION NUMBER: US/09/171,705
 : PRIOR FILING DATE: 1998-10-23
 : NUMBER OF SEQ. ID NOS: 78
 : SOFTWARE: PatentIn Ver. 2.0
 : SEQ ID NO 26
 :
 : LENGTH: 16
 :
 : TYPE: PRT
 : ORGANISM: Artificial Sequence
 : FEATURE:
 : OTHER INFORMATION: Description of Artificial Sequence: DERIVED FROM
 : OTHER INFORMATION: SEQUENCE OF HUMAN CARTILAGE (HC) -39 PROTEIN
 : US-09-657-757-26

Query Match	33.3%	Score 32	DB 2	Length 16
Best Local Similarity	70.0%	Pred. No. 59		
Matches	7	Conservative	2	Mismatches 0
				Gaps 0

```
Qy      9 LTTAAVSPGK 18
          ||::||:|
Db      2 LLSAALSAGK 11
```

RESULT 9
 US-09-870-089B-13
 Sequence 13, Application US/09870089B
 Patent No. 6737062
 GENERAL INFORMATION:
 APPLICANT: Charles A. Nicolette
 TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
 FILE REFERENCE: 68126881209900
 CURRENT APPLICATION NUMBER: US/09/870,089B
 CURRENT FILING DATE: 2001-05-30
 NUMBER OF SEQ ID NOS: 14

Best Local Similarity 54.5%; Pred. No. 1.1e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 1 DAFPHGYLT 11
Db 7 DAEQPHQFV 17

RESULT 13

US-08-822-586-11
Sequence 11, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
APPLICANT: AMALIO TELENTE
TITLE OF INVENTION: AN ENCBAB OPERON OF MYCOBACTERIA AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822.586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal fragment
US-08-822-586-11

Query Match 31.2%; Score 30; DB 2; Length 10;
Best Local Similarity 85.7%; Pred. No. 75;
Matches 6; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GYLTTAA 13
Db 4 GYLTTVA 10

RESULT 14

US-08-766-596A-66
Sequence 66, Application US/08766596A
Patent No. 6462171
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
APPLICANT: BAUMANN, Marc
APPLICANT: FAUGNION, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
TITLE OF INVENTION: COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES

TITLE OF INVENTION: ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
TITLE OF INVENTION: DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-766-596A-66

Query Match 31.2%; Score 30; DB 2; Length 11;
Best Local Similarity 63.6%; Pred. No. 84;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 7 GYLTTAAVSFG 17
Db 1 GYLTTVAAVFRG 11

RESULT 15
US-09-560-915-11
Sequence 11, Application US/09560915
Patent No. 638764
GENERAL INFORMATION:
APPLICANT: CIVELLI, Olivier
APPLICANT: Lhn, Steven
TITLE OF INVENTION: Therapeutic Compositions and Methods
TITLE OF INVENTION: Relating To Proinactin Releasing Peptide (PrRrP)
FILE REFERENCE: P-UC 3534
CURRENT APPLICATION NUMBER: US/09/560,915
CURRENT FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human GPR10 variant
US-09-560-915-11

Query Match 31.2%; Score 30; DB 2; Length 12;

Best Local Similarity 45.5%; Pred. No. 93;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAVS 15
Db 1 PHQNMNTVSV 11

RESULT 15

US-09-932-161-11
; Sequence 11, Application US/09932161
; Patent No. 6884596
; GENERAL INFORMATION:
; APPLICANT: Civeilli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; PRIOR FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 11
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-932-161-11

Query Match 31.2%; Score 30; DB 2; Length 12;
Best Local Similarity 45.5%; Pred. No. 93;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAVS 15
Db 1 PHQNMNTVSV 11

RESULT 17

US-09-716-964B-210
; Sequence 210, Application US/09716964B
; Patent No. 6897053
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurleva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kiriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/09/716,964B
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-09-716-964B-210

Query Match 30.2%; Score 29; DB 2; Length 11;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYYL 10
Db 7 HGYYL 11

RESULT 18

US-09-560-915-4
; Sequence 4, Application US/09560915
; Patent No. 6383764
; GENERAL INFORMATION:
; APPLICANT: Civeilli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-560-915-4

Query Match 30.2%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14
Db 1 PHQNMNTVSV 10

RESULT 19

US-09-560-915-12
; Sequence 12, Application US/09560915
; Patent No. 6383764
; GENERAL INFORMATION:
; APPLICANT: Civeilli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating To Prolactin Releasing Peptide (PRRP)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-560-915-12

Query Match 30.2%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14
Db 1 PHQNMNTVSV 10

RESULT 20

US-09-932-161-4
; Sequence 4, Application US/09932161

```
/ Patent No. 6884596
/ GENERAL INFORMATION:
/ APPLICANT: Civeilli, Olivier
/ APPLICANT: Lin, Steven
/ TITLE OF INVENTION: Screening and Therapeutic Methods For
/ FILE REFERENCE: P-UC 4679
/ CURRENT APPLICATION NUMBER: US/09/932.161
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: US 09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-09-932-161-4
```

```
Query Match          30.2%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 PHGYLTAAY 14
      |||:|:|
DB      1 PHGQNMVSV 10
```

```
RESULT 21
US-09-932-161-12
/ Sequence 12, Application US/09932161
/ Patent No. 6884596
/ GENERAL INFORMATION:
/ APPLICANT: Civeilli, Olivier
/ APPLICANT: Lin, Steven
/ TITLE OF INVENTION: Screening and Therapeutic Methods For
/ FILE REFERENCE: P-UC 4679
/ CURRENT APPLICATION NUMBER: US/09/932.161
/ PRIOR FILING DATE: 2001-08-17
/ PRIOR APPLICATION NUMBER: US 09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: human GPR10 variant
US-09-932-161-12
```

```
Query Match          30.2%; Score 29; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 1.4e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      5 PHGYLTAAY 14
      |||:|:|
DB      1 PHGQNMVSV 10
```

```
RESULT 22
US-09-747-287A-205
/ Sequence 205, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
/ CURRENT FILING DATE: 2000-12-22
```

```
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 205
/ LENGTH: 16
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-747-287A-205
```

```
Query Match          30.2%; Score 29; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 2e+02;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
QY      4 EPHGYLTAAYSPG 17
      :|||:|:|
DB      2 DPGYVHADAPVPRG 15
```

```
RESULT 23
US-09-708-906-12
/ Sequence 12, Application US/09708906
/ Patent No. 6528620
/ GENERAL INFORMATION:
/ APPLICANT: Ayer, Donald E.
/ APPLICANT: Billin, Andrew N.
/ TITLE OF INVENTION: STD-POLYAMIDE FUSIONS: A POTENT METHOD OF REGULATING
/ FILE REFERENCE: 1321.2.37
/ CURRENT APPLICATION NUMBER: US/09/708,906
/ PRIOR FILING DATE: 2000-11-08
/ PRIOR APPLICATION NUMBER: 60/163,960
/ PRIOR FILING DATE: 1999-11-08
/ NUMBER OF SEQ ID NOS: 27
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 12
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Caenorhabditis elegans
US-09-708-906-12
```

```
Query Match          30.2%; Score 29; DB 2; Length 18;
Best Local Similarity 85.7%; Pred. No. 2.3e+02;
Matches 6; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      7 GYLLTA 13
      :|||:|:|
DB      3 GHLLTA 9
```

```
RESULT 24
5258287-19
/ Patent No. 5258287
/ APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.
/ TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
/ OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
/ NUMBER OF SEQUENCES: 58
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/07/171,623
/ FILING DATE: 22-MAR-1988
/ SEQ ID NO:19:
/ LENGTH: 20
5258287-19
```

Query Match 30.2%; Score 29; DB 6; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17
||| |
2 YLLPAPPAPG 11

Db

RESULT 25
5258287-22
; Patent No. 5258287
; APPLICANT: BAXTER, ROBERT C.; WOOD, WILLIAM I.
; TITLE OF INVENTION: DNA ENCODING AND METHODS OF PRODUCTION
; OF INSULIN-LIKE GROWTH FACTOR BINDING PROTEIN BP53
; NUMBER OF SEQUENCES: 58
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/171,623
; FILING DATE: 22-MAR-1988
; SEQ ID NO:22:
; LENGTH: 20
5258287-22

Query Match 30.2%; Score 29; DB 6; Length 20;
Best Local Similarity 60.0%; Pred. No. 2.6e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17
||| |
2 YLLPAPPAPG 11

Db

RESULT 26
US-08-875-309-13
; Sequence 13, Application US/08875309
; Patent No. 6180600
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksel, Swati
; APPLICANT: Koringold, Robert
; APPLICANT: Huang, Ziwei
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 6180600r18
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/875,309
; FILING DATE: 26-NOV-1997
; CLASSIFICATION: 424
; APPLICATION NUMBER: PCT/US96/00310
; FILING DATE: 17-JAN-1996
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,952
; FILING DATE: 17-JAN-1995
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1772
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-875-309-13

Query Match 29.2%; Score 28; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEHGYLTLAAVSP 16
||| |
1 FQPRG---AAASP 10

Db

RESULT 27
PCT-US96-00310-13
; Sequence 13, Application PC/TUS9600310
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Choksel, Swati
; APPLICANT: Koringold, Robert
; APPLICANT: Huang, Ziwei
; TITLE OF INVENTION: CD8 Antagonists
; NUMBER OF SEQUENCES: 14
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00310
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/372,952
; FILING DATE: 17-JAN-1995
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1752
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3100
; TELEFAX: 215-568-3439
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00310-13

Query Match 29.2%; Score 28; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.9e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEHGYLTLAAVSP 16
||| |
1 FQPRG---AAASP 10

Db

RESULT 28
US-08-875-309-14
Sequence 14, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Chokshi, Swati
APPLICANT: Korgold, Robert
APPLICANT: Huang, Zimei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 6180600r1s
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TCU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: protein
US-08-875-309-14

Query Match 29.2% Score 28; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEHGYLTAASP 16
DB 2 FQPRG---AAASP 11

RESULT 29
PCT-US96-00310-14
Sequence 14, Application PC/TUS9600310
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Chokshi, Swati
APPLICANT: Korgold, Robert
APPLICANT: Huang, Zimei
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & Norris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia

STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TCU-1752
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
TOPOLOGY: circular
MOLECULE TYPE: protein
PCT-US96-00310-14

Query Match 29.2% Score 28; DB 4; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.3e+02;
Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;

QY 3 FEHGYLTAASP 16
DB 2 FQPRG---AAASP 11

RESULT 30
US-08-190-802A-17
Sequence 17, Application US/08190802A
Patent No. 5519003
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Dehlinger & Associates
STREET: P.O. Box 60850
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94306-0850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/190,802A
FILING DATE: 01-FEB-1994
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Fabian, Gary R.
REGISTRATION NUMBER: 33,875
REFERENCE/DOCKET NUMBER: 8600-0139
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 324-0880
TELEFAX: (415) 324-0960

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GBH Peptide rV, Fig. 24
US-08-190-802A-17

Query Match 29.2%; Score 28; DB 1; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTLAAVSP 16
|||
1 YLNTVTVP 9

RESULT 31
US-08-875-309-17
Sequence 17, Application US/08875309
Patent No. 6180600
GENERAL INFORMATION:
APPLICANT: Jameson, Bradford A.
APPLICANT: Choksi, Swati
APPLICANT: Kohnigold, Robert
APPLICANT: Huang, Ziwel
TITLE OF INVENTION: CD8 Antagonists
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSER: Woodcock Washburn Kurtz Mackiewicz & No. 61806000ris
STREET: One Liberty Place, 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: USA
ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Wordperfect
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/875,309
FILING DATE: 26-NOV-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/00310
FILING DATE: 17-JAN-1996
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/372,952
FILING DATE: 17-JAN-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Deluca, Mark
REGISTRATION NUMBER: 33,229
REFERENCE/DOCKET NUMBER: TJU-1772
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-875-309-17
Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 2.7e+02;

Matches 7; Conservative 1; Mismatches 2; Indels 4; Gaps 1;
QY 3 FEPHGILTLAAVSP 16
|||
5 FQPRG---AAASP 14

RESULT 32
US-08-477-346-17
Sequence 17, Application US/08477346
Patent No. 6262023
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,346
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/487,072
FILING DATE: 07-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGER, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GBH Peptide rV, Fig. 24
US-08-477-346-17
Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 8 YLTLAAVSP 16
|||
1 YLNTVTVP 9
RESULT 33
US-08-473-089-17
Sequence 17, Application US/08473089
Patent No. 6342368
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
APPLICANT: Ron, Dorit
TITLE OF INVENTION: WD-40 - Derived Peptides and Uses
TITLE OF INVENTION: Thereof

NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
ADDRESSER: Morrison & Peester
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/473,089
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MURASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.22
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-0763
TELEFAX: (202) 887-1500
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GBH Peptide rV, Fig. 24
US-08-473-089-17

Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSP 16
|||
1 YLNTVTVSP 9

Db

RESULT 34
US-09-009-953-176
Sequence 176, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997

APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 176:
US-09-009-953-176

Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTTAAVSPG 17
|||
6 LTPALISPG 14

Db

RESULT 35
US-09-009-953-183
Sequence 183, Application US/09009953
Patent No. 6413517
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
TITLE OF INVENTION: Identification of Broadly
Reactive DR Restricted Epitopes
NUMBER OF SEQUENCES: 274
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,953
FILING DATE: 21-Jan-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/036,713
FILING DATE: 23-JAN-1997
APPLICATION NUMBER: US 60/037,432
FILING DATE: 07-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 018623-011520US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
TELEFAX: 415-576-0300
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 183:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 183;
US-09-009-953-183

Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 YLTAAVSPG 17
DB 3 LEPALISPG 11

RESULT 36

US-08-487-072A-17
Sequence 17, Application US/08487072A
Patent No. 6423684
GENERAL INFORMATION:
APPLICANT: Mochly-Rosen, Daria
TITLE OF INVENTION: MD-40 - Derived peptides and uses
TITLE OF INVENTION: Thereof
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESSES:
ADDRESSER: Morrison & Foerster
STREET: 2000 Pennsylvania Avenue, NW
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20006-1812
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,072A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: MORASHIGE, KATE H.
REGISTRATION NUMBER: 29,959
REFERENCE/DOCKET NUMBER: 2550-0025.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 887-1500
TELEFAX: (202) 887-0763
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
INDIVIDUAL ISOLATE: GRH Peptide rv, Fig. 24
US-08-487-072A-17

Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.7e+02;
Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSP 16
DB 1 YLNTVTSP 9

RESULT 37
US-08-469-318-188
Sequence 188, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:

TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-469-318-188

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSPG 17
DB 1 YVIEGRISPG 10

RESULT 38
US-08-469-318-189
Sequence 189, Application US/08469318
Patent No. 6022535
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/446,872
FILING DATE:
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-469-318-189

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTAAVSPG 17
DB 1 YVIEGRISPG 10

RESULT 39

```

US-08-468-609A-188
; Sequence 188, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maïre H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 188:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-609A-188

Query Match      29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      8 YLLTAAVSPG 17
      |:::|
      1 YVIEGRISPG 10

RESULT 40
US-08-468-609A-189
; Sequence 189, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maïre H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-609A-189

```

```

; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60680
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,609A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/192,325
; FILING DATE: 14-FEB-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Bennett, Dennis A.
; REGISTRATION NUMBER: 34,547
; REFERENCE/DOCKET NUMBER: C-2790/3
; TELEPHONE: (314)737-6986
; TELEFAX: (314)737-6972
; INFORMATION FOR SEQ ID NO: 189:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 18 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; US-08-468-609A-189

Query Match      29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      8 YLLTAAVSPG 17
      |:::|
      1 YVIEGRISPG 10

RESULT 41
US-08-468-609A-188
; Sequence 188, Application US/08468609A
; Patent No. 6030812
; GENERAL INFORMATION:
; APPLICANT: Abrams, Mark A.
; APPLICANT: Bauer, S. C.
; APPLICANT: Bradford-Goldberg, Sarah R.
; APPLICANT: Caparon, Maïre H.
; APPLICANT: Easton, Alan M.
; APPLICANT: Klein, Barbara K.
; APPLICANT: McKearn, John P.
; APPLICANT: Olin, Peter O.
; APPLICANT: Paik, Kuman
; APPLICANT: Thomas, John W.
; TITLE OF INVENTION: Fusion Proteins Comprising Multiply Mutated Interleukin-3 (IL-
; NUMBER OF SEQUENCES: 197
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
; ADDRESSEE: Corporate Patent Dept.
; STREET: P. O. Box 5110
; CITY: Chicago

```

STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-872A-188

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLITAAVSPG 17
|:::|
DB 1 YVIEGRISPG 10

RESULT 42
US-08-446-872A-189
Sequence 189, Application US/08446872A
Patent No. 6361977
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Maïre H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/446,872A

FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6986
TELEFAX: (314)737-6972
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-446-872A-189

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLITAAVSPG 17
|:::|
DB 1 YVIEGRISPG 10

RESULT 43
US-08-762-227A-188
Sequence 188, Application US/08762227A
Patent No. 6436387
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
APPLICANT: Bauer, S. C.
APPLICANT: Bradford-Goldberg, Sarah R.
APPLICANT: Caparon, Maïre H.
APPLICANT: Easton, Alan M.
APPLICANT: Klein, Barbara K.
APPLICANT: McKearn, John P.
APPLICANT: Olin, Peter O.
APPLICANT: Paik, Kuman
APPLICANT: Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
TITLE OF INVENTION: Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
ADDRESSEE: Corporate Patent Dept.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547

REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
MOLECULE TYPE: peptide
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-08-762-227A-188

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17
|:::|
DB 1 YVIEGRISPG 10

RESULT 44
US-08-762-227A-189
Sequence 189, Application US/08762227A
Patent No. 6436387
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Bartford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Palk, Kuman
Thomas, John W.
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
Fusion Protein
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co.,
STREET: P. O. Box 5110
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
REFERENCE/DOCKET NUMBER: C-2790/5
TELECOMMUNICATION INFORMATION:
TELEPHONE: (708)470-6501
TELEFAX: (708)470-6881
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids

TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-08-762-227A-189

Query Match 29.2%; Score 28; DB 2; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17
|:::|
DB 1 YVIEGRISPG 10

RESULT 45
PCT-US95-01185-188
Sequence 188, Application PC/TUS9501185
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
Fusion Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325

RESULT 46
PCT-US95-01185-189
Sequence 189, Application PC/TUS9501185
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis Fusion
Fusion Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/01185
FILING DATE: 02-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/192325

FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 189;
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-01185-189

Query Match 29.2%; Score 28; DB 4; Length 18;
Best Local Similarity 40.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLITAAVSPG 17
DB 1 YVIEGRISPG 10

RESULT 47
US-08-416-950-7
Sequence 7, Application US/08416950
Patent No. 5780036
GENERAL INFORMATION:
APPLICANT: CHISARI, Francis V.
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Hourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,950
FILING DATE:
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US
FILING DATE:
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14740-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-416-950-7

Query Match 29.2%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
QY 5 PHGYLTAAY 14

DB 1 PHHYALRQAI 10

RESULT 48
US-08-464-235-18
Sequence 18, Application US/08464235
Patent No. 5788969
GENERAL INFORMATION:
APPLICANT: CHISARI, Francis V.
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,235
FILING DATE: 05-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/024,120
FILING DATE: 26-FEB-1993
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14740-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-464-235-18

Query Match 29.2%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
DB 1 PHHYALRQAI 10

RESULT 49
US-08-468-279-35
Sequence 35, Application US/08468279
Patent No. 5840303
GENERAL INFORMATION:
APPLICANT: CHISARI, Francis V.
APPLICANT: FERRARI, Carlo
APPLICANT: PENNA, Amalia
APPLICANT: MISALE, Gabriele
TITLE OF INVENTION: T-LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 38
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco

STATE: CA
COUNTRY: USA
ZIP: 94105
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,279
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14740-2-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-468-279-35

Query Match 29.2%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
DB 1 PHRYALRQAI 10

RESULT 50
US-08-469-830-7
Sequence 7, Application US/08469830
Patent No. 593224
GENERAL INFORMATION:
APPLICANT: CHISARI, Francis V.
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend Kourie and Crew
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: U.S.A.
ZIP: 94105-1492
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,830
FILING DATE: 06-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14740-2-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-469-830-7

Query Match 29.2%; Score 28; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
DB 1 PHRYALRQAI 10

RESULT 51
US-08-463-486-18
Sequence 18, Application US/08463486
Patent No. 6235288
GENERAL INFORMATION:
APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
TITLE OF INVENTION: LYMPHOCYTE RESPONSES TO HEPATITIS B VIRUS
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Townsend and Townsend
STREET: One Market Plaza, Stewart Street Tower
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94105

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,486
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/024,120
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14740-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-463-486-18

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLITAAV 14
|||
Db 1 PHHYALROAI 10

RESULT 52
US-08-464-496-11
Sequence 11, Application US/08464496
Patent No. 6322789
GENERAL INFORMATION:
APPLICANT: Epimmune, Inc.
APPLICANT: Vitiello, Maria
APPLICANT: Chesnut, Robert
TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
TITLE OF INVENTION: EPTIOPES
FILE REFERENCE: 39963-20001.13
CURRENT APPLICATION NUMBER: US/08/464,496
CURRENT FILING DATE: 1995-06-05
PRIOR APPLICATION NUMBER: 07/935,811
PRIOR FILING DATE: 1992-08-26
PRIOR APPLICATION NUMBER: 07/874,491
PRIOR FILING DATE: 1992-04-27
PRIOR APPLICATION NUMBER: 07/827,682
PRIOR FILING DATE: 1992-01-29
PRIOR APPLICATION NUMBER: 07/749,568
PRIOR FILING DATE: 1991-08-26
NUMBER OF SEQ ID NOS: 75
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 20
TYPE: PRT
ORGANISM: HBV HBC 50-69
US-08-464-496-11

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLITAAV 14
|||
Db 1 PHHYALROAI 10

RESULT 53
US-08-197-484-101
Sequence 101, Application US/08197484
Patent No. 6419931
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
APPLICANT: CHESTNUT, Robert W.
APPLICANT: SETTE, Alessandro D.
APPLICANT: GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend Kourile and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994

CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "HTL-inducing peptide
US-08-197-484-101
specific for HBV, HBC50-69"

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLITAAV 14
|||
Db 1 PHHYALROAI 10

RESULT 54
US-08-591-502B-7
Sequence 7, Application US/08591502B
Patent No. 6607727
GENERAL INFORMATION:
APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Releasee #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/591,502B
FILING DATE: 20-May-1996
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,540
FILING DATE: 26-AUG-1991
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992

APPLICATION NUMBER: US 08/100,870
FILING DATE: 02-AUG-1993
APPLICATION NUMBER: WO PCT/US94/08685
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen Lauver
REGISTRATION NUMBER: 32,762
REFERENCE/DOCKET NUMBER: 014740-000230US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-08-591-502B-7

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
DB 1 PHHYALAKRAI 10

RESULT 55
US-09-790-497A-446
Sequence 446, Application US/09790497A
Patent No. 6649735
GENERAL INFORMATION:
APPLICANT: De Levy, Robert
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
FILE REFERENCE: 2752-16
CURRENT APPLICATION NUMBER: US/09/790,497A
CURRENT FILING DATE: 2001-02-23
PRIOR APPLICATION NUMBER: 09/576,824
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 08/723,425
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: PCT/EP93/00517
PRIOR FILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: EP 92400598.6
PRIOR FILING DATE: 1992-03-06
NUMBER OF SEQ ID NOS: 600
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 446
LENGTH: 20
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-790-497A-446

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTRAAVSPG 17
DB 10 LTRAAVSPG 18

RESULT 56

US-09-576-824A-446
Sequence 446, Application US/09576824A
Patent No. 667387
GENERAL INFORMATION:
APPLICANT: De Levy, Robert
TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
FILE REFERENCE: 2752-11
CURRENT APPLICATION NUMBER: US/09/576,824A
CURRENT FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 08/723,425
PRIOR FILING DATE: 1996-09-30
PRIOR APPLICATION NUMBER: 09/146,028
PRIOR FILING DATE: 1993-11-22
PRIOR APPLICATION NUMBER: PCT/EP93/00517
PRIOR FILING DATE: 1993-03-08
PRIOR APPLICATION NUMBER: EP 92400598.6
PRIOR FILING DATE: 1992-03-06
NUMBER OF SEQ ID NOS: 600
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 446
LENGTH: 20
TYPE: PRT
ORGANISM: Hepatitis C virus
US-09-576-824A-446

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTRAAVSPG 17
DB 10 LTRAAVSPG 18

RESULT 57
US-09-325-917A-4
Sequence 47A, Application US/09325917A
Patent No. 6913316
GENERAL INFORMATION:
APPLICANT: Higazi, Abd Al-Roof
TITLE OF INVENTION: Medical Uses of scdPA/suPAR Complex
FILE REFERENCE: 2741.1001-000
CURRENT APPLICATION NUMBER: US/09/325,917A
CURRENT FILING DATE: 1999-06-04
PRIOR APPLICATION NUMBER: PCT/IL97/00402
PRIOR FILING DATE: 1999-12-09
PRIOR APPLICATION NUMBER: 60/032,676
PRIOR FILING DATE: 1996-12-09
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patscseq for Windows Version 4.0
SEQ ID NO 4
LENGTH: 20
TYPE: PRT
ORGANISM: unknown
FEATURE:
OTHER INFORMATION: homo sapien
US-09-325-917A-4

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 55.6%; Pred. No. 3.9e+02;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 10 LTRAAVSPG 18
DB 9 VTLVSVSPG 17

RESULT 58

US-09-863-054-18
; Sequence 18, Application US/09863054
; Patent No. 6919203
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for inducing cytotoxic T
; Lymphocyte Responses to Hepatitis B Virus
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/863,054
; FILING DATE: 21-May-2001
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/935,898
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 08/024,120
; FILING DATE: 26-FEB-1993
; APPLICATION NUMBER: US 08/396,283
; FILING DATE: 27-FEB-1995
; APPLICATION NUMBER: US 08/463,486
; FILING DATE: 05-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Lockyer, Jean M.
; REGISTRATION NUMBER: 44,879
; REFERENCE/DOCKET NUMBER: 014740-000421US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-863-054-18

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
Db 1 PHHYALRQAI 10

RESULT 59
PCT-US92-07218-11
; Sequence 11, Application PC/TUS9207218
; GENERAL INFORMATION:
; APPLICANT: Vitello, Maria A.
; APPLICANT: Chesnut, Robert W.
; TITLE OF INVENTION: HLA-RESTRICTED HEPATITIS B VIRUS CTL
; TITLE OF INVENTION: EPITOPES
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: California

COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US92/07218
; FILING DATE: 19920826
; CLASSIFICATION: 424
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,568
; FILING DATE: 26-AUG-1991
; APPLICATION NUMBER: US 07/827,682
; FILING DATE: 29-JAN-1992
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/874,491
; FILING DATE: 27-APR-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 14137-26-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-543-5043
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: AMINO ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
PCT-US92-07218-11

Query Match 29.2%; Score 28; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
Db 1 PHHYALRQAI 10

RESULT 60
PCT-US94-02195-18
; Sequence 18, Application PC/TUS9402195
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: PEPTIDES FOR INDUCING CYTOTOXIC T
; Lymphocyte Responses to Hepatitis B Virus
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend
; STREET: One Market Plaza, Stewart Street Tower
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94105
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/02195
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Parmelee, Steven W.
; REGISTRATION NUMBER: 31,990
; REFERENCE/DOCKET NUMBER: 14740-4

TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEFAX: 415-543-5043
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULAR TYPE: peptide
PCT-US94-02195-18

Query Match 29.2%; Score 28; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PHGYLTAHV 14
Db 1 PHHYALRQAI 10

RESULT 61
PCT-US95-02121-101
Sequence 101, Application PC/TUS9502121
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
TITLE OF INVENTION: CTL IMMUNITY
NUMBER OF SEQUENCES: 153
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/02121
FILING DATE: 16-FEB-1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/197,484
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULAR TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note="HTL-inducing peptide
OTHER INFORMATION: specific for HBV, HBC50-69"
PCT-US95-02121-101

Query Match 29.2%; Score 28; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.9e+02;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 5 PHGYLTAHV 14
Db 1 PHHYALRQAI 10

RESULT 62
US-08-652-877-52
Sequence 52, Application US/08652877
Patent No. 6187548
GENERAL INFORMATION:
APPLICANT: Akersstrom, Goran
APPLICANT: Juhlin, Claes
APPLICANT: Raak, Lars
APPLICANT: Crumley, Gregg R.
APPLICANT: Morse, Clarence C.
APPLICANT: Murray, Edward M.
TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
TITLE OF INVENTION: Thereof and DNA Encoding Same
NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSER: Rhone-Poulenc Rorer Inc.
STREET: 500 Arcola Rd., 3c43
CITY: Collegeville
STATE: PA
COUNTRY: USA
ZIP: 19426-0107
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Macintosh
OPERATING SYSTEM: System 7.5.1
SOFTWARE: Word 6.0 (Patentin)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/652,877
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/15203
FILING DATE: 22-NOV-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/344,836
FILING DATE: 23-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/487,314
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
NAME: Savitzky, Martin
REGISTRATION NUMBER: 29,699
REFERENCE/DOCKET NUMBER: A1355E-US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-454-3816
TELEFAX: 610-454-3808
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULAR TYPE: peptide
HYPOTHEICAL: NO
FRAGMENT TYPE: internal
US-08-652-877-52

Query Match 28.6%; Score 27.5; DB 2; Length 11;
Best Local Similarity 38.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

Qy 4 EPHGYLTAHVSP 16

DB :||: :||
2 DPNGYMM--MSP 11

RESULT 63

US-08-476-515A-52
; Sequence 52, Application US/08476515A
; Patent No. 6239270
; GENERAL INFORMATION:
; APPLICANT: Aketrom, Goran
; APPLICANT: Junlin, Claes
; APPLICANT: Raek, Lars
; APPLICANT: Crumley, Gregg R.
; APPLICANT: Morse, Clarence C.
; APPLICANT: Murray, Edward M.
; APPLICANT: Hjaln, Goran
; TITLE OF INVENTION: Human Calcium Sensor Protein, Fragments
; NUMBER OF SEQUENCES: 84
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Martin Savitzky
; STREET: Rhone-Poulenc Rorer Inc., 500 Arcola Rd.,
; STREET: 3C43,
; CITY: Collegeville
; STATE: PA
; COUNTRY: USA
; ZIP: 19426-0107
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: Windows 95
; SOFTWARE: Word 7.0 (Patentin)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/476,515A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/344,836
; FILING DATE: 23-NOV-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/SE94/00483
; FILING DATE: 24-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: SE 9301764-8
; FILING DATE: 24-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Savitzky, Martin
; REGISTRATION NUMBER: 29,699
; REFERENCE/DOCKET NUMBER: A1355D
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-454-3816
; TELEFAX: 610-454-3808
; INFORMATION FOR SEQ ID NO: 52:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 11 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; FRAGMENT TYPE: internal
; US-08-476-515A-52

Query Match 28.6%; Score 27.5; DB 2; Length 11;
Best Local Similarity 38.5%; Pred. No. 2.3e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

QY 4 EPHGYLTAAVSP 16
DB 2 DPNGYMM--MSP 11

RESULT 64

US-08-408-604A-27
; Sequence 27, Application US/08408604A
; Patent No. 5801149
; GENERAL INFORMATION:
; APPLICANT: Shoelson, Steven
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
; NUMBER OF SEQUENCES: 211
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: LAHIVE & COCKFIELD
; STREET: 60 State Street, Suite 510
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
; ZIP: 02109-1875
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/408,604A
; FILING DATE: 21-MAR-1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/134,558
; FILING DATE: 08-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/959,949
; FILING DATE: 09-OCT-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/722,359
; FILING DATE: 19-JUNE-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Myers, Louis
; REGISTRATION NUMBER: 35,965
; REFERENCE/DOCKET NUMBER: JDP-014CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617)227-7400
; TELEFAX: (617)227-5941
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 17
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; US-08-408-604A-27

Query Match 28.6%; Score 27.5; DB 1; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

QY 4 EPHGYLTAAVSP 16
DB 5 DPNGYMM--MSP 14

RESULT 65

PCT-US93-09626-27
; Sequence 27, Application PC/TUS9309626
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: INHIBITION OF SIGNAL TRANSDUCTION MOLECULES
; NUMBER OF SEQUENCES: 48
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: ASCII (text)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/09626
; APPLICATION NUMBER: 07/959,949
; FILING DATE: October 9, 1992

APPLICATION NUMBER: 07/722,359
FILING DATE: June 19, 1991
INFORMATION FOR SEQ ID NO: 27
SEQUENCE CHARACTERISTICS:
LENGTH: 17
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
PCT-US93-09626-27

Query Match 28.6%; Score 27.5; DB 4; Length 17;
Best Local Similarity 38.5%; Pred. No. 3.9e+02;
Matches 5; Conservative 5; Mismatches 0; Indels 3; Gaps 1;

QY 4 EPHGYLITAAVSP 16
DB 5 DPNGYMM--MSP 14

RESULT 66
US-08-256-747C-15
Sequence 15, Application US/08256747C
Patent No. 6037448
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: GILLAM, Shirley
APPLICANT: OU, Dawei
APPLICANT: TINGLE, Aubrey
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
NUMBER OF SEQUENCES: 78
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6th Floor, 330 University Avenue
STREET: 6th Floor 701, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/256,747C
FILING DATE: 06-OCT-1994
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Stewart, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-370
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-256-747C-15

Query Match 28.6%; Score 27.5; DB 2; Length 20;

Best Local Similarity 44.4%; Pred. No. 4.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 DAEPPHYLITAAVSPK 18
DB 4 DADDP---LIRTAPEGGR 18

RESULT 67
US-08-834-130A-15
Sequence 15, Application US/08834130A

Patent No. 6180758
GENERAL INFORMATION:
APPLICANT: CHONG, Pele
APPLICANT: GILLAM, Shirley
APPLICANT: OU, Dawei
APPLICANT: TINGLE, Aubrey
TITLE OF INVENTION: SYNTHETIC PEPTIDES FOR A RUBELLA VACCINE
NUMBER OF SEQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: 6th Floor, 330 University Avenue
STREET: 6th Floor, 330 University Avenue
CITY: Toronto
STATE: Ontario
COUNTRY: Canada
ZIP: M5G 1R7
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/834,130A
FILING DATE: 14-APR-1997
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: STEWART, Michael I.
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-686 MIS:jb
TELECOMMUNICATION INFORMATION:
TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-834-130A-15

Query Match 28.6%; Score 27.5; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 4.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 DAEPPHYLITAAVSPK 18
DB 4 DADDP---LIRTAPEGGR 18

RESULT 68
5164481-6
Patent No. 5164481
APPLICANT: LACROIX, MARTIAL, ZREIN, MAAN, DIONNE, GERVAIS
TITLE OF INVENTION: PEPTIDES AND ANALOGUES AND MIXTURES
FOR DETECTING AND ELICITING ANTIBODIES TO RUBELLA VIRUS
NUMBER OF SEQUENCES: 11
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/397,767
FILING DATE: 23-AUG-1989
SEQ ID NO: 6
LENGTH: 20
5164481-6

Query Match 28.6%; Score 27.5; DB 6; Length 20;

Best Local Similarity 44.4%; Pred. No. 4.7e+02;
Matches 8; Conservative 2; Mismatches 5; Indels 3; Gaps 1;

QY 1 DAEPPHYLITAAVSPK 18
DB 2 DADDP---LIRTAPEGGR 16

RESULT 69
US-08-822-586-19

Sequence 19, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal fragment
US-08-822-586-19
Query Match 28.1%; Score 27; DB 2; Length 10;
Best Local Similarity 71.4%; Pred No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 GYLTTAA 13
DB 4 GYLTTAA 10
RESULT 70
US-08-822-586-23
Sequence 23, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE

COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE:
DESCRIPTION: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal fragment
US-08-822-586-23
Query Match 28.1%; Score 27; DB 2; Length 10;
Best Local Similarity 71.4%; Pred No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
QY 7 GYLTTAA 13
DB 4 GYLTTAA 10
RESULT 71
US-08-822-586-27
Sequence 27, Application US/08822586
Patent No. 6015890
GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS, JR., JAMES M. MUSSER AND
TITLE OF INVENTION: AN EMBICAB OPERON OF MYCOBACTERIA AND
TITLE OF INVENTION: MUTANTS THEREOF
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSER: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
CITY: NEW YORK
STATE: NEW YORK
COUNTRY: U.S.A.
ZIP: 10016
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 MB STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,586
FILING DATE: MARCH 20, 1997
ATTORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REFERENCE/DOCKET NUMBER: 96700/437
TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
LENGTH: 10 amino acids
TYPE: amino acid

STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
DESCRIPTION: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: Internal fragment
US-08-822-586-27

Query Match 28.1%; Score 27; DB 2; Length 10;
Best Local Similarity 71.4%; Pred. No. 2.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLTTAA 13
DB 4 GYLTTAA 10

RESULT 72
US-08-802-981-161
Sequence 161, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
City: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 161:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Fluorophore 1 linked to the alpha-amino group C
FEATURE:
NAME/KEY: Modified-site
LOCATION: 9
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = Fluorophore 1 linked to the epsilon-amino group C
US-08-802-981-161
Query Match 28.1%; Score 27; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;

Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 4 DGIDPKGY 11

RESULT 73
US-09-747-287A-215
Sequence 215, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
TITLE OF INVENTION: HOW-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3
SEQ ID NO 215
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Synthetic peptide. Artificial protease substrate.
US-09-747-287A-215

Query Match 28.1%; Score 27; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 4 DGIDPKGY 11

RESULT 74
US-09-394-019C-169
Sequence 169, Application US/09394019C
Patent No. 6936687
GENERAL INFORMATION:
APPLICANT: Oncolmmun, Inc.
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: Packard, Beverly
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
FILE REFERENCE: 300-903820US
CURRENT APPLICATION NUMBER: US/09/394,019C
CURRENT FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: PCT/US98/00300
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/802,981
PRIOR FILING DATE: 1997-02-20
NUMBER OF SEQ ID NOS: 405
SOFTWARE: PatentIn version 3.2
SEQ ID NO 169
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Synthetic peptide substrate
FEATURE:
NAME/KEY: misc feature
OTHER INFORMATION: Artificial = synthetic protease indicator

NAME/KEY: MOD_RES
LOCATION: (1)-(1)
OTHER INFORMATION: D is derivatized with fluorophore
FEATURE:
NAME/KEY: MOD_RES
LOCATION: (9)-(9)
OTHER INFORMATION: K is derivatized with fluorophore
US-09-394-019C-169

Query Match 28.1%; Score 27; DB 2; Length 11;
Best Local Similarity 50.0%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8
DB 4 DGDIPKGY 11

RESULT 75

US-08-802-981-162
Sequence 162, Application US/08802981
Patent No. 6037137

GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom

REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 162:

SEQUENCE CHARACTERISTICS:

LENGTH: 12 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: peptide

FEATURE:
NAME/KEY: Modified-site

LOCATION: 1
OTHER INFORMATION: /product= "OTHER"

OTHER INFORMATION: /note= "Xaa = fluorophore 1 linked to the alpha-amino group of

OTHER INFORMATION: Ptc"

FEATURE:
NAME/KEY: Modified-site

LOCATION: 10
OTHER INFORMATION: /product= "OTHER"

OTHER INFORMATION: /note= "Xaa = fluorophore 1 linked to the epsilon-amino group

OTHER INFORMATION: Lys"

US-08-802-981-162

Query Match 28.1%; Score 27; DB 2; Length 12;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFPHGY 8
DB 5 DGDIPKGY 12

RESULT 76

US-09-929-266-13

Sequence 13, Application US/09929266
Patent No. 6824981

GENERAL INFORMATION:

APPLICANT: Brian T. Chait
APPLICANT: Darin R. Lattimer
APPLICANT: Paul M. Lizardi
APPLICANT: Eric R. Kershner
APPLICANT: Jon S. Morrow
APPLICANT: Matthew B. Roth
APPLICANT: Martin J. Matresich
APPLICANT: Kevin J. McConnell

TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173.000302

CURRENT APPLICATION NUMBER: US/09/929,266

PRIOR FILING DATE: 2001-08-13

PRIOR APPLICATION NUMBER: 60/224,939

PRIOR FILING DATE: 2000-08-11

PRIOR APPLICATION NUMBER: 60/283,498

PRIOR FILING DATE: 2000-04-12

NUMBER OF SEQ ID NOS: 33

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 13

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Description of Artificial Sequence; No. 6824981e=synthetic

US-09-929-266-13

Query Match 28.1%; Score 27; DB 2; Length 12;

Best Local Similarity 40.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTAASBPG 17
DB 1 YFTSGCDPG 10

RESULT 77

US-09-747-287A-216

Sequence 216, Application US/09747287A
Patent No. 6893868

GENERAL INFORMATION:

APPLICANT: KOMORIYA, AKIRA

APPLICANT: PACKARD, BEVERLY S.

TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME

TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES

FILE REFERENCE: 300-948600US

CURRENT APPLICATION NUMBER: US/09/747,287A

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: US 09/349,019

PRIOR FILING DATE: 1999-09-10

PRIOR APPLICATION NUMBER: US08/802,981

PRIOR FILING DATE: 1997-02-20

PRIOR APPLICATION NUMBER: PCT/US00/24882

PRIOR FILING DATE: 2000-09-11

NUMBER OF SEQ ID NOS: 246

SOFTWARE: Patentin version 3.3

SEQ ID NO 216

LENGTH: 12

TYPE: PRT

ORGANISM: Artificial

FEATURE:
OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-216

Query Match 28.1%; Score 27; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 5 DGIDPKGY 12

RESULT 78
US-09-394-019C-170
Sequence 170, Application US/09394019C
Patent No. 6936687
GENERAL INFORMATION:
APPLICANT: Oncoimmunin, Inc.
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
FILE REFERENCE: 300-903820US
CURRENT APPLICATION NUMBER: US/09/394,019C
CURRENT FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: PCT/US98/00300
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: US 08/802,981
PRIOR FILING DATE: 1997-02-20
NUMBER OF SEQ ID NOS: 405
SOFTWARE: PatentIn version 3.2
SEQ ID NO 170
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide substrate
NAME/KEY: misc_feature
OTHER INFORMATION: Artificial = synthetic protease indicator
FEATURE:
NAME/KEY: MOD RES
LOCATION: (1)..(1)
OTHER INFORMATION: P is derivatized with fluorophore
FEATURE:
NAME/KEY: MOD RES
LOCATION: (10)..(10)
OTHER INFORMATION: K is derivatized with fluorophore
US-09-394-019C-170

Query Match 28.1%; Score 27; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 5 DGIDPKGY 12

RESULT 79
US-08-802-981-42
Sequence 42, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor

CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 42:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product= "A1b"
US-08-802-981-42

Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

RESULT 80
US-08-802-981-43
Sequence 43, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:

OTHER INFORMATION: /product= "Alb"
US-08-802-981-46
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "Alb"
US-08-802-981-43
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFPHGY 8
| : | | |
DB 6 DGIIDPKGY 13
RESULT 81
US-08-802-981-46
Sequence 46, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 46:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /notes="Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached
OTHER INFORMATION: to the alpha-amino group of Lys"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3

OTHER INFORMATION: /product= "Alb"
US-08-802-981-46
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFPHGY 8
| : | | |
DB 6 DGIIDPKGY 13
RESULT 82
US-08-802-981-51
Sequence 51, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /notes="Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached
OTHER INFORMATION: to the alpha-amino group of Lys"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "Alb"
US-08-802-981-51
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFPHGY 8
| : | | |
DB 6 DGIIDPKGY 13

RESULT 83
US-08-802-981-170
; Sequence 170, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 170:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached
; OTHER INFORMATION: the alpha-amino group and 5'-carboxytetramethylrhodamine
; OTHER INFORMATION: attached to the epsilon-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 3
; OTHER INFORMATION: /product= "Alb"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-170
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13
RESULT 84
US-08-802-981-171
; Sequence 171, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Alb"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-171
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13
RESULT 85
US-08-802-981-175
; Sequence 175, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Alb"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-175
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 171:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Alb"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-171
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13
RESULT 85
US-08-802-981-175
; Sequence 175, Application US/08802981
; Patent No. 6037137
; GENERAL INFORMATION:
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly S.
; TITLE OF INVENTION: Compositions for the Detection of Enzyme
; TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
; NUMBER OF SEQUENCES: 231
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/802,981
; FILING DATE: 20-FEB-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Hunter, Tom
; REGISTRATION NUMBER: 38,498
; REFERENCE/DOCKET NUMBER: 016865-000300US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 175:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 13 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 1
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 4
; OTHER INFORMATION: /product= "Alb"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 11
; OTHER INFORMATION: /product= "OTHER"
; OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
; OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-175
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 175:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = 9-fluorenylmethoxycarbonyl (Fmoc) group attached to the alpha-amino group and 5'-carboxytetramethylrhodamine
OTHER INFORMATION: attached to the epsilon-amino group of Lys"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 4
OTHER INFORMATION: /product= "Aib"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-175
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPXGY 13
RESULT 86
US-08-802-981-176
Sequence 176, Application US/08802981
Patent No. 6037137
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
APPLICANT: Packard, Beverly S.
TITLE OF INVENTION: Compositions for the Detection of Enzyme
TITLE OF INVENTION: Activity in Biological Samples and Methods of Use Thereof
NUMBER OF SEQUENCES: 231
CORRESPONDENCE ADDRESS:
ADDRESSER: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA

ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/802,981
FILING DATE: 20-FEB-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
REFERENCE/DOCKET NUMBER: 016865-000300US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 176:
SEQUENCE CHARACTERISTICS:
LENGTH: 13 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Modified-site
LOCATION: 1
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
OTHER INFORMATION: epsilon-amino group of Lys"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 3
OTHER INFORMATION: /product= "Aib"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 11
OTHER INFORMATION: /product= "OTHER"
OTHER INFORMATION: /note= "Xaa = 5'-carboxytetramethylrhodamine attached to the
OTHER INFORMATION: epsilon-amino group of Lys"
US-08-802-981-176
Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
QY 1 DAFEPHGY 8
DB 6 DGIDPXGY 13
RESULT 87
US-09-747-287A-40
Sequence 40, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.
TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 246
SOFTWARE: Patent in version 3.3
SEQ ID NO 40
LENGTH: 13

TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-40

Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

RESULT 88
US-09-747-287A-41
Sequence 41, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3
SEQ ID NO 41
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-41

Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

RESULT 89
US-09-747-287A-44
Sequence 44, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3
SEQ ID NO 44

LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-44

Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

RESULT 90
US-09-747-287A-50
Sequence 50, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3
SEQ ID NO 50
LENGTH: 13
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide.
US-09-747-287A-50

Query Match 28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 6 DGIDPKGY 13

RESULT 91
US-09-747-287A-224
Sequence 224, Application US/09747287A
Patent No. 6893868
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287A
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
NUMBER OF SEQ ID NOS: 246
SOFTWARE: PatentIn version 3.3

```
/ SEQ ID NO 224
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-224
```

```
Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAFEPHGY 8
   | : | | |
Db 6 DGIDPKGY 13
```

```
RESULT 92
US-09-747-287A-225
/ Sequence 225, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 225
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-225
```

```
Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAFEPHGY 8
   | : | | |
Db 6 DGIDPKGY 13
```

```
RESULT 93
US-09-747-287A-229
/ Sequence 229, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
```

```
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 229
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-229
```

```
Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAFEPHGY 8
   | : | | |
Db 6 DGIDPKGY 13
```

```
RESULT 94
US-09-747-287A-230
/ Sequence 230, Application US/09747287A
/ Patent No. 6893868
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOWO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287A
/ CURRENT FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 246
/ SOFTWARE: PatentIn version 3.3
/ SEQ ID NO 230
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa is aminobutyric acid
US-09-747-287A-230
```

```
Query Match          28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAFEPHGY 8
   | : | | |
Db 6 DGIDPKGY 13
```

```
RESULT 95
US-09-394-019C-5
```

```
/ Sequence 5, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 5
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: X is Alb or Pro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-5
```

```
Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
Db      6 DGIDPKGY 13
```

```
RESULT 96
US-09-394-019C-6
/ Sequence 6, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 6
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: MOD_RES
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: X is Alb or Pro
/ FEATURE:
/ NAME/KEY: misc_feature
```

```
/ LOCATION: (4)..(4)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-6
```

```
Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
Db      6 DGIDPKGY 13
```

```
RESULT 97
US-09-394-019C-9
/ Sequence 9, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 9
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: BLOCKED with Fmoc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: X is Alb or Pro
/ FEATURE:
/ NAME/KEY: misc_feature
/ LOCATION: (3)..(3)
/ OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-394-019C-9
```

```
Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
Db      6 DGIDPKGY 13
```

```
RESULT 98
US-09-394-019C-15
/ Sequence 15, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncolimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ APPLICANT: Packard, Beverly
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
```

```
/ CURRENT FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 15
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: BLOCKED with Fmoc
US-09-394-019C-15
```

```
Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 DAFEPHGY 8
| : |||
Db      6 DGIDPKGY 13
```

```
RESULT 99
US-09-394-019C-178
/ Sequence 178, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncoimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ CURRENT FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 178
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ FEATURE:
/ NAME/KEY: misc.feature
/ OTHER INFORMATION: ARTIFICIAL/UNKNOWN = synthetic protease indicator
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: K is blocked with Fmoc
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (11)..(11)
/ OTHER INFORMATION: K is derivatized with fluorophore
US-09-394-019C-178
```

```
Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      1 DAFEPHGY 8
| : |||
Db      6 DGIDPKGY 13
```

```
RESULT 100
US-09-394-019C-179
/ Sequence 179, Application US/09394019C
/ Patent No. 6936687
/ GENERAL INFORMATION:
/ APPLICANT: Oncoimmunin, Inc.
/ APPLICANT: Komoriya, Akira
/ TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
/ FILE REFERENCE: 300-903820US
/ CURRENT APPLICATION NUMBER: US/09/394,019C
/ CURRENT FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: PCT/US98/00300
/ PRIOR FILING DATE: 1998-02-20
/ PRIOR APPLICATION NUMBER: US 08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ NUMBER OF SEQ ID NOS: 405
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 179
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide substrate
/ FEATURE:
/ NAME/KEY: misc.feature
/ OTHER INFORMATION: ARTIFICIAL/UNKNOWN = synthetic protease indicator
/ FEATURE:
/ NAME/KEY: MOD_RES
/ LOCATION: (1)..(1)
/ OTHER INFORMATION: K is derivatized with fluorophore
/ NAME/KEY: MOD_RES
/ LOCATION: (11)..(11)
/ OTHER INFORMATION: K is derivatized with fluorophore
US-09-394-019C-179
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Query Match      28.1%; Score 27; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 3.4e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
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Qy      1 DAFEPHGY 8
| : |||
Db      6 DGIDPKGY 13
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Search completed: January 20, 2006, 19:14:15
OOD time : 19.8654 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:11:21 ! Search time 64,9038 Seconds
(without alignments)
115,878 Million cell updates/sec

Title: US-09-662-293-6
Perfect score: 96
Sequence: 1 DAFPHGYLTAAVSPK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 380452

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA_Main:
1: /cgn2_6/ptodaca/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodaca/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodaca/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodaca/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodaca/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodaca/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed.
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	96	100.0	18	4	US-10-218-743-6
2	35.5	37.0	19	4	US-10-603-566-43
3	35.5	37.0	19	5	US-10-893-485-43
4	33	34.4	6	4	US-10-699-088-957
5	33	34.4	6	5	US-10-699-113-46
6	33	34.4	6	5	US-10-699-114-957
7	33	34.4	6	5	US-10-806-924-9
8	33	34.4	12	3	US-09-932-161-8
9	33	34.4	12	4	US-10-096-777-8
10	32	33.3	12	3	US-09-932-161-9
11	32	33.3	12	4	US-10-096-777-8
12	31	32.3	9	3	US-09-870-089-13
13	31	32.3	9	5	US-10-813-859-13
14	31	32.3	18	5	US-10-661-156-133
15	31	32.3	19	3	US-09-839-884-63
16	31	32.3	19	3	US-09-839-884-63
17	31	32.3	19	3	US-09-839-884-63
18	30	31.2	11	4	US-10-994-815-63
19	30	31.2	12	4	US-10-235-833-66
20	30	31.2	12	4	US-09-932-161-11
21	29	30.2	6	4	US-10-699-088-758
22	29	30.2	6	4	US-10-699-113-758
23	29	30.2	6	5	US-10-699-114-758
24	29	30.2	6	5	US-10-806-924-721
25	29	30.2	11	4	US-10-671-403-210
26	29	30.2	11	4	US-10-671-419-210
27	29	30.2	11	4	US-10-670-844-210

28	29	30.2	11	4	US-10-671-134-210	Sequence 210, App
29	29	30.2	11	4	US-10-673-098-210	Sequence 210, App
30	29	30.2	11	4	US-10-672-638-210	Sequence 210, App
31	29	30.2	11	4	US-10-673-127-210	Sequence 210, App
32	29	30.2	11	4	US-10-670-817-210	Sequence 210, App
33	29	30.2	11	4	US-10-673-119-210	Sequence 210, App
34	29	30.2	11	4	US-10-671-207-210	Sequence 210, App
35	29	30.2	11	5	US-10-673-120-210	Sequence 210, App
36	29	30.2	11	5	US-10-257-603A-8	Sequence 8, App11
37	29	30.2	11	5	US-10-671-412-210	Sequence 210, App
38	29	30.2	11	5	US-10-671-859-210	Sequence 210, App
39	29	30.2	11	5	US-10-671-106-210	Sequence 210, App
40	29	30.2	12	3	US-09-932-161-4	Sequence 4, App11
41	29	30.2	12	3	US-09-932-161-12	Sequence 12, App1
42	29	30.2	12	4	US-10-096-777-4	Sequence 4, App11
43	29	30.2	12	4	US-10-096-777-12	Sequence 12, App1
44	29	30.2	16	3	US-09-747-287-205	Sequence 205, App
45	29	30.2	19	4	US-10-300-694A-114	Sequence 114, App
46	28.5	29.7	16	5	US-10-918-015A-15	Sequence 15, App1
47	28	29.2	6	4	US-10-699-088-232	Sequence 232, App
48	28	29.2	6	4	US-10-699-088-240	Sequence 240, App
49	28	29.2	6	5	US-10-699-113-232	Sequence 232, App
50	28	29.2	6	5	US-10-699-113-240	Sequence 240, App
51	28	29.2	6	5	US-10-699-114-232	Sequence 232, App
52	28	29.2	6	5	US-10-699-114-240	Sequence 240, App
53	28	29.2	6	5	US-10-806-924-195	Sequence 195, App
54	28	29.2	6	5	US-10-806-924-203	Sequence 203, App
55	28	29.2	13	5	US-10-862-195-1482	Sequence 1482, App
56	28	29.2	14	3	US-09-906-179A-203	Sequence 203, App1
57	28	29.2	14	4	US-10-447-161-1	Sequence 1, App11
58	28	29.2	15	4	US-10-103-395-176	Sequence 176, App
59	28	29.2	15	4	US-10-103-395-183	Sequence 183, App
60	28	29.2	15	4	US-10-203-315A-1174	Sequence 1174, App
61	28	29.2	15	5	US-10-886-773-49	Sequence 49, App1
62	28	29.2	15	5	US-10-414-522-25	Sequence 25, App1
63	28	29.2	15	5	US-10-505-929-202	Sequence 202, App
64	28	29.2	18	4	US-10-083-446-188	Sequence 188, App
65	28	29.2	18	4	US-10-083-446-189	Sequence 189, App
66	28	29.2	18	5	US-10-948-576-188	Sequence 188, App
67	28	29.2	18	5	US-10-948-576-189	Sequence 189, App
68	28	29.2	20	3	US-09-863-054-18	Sequence 18, App1
69	28	29.2	20	4	US-10-128-711-101	Sequence 101, App
70	28	29.2	20	4	US-10-359-431-7	Sequence 7, App11
71	28	29.2	20	4	US-10-397-411-13	Sequence 13, App1
72	28	29.2	20	5	US-10-776-013-250	Sequence 250, App
73	28	29.2	20	5	US-10-881-453-18	Sequence 18, App1
74	28	29.2	20	5	US-10-621-575-446	Sequence 446, App
75	28	29.2	20	5	US-10-931-566-22	Sequence 22, App1
76	28	29.2	20	6	US-11-068-110-18	Sequence 18, App1
77	27	28.1	9	4	US-10-461-864-5	Sequence 5, App11
78	27	28.1	11	3	US-09-747-287-215	Sequence 215, App
79	27	28.1	11	3	US-09-874-350A-186	Sequence 186, App
80	27	28.1	11	4	US-10-014-340-731	Sequence 731, App
81	27	28.1	11	4	US-10-285-194-364	Sequence 364, App
82	27	28.1	11	4	US-10-468-543-79	Sequence 79, App1
83	27	28.1	12	3	US-09-486-734A-28	Sequence 28, App1
84	27	28.1	12	3	US-09-929-566-13	Sequence 13, App1
85	27	28.1	12	3	US-09-747-287-216	Sequence 216, App
86	27	28.1	12	3	US-09-747-287-216	Sequence 216, App
87	27	28.1	12	3	US-09-874-350A-187	Sequence 187, App
88	27	28.1	12	5	US-10-825-568-13	Sequence 13, App1
89	27	28.1	13	3	US-09-747-287-40	Sequence 40, App1
90	27	28.1	13	3	US-09-747-287-41	Sequence 41, App1
91	27	28.1	13	3	US-09-747-287-44	Sequence 44, App1
92	27	28.1	13	3	US-09-747-287-50	Sequence 50, App1
93	27	28.1	13	3	US-09-747-287-224	Sequence 224, App
94	27	28.1	13	3	US-09-747-287-225	Sequence 225, App
95	27	28.1	13	3	US-09-747-287-229	Sequence 229, App
96	27	28.1	13	3	US-09-747-287-230	Sequence 230, App
97	27	28.1	13	3	US-09-874-350A-6	Sequence 6, App11
98	27	28.1	13	3	US-09-874-350A-7	Sequence 7, App11
99	27	28.1	13	3	US-09-874-350A-10	Sequence 10, App1
100	27	28.1	13	3	US-09-874-350A-16	Sequence 16, App1
	27	28.1	13	3	US-09-874-350A-195	Sequence 195, App

ALIGNMENTS

RESULT 1
US-10-218-743-6

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; Sequence 6, Application US/10218743
; Publication No. US20030096779A1
; GENERAL INFORMATION:
; APPLICANT: McCall, Catherine A.
; APPLICANT: Hunter, Shirley Wu
; APPLICANT: Weber, Eric R.
; TITLE OF INVENTION: NOVEL DERMATOPHAGOIDES NUCLEIC ACID MOLECULES, PROTEINS
; TITLE OF INVENTION: AND USES THEREOF
; FILE REFERENCE: AL-2-C3
; CURRENT APPLICATION NUMBER: US/10/218,743
; CURRENT FILING DATE: 2002-08-13
; PRIOR APPLICATION NUMBER: US/09/292,225
; PRIOR FILING DATE: 1999-04-15
; PRIOR APPLICATION NUMBER: 60/098,909
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/085,295
; PRIOR FILING DATE: 1998-05-13
; PRIOR APPLICATION NUMBER: 60/098,565
; PRIOR FILING DATE: 1998-04-17
; PRIOR APPLICATION NUMBER: 09/062,013
; PRIOR FILING DATE: 1998-04-17
; NUMBER OF SEQ ID NOS: 49
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 18
; TYPE: PRT
; ORGANISM: Dermatophagoides farinae
US-10-218-743-6
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Query Match          100.0%; Score 96; DB 4; Length 18;
Best Local Similarity 100.0%; Pred. No. 1.2e+08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY      1 DAEPPHYLTAAVSPGK 18
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Db       1 DAEPPHYLTAAVSPGK 18
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RESULT 2
US-10-603-566-43

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; Sequence 43, Application US/10603566
; Publication No. US20040086966A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenberghe, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/22212
; CURRENT APPLICATION NUMBER: US/10/603,566
; CURRENT FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 91
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-603-566-43
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Query Match          37.0%; Score 35.5; DB 4; Length 19;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
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QY      4 BPHGYLTAAVSPGK 18
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Db       6 DPHGYFL-----PGQ 15
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RESULT 3
US-10-893-485-43

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; Sequence 43, Application US/10893485
; Publication No. US20050155090A1
; GENERAL INFORMATION:
; APPLICANT: Wiltamer, Valerie
; APPLICANT: Communi, David
; APPLICANT: Vandenberghe, Ann
; APPLICANT: Detheux, Michel
; APPLICANT: Parentier, Marc
; TITLE OF INVENTION: Compositions and Methods Comprising a Ligand of Chemerin
; FILE REFERENCE: 9409/2045C
; CURRENT APPLICATION NUMBER: US/10/893,485
; CURRENT FILING DATE: 2004-07-16
; PRIOR APPLICATION NUMBER: US 60/303,858
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: US10/603,566
; PRIOR FILING DATE: 2003-06-25
; PRIOR APPLICATION NUMBER: US 09/905,253
; PRIOR FILING DATE: 2001-07-13
; PRIOR APPLICATION NUMBER: US 10/201,187
; PRIOR FILING DATE: 2001-07-23
; NUMBER OF SEQ ID NOS: 97
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 43
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Mus musculus
US-10-893-485-43
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Query Match          37.0%; Score 35.5; DB 5; Length 19;
Best Local Similarity 46.7%; Pred. No. 1.2e+02;
Matches 7; Conservative 2; Mismatches 1; Indels 5; Gaps 1;
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QY      4 BPHGYLTAAVSPGK 18
        :|||
Db       6 DPHGYFL-----PGQ 15
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RESULT 4
US-10-699-088-957

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; Sequence 957, Application US/10699088
; Publication No. US20040209282A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
; TITLE OF INVENTION: SYSTEMS CONTAINING THE TAGGED POLYPEPTIDES
; FILE REFERENCE: 25865-1754
; CURRENT APPLICATION NUMBER: US/10/699,088
; CURRENT FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-088-957
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Query Match 34.4%; Score 33; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
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Db 1 EPHGY 5

RESULT 5
US-10-699-113-46
; Sequence 46, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Kumble, Krishnamand
; APPLICANT: Schultz, Rainer
; APPLICANT: Schultz, Kenneth
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
; FILE REFERENCE: 25885-1755
; CURRENT APPLICATION NUMBER: US/10/699,113
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/446,687
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 46
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: synthetic peptide
US-10-699-113-46

Query Match 34.4%; Score 33; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
|||||
Db 1 EPHGY 5

RESULT 6
US-10-699-114-957
; Sequence 957, Application US/10699114
; Publication No. US20050042623A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Atkinson
; APPLICANT: Krishnamand Kumble
; APPLICANT: Lynne Jersaltis
; APPLICANT: Glazette Sperinde
; TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND METH
; FILE REFERENCE: 25885-1759
; CURRENT APPLICATION NUMBER: US/10/699,114
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 957
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-114-957

Query Match 34.4%; Score 33; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
|||||
Db 1 EPHGY 5

RESULT 7
US-10-806-924-9
; Sequence 9, Application US/10806924
; Publication No. US20050095648A1
; GENERAL INFORMATION:
; APPLICANT: Geyesen, H. Mario
; APPLICANT: Ault-Riche, Dana
; TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
; TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
; FILE REFERENCE: 25885-1760
; CURRENT APPLICATION NUMBER: US/10/806,924
; CURRENT FILING DATE: 2004-03-22
; NUMBER OF SEQ ID NOS: 911
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-806-924-9

Query Match 34.4%; Score 33; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHGY 8
|||||
Db 1 EPHGY 5

RESULT 8
US-09-932-161-8
; Sequence 8, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
; APPLICANT: Civeili, Olivier
; APPLICANT: Ian, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-932-161-8

Query Match 34.4%; Score 33; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
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Db 1 PHGQNTTASY 10

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RESULT 9
US-10-096-777-8
; Sequence 8, Application US/10096777
; Publication No. US20030171270A1
; GENERAL INFORMATION:
; APPLICANT: Clivell, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-10-096-777-8

Query Match          34.4%; Score 33; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 1.9e+02;
Matches 6; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY      5 PHGYLTTAAV 14
DB      1 PHGQNMTVAV 10

RESULT 10
US-09-932-161-9
; Sequence 9, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
; APPLICANT: Clivell, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-932-161-9

Query Match          33.3%; Score 32; DB 3; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 PHGYLTTAAV 14
DB      1 PHGQNMTVAV 10
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; TITLE OF INVENTION: Therapeutic Compositions and Methods
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; PRIOR FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-10-096-777-9

Query Match          33.3%; Score 32; DB 4; Length 12;
Best Local Similarity 60.0%; Pred. No. 2.7e+02;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      5 PHGYLTTAAV 14
DB      1 PHGQNMTVAV 10

RESULT 12
US-09-870-089B-13
; Sequence 13, Application US/09870089B
; Publication No. US20030175252A1
; GENERAL INFORMATION:
; APPLICANT: Charles A. Nicolette
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 68126881209900
; CURRENT APPLICATION NUMBER: US/09/870,089B
; CURRENT FILING DATE: 2001-05-30
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: ATP4/CREB-2
US-09-870-089B-13

Query Match          32.3%; Score 31; DB 3; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 PEPHGV 8
DB      3 FKPHPG 8

RESULT 13
US-10-813-859-13
; Sequence 13, Application US/10813859
; Publication No. US20050048068A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Charles, Nicolette A.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS FOR OVARIAN CANCER
; FILE REFERENCE: 5032US-DIV
; CURRENT APPLICATION NUMBER: US/10/813,859
; CURRENT FILING DATE: 2004-03-31
; PRIOR APPLICATION NUMBER: US 09/870,089
; PRIOR FILING DATE: 2001-05-31
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 13
; LENGTH: 9
; TYPE: PRT
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```
/ ORGANISM: Homo sapiens
US-10-813-859-13

Query Match      32.3%; Score 31; DB 5; Length 9;
Best Local Similarity 66.7%; Pred. No. 1.7e+06;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY      3 FEPHGY 8
      |||||
Db      3 FEPHGF 8

RESULT 14
US-10-661-156-133
/ Sequence 133, Application US/10661156
/ Publication No. US20050100963A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bussat, Philippe
/ APPLICANT: Fan, Hong
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddi
/ APPLICANT: Shrivastava, Rajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR and VEGF/KDR Binding Peptides and
/ FILE REFERENCE: D0617.70012US00
/ CURRENT APPLICATION NUMBER: US/10/661,156
/ CURRENT FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 617
/ SOFTWARE: FASTSEQ for Windows Version 4.0
/ SEQ ID NO 133
/ LENGTH: 18
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-661-156-133

Query Match      32.3%; Score 31; DB 5; Length 18;
Best Local Similarity 55.6%; Pred. No. 6.3e+02;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
```

```
/ APPLICANT: Aebersold, Rudolf H.
/ APPLICANT: Gyl, Michael H
/ APPLICANT: Gyl, Steven
/ APPLICANT: Scott, C R
/ APPLICANT: Turecek, Frantisek
/ APPLICANT: Gerber, Scott A
/ APPLICANT: Rist, Beate
/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
/ FILE REFERENCE: 64-98A
/ CURRENT APPLICATION NUMBER: US/09/839,884
/ CURRENT FILING DATE: 2001-04-20
/ PRIOR APPLICATION NUMBER: 09/383,062
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 60/097,788
/ PRIOR FILING DATE: 1998-08-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 63
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Unidentified
US-09-839-884-63

Query Match      32.3%; Score 31; DB 3; Length 19;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 DAEFGHYLT 11
      |||||
Db      7 DAEFGHGFVT 17

RESULT 16
US-09-839-884-63
/ Sequence 63, Application US/09839884
/ Publication No. US2003008732A9
/ GENERAL INFORMATION:
/ APPLICANT: Aebersold, Rudolf H.
/ APPLICANT: Gyl, Michael H
/ APPLICANT: Gyl, Steven
/ APPLICANT: Turecek, Frantisek
/ APPLICANT: Gerber, Scott A
/ APPLICANT: Rist, Beate
/ TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
/ FILE REFERENCE: 64-98A
/ CURRENT APPLICATION NUMBER: US/09/839,884
/ CURRENT FILING DATE: 2001-04-20
/ PRIOR APPLICATION NUMBER: 09/383,062
/ PRIOR FILING DATE: 1999-08-25
/ PRIOR APPLICATION NUMBER: 60/097,788
/ PRIOR FILING DATE: 1998-08-25
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 63
/ LENGTH: 19
/ TYPE: PRT
/ ORGANISM: Unknown
/ FEATURE:
/ OTHER INFORMATION: Description of Unknown Organism: Unidentified
US-09-839-884-63

Query Match      32.3%; Score 31; DB 3; Length 19;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY      1 DAEFGHYLT 11
      |||||
Db      7 DAEFGHGFVT 17
```

RESULT 17
US-10-994-815-63
Sequence 63, Application US/10994815
Publication No. US20050233399A1
GENERAL INFORMATION:
APPLICANT: Aebbersold, Rudolf H.
APPLICANT: Gelb, Michael H.
APPLICANT: Gysel, Steven
APPLICANT: Scott, C R
APPLICANT: Turecek, Frantisek
APPLICANT: Gerber, Scott A
APPLICANT: Rist, Beate
TITLE OF INVENTION: Rapid Quantitative Analysis of Proteins or Protein
TITLE OF INVENTION: Function in Complex Mixture
FILE REFERENCE: 64-98A
CURRENT APPLICATION NUMBER: US/10/994,815
CURRENT FILING DATE: 2004-11-23
PRIOR APPLICATION NUMBER: US/09/839,884
PRIOR FILING DATE: 2001-04-20
PRIOR APPLICATION NUMBER: 09/383,062
PRIOR FILING DATE: 1999-08-25
PRIOR APPLICATION NUMBER: 60/097,788
PRIOR FILING DATE: 1998-08-25
NUMBER OF SEQ ID NOS: 64
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 63
LENGTH: 19
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Unidentified
US-10-994-815-63

Query Match 32.3%; Score 31; DB 5; Length 19;
Best Local Similarity 54.5%; Pred. No. 6.7e+02;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAEPHGYLIT 11
DB 7 DAEPHGYLIT 17

RESULT 18
US-10-235-483-66
Sequence 66, Application US/10235483
Publication No. US20030087407A1
GENERAL INFORMATION:
APPLICANT: SOTO-JARA, Claudio
BAUMANN, Marc
FRANGIONE, Blas
TITLE OF INVENTION: PEPTIDES AND PHARMACEUTICAL
COMPOSITIONS THEREOF FOR TREATMENT OF DISORDERS OR DISEASES
ASSOCIATED WITH PROTEIN FOLDING INTO AMYLOID OR AMYLOID-LIKE
DEPOSITS
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSES: BROWDY AND NEIMARK
STREET: 419 Seventh Street, N.W., Suite 400
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/235,483
FILING DATE: 06-Sep-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/766,596
FILING DATE: <Unknown>
APPLICATION NUMBER: US 08/630,645
FILING DATE: 10-APR-1996
APPLICATION NUMBER: US 08/478,326
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: YUN, Allen C.
REGISTRATION NUMBER: 37,971
REFERENCE/DOCKET NUMBER: SOTO-JARA-1A
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-628-5197
TELEFAX: 202-737-3528
INFORMATION FOR SEQ ID NO: 66:
SEQUENCE CHARACTERISTICS:
LENGTH: 11 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 66:
US-10-235-483-66

Query Match 31.2%; Score 30; DB 4; Length 11;
Best Local Similarity 63.6%; Pred. No. 5.3e+02;
Matches 7; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 7 GYLITVAVSPG 17
DB 1 GYLITVAVSPG 11

RESULT 19
US-09-932-161-11
Sequence 11, Application US/09932161
Patent No. US20020037533A1
GENERAL INFORMATION:
APPLICANT: Clavell, Olivier
APPLICANT: Lin, Steven
TITLE OF INVENTION: Screening and Therapeutic Methods For
FILE REFERENCE: P-UC 4679
CURRENT APPLICATION NUMBER: US/09/932,161
CURRENT FILING DATE: 2001-08-17
PRIOR APPLICATION NUMBER: US 09/560,915
PRIOR FILING DATE: 2000-04-28
NUMBER OF SEQ ID NOS: 24
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 11
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: human GPR10 variant
US-09-932-161-11

Query Match 31.2%; Score 30; DB 3; Length 12;
Best Local Similarity 45.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLITAAVS 15
DB 1 PHGYLITAAVS 11

RESULT 20
US-10-096-777-11
Sequence 11, Application US/10096777
Publication No. US20030171270A1
GENERAL INFORMATION:
APPLICANT: Clavell, Olivier
APPLICANT: Lin, Steven

```
/ TITLE OF INVENTION: Therapeutic Compositions and Methods
/ TITLE OF INVENTION: Relating to Protectin Releasing Peptide (PrpP)
/ FILE REFERENCE: P-UC 3534
/ CURRENT APPLICATION NUMBER: US/10/096,777
/ PRIOR FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: US/09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 11
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: human GPR10 variant
US-10-096-777-11
```

```
Query Match          31.2%; Score 30; DB 4; Length 12;
Best Local Similarity 45.5%; Pred. No. 5.9e+02;
Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 5 PHGYLTAAVS 15
   ||| : |||
Db 1 PHGQNTVSYVA 11
```

```
RESULT 21
US-10-699-088-758
/ Sequence 758, Application US/10699088
/ Publication No. US20040209282A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
/ TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
/ FILE REFERENCE: 25885-1754
/ CURRENT APPLICATION NUMBER: US/10/699,088
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-088-758
```

```
Query Match          30.2%; Score 29; DB 4; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 EPHGY 8
   : |||
Db 1 KPHGY 5
```

```
RESULT 22
US-10-699-113-758
/ Sequence 758, Application US/10699113
/ Publication No. US20040241748A1
/ GENERAL INFORMATION:
/ APPLICANT: Ault-Riche, Dana
/ APPLICANT: Kumble, Krishnamand
/ APPLICANT: Schultz, Rainer
/ TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
/ FILE REFERENCE: 25885-1755
/ CURRENT APPLICATION NUMBER: US/10/699,113
```

```
/ CURRENT FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/446,687
/ PRIOR FILING DATE: 2003-02-10
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-113-758
```

```
Query Match          30.2%; Score 29; DB 5; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 EPHGY 8
   : |||
Db 1 KPHGY 5
```

```
RESULT 23
US-10-699-114-758
/ Sequence 758, Application US/10699114
/ Publication No. US20050042623A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
/ APPLICANT: Bruce Atkinson
/ APPLICANT: Krishnamand Kumble
/ APPLICANT: Lynne Jesaitis
/ TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND MET
/ FILE REFERENCE: 25885-1759
/ CURRENT APPLICATION NUMBER: US/10/699,114
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 758
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-114-758
```

```
Query Match          30.2%; Score 29; DB 5; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 4 EPHGY 8
   : |||
Db 1 KPHGY 5
```

```
RESULT 24
US-10-806-924-721
/ Sequence 721, Application US/10806924
/ Publication No. US20050095648A1
/ GENERAL INFORMATION:
/ APPLICANT: Geysen, H. Mario
/ APPLICANT: Ault-Riche, Dana
/ TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
/ FILE REFERENCE: 25885-1760
/ CURRENT APPLICATION NUMBER: US/10/806,924
/ CURRENT FILING DATE: 2004-03-22
/ NUMBER OF SEQ ID NOS: 911
```

```
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 721
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-806-924-721

Query Match          30.2%; Score 29; DB 5; Length 6;
Best Local Similarity 80.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      4 BPHGY 8
        :||||
Db       1 KPHGY 5

RESULT 25
US-10-671-403-210
/ Sequence 210, Application US/10671403
/ Publication No. US20040038289A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kurlyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,403
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-403-210

Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
        :||||
Db       7 HGYYL 11

RESULT 26
US-10-671-419-210
/ Sequence 210, Application US/10671419
/ Publication No. US20040038290A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kurlyan, John
```

```
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,419
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-670-844-210

Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
        :||||
Db       7 HGYYL 11

RESULT 27
US-10-670-844-210
/ Sequence 210, Application US/10670844
/ Publication No. US20040043414A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kurlyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/670,844
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-670-844-210

Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
```


Db 7 HGVL 11

RESULT 28

US-10-671-134-210
; Sequence 210, Application US/10671134
; Publication No. US20040043415A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurleva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/671,134
; PRIOR FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-134-210

Query Match 30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVL 10
Db 7 HGVL 11

RESULT 29
US-10-673-098-210
; Sequence 210, Application US/10673098
; Publication No. US20040048309A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurleva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/673,098
; PRIOR FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; SOFTWARE: PatentIn Ver. 2.1

NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-098-210

Query Match 30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVL 10
Db 7 HGVL 11

RESULT 30
US-10-672-638-210
; Sequence 210, Application US/10672638
; Publication No. US20040077012A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurleva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kuriyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/672,638
; PRIOR FILING DATE: 2003-10-09
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-672-638-210

Query Match 30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVL 10
Db 7 HGVL 11

RESULT 31
US-10-673-127-210
; Sequence 210, Application US/10673127
; Publication No. US20040081995A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurleva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina

```
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/673,127
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-127-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 HGYL 10
        |||||
Db      7 HGYL 11
```

```
RESULT 32
/ Sequence 210, Application US/10670817
/ Publication No. US20040106137A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/670,817
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-670-817-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 HGYL 10
        |||||
Db      7 HGYL 11
```

```
RESULT 33
/ Sequence 210, Application US/10673119
/ Publication No. US20040110210A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/673,119
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-119-210
```

```
Query Match          30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      6 HGYL 10
        |||||
Db      7 HGYL 11
```

```
RESULT 34
/ Sequence 210, Application US/10671207
/ Publication No. US2004019796A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ TITLE OF INVENTION: USE THEREOF
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,207
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
```

/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-207-210

Query Match 30.2%; Score 29; DB 4; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGYL 10
| | | | |
Db 7 HGYL 11

RESULT 35
US-10-673-120-210
/ Sequence 210, Application US/10673120
/ Publication No. US20050048510A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/673,120
/ CURRENT FILING DATE: 2003-09-26
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-673-120-210

Query Match 30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGYL 10
| | | | |
Db 7 HGYL 11

RESULT 36
US-10-257-603A-8
/ Sequence 8, Application US/10257603A
/ Publication No. US20050100551A1
/ GENERAL INFORMATION:
/ APPLICANT: Zieginski, Christoph
/ APPLICANT: Pehamberger, Hubert
/ APPLICANT: Breiteneder, Helmo
/ APPLICANT: Jensen-Jarolim, Erika

/ APPLICANT: Scheiner, Otto
/ TITLE OF INVENTION: Vaccine Against Cancerous Diseases
/ FILE REFERENCE: 37488-00100
/ CURRENT APPLICATION NUMBER: US/10/257,603A
/ CURRENT FILING DATE: 2002-10-15
/ PRIOR APPLICATION NUMBER: PCT/EP01/04251
/ PRIOR FILING DATE: 2001-04-12
/ PRIOR APPLICATION NUMBER: DE 200 18 403.0
/ PRIOR FILING DATE: 2000-04-13
/ PRIOR APPLICATION NUMBER: DE 100 41 342.0
/ PRIOR FILING DATE: 2000-08-23
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 8
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: homo sapiens
US-10-257-603A-8

Query Match 30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 71.4%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFPHG 7
| | | | |
Db 4 DPFPHG 10

RESULT 37
US-10-671-412-210
/ Sequence 210, Application US/10671412
/ Publication No. US20050100920A1
/ GENERAL INFORMATION:
/ APPLICANT: O'Donnell, Michael E.
/ APPLICANT: Yuzhakov, Alexander
/ APPLICANT: Yurleva, Olga
/ APPLICANT: Jeruzalmi, David
/ APPLICANT: Bruck, Irina
/ APPLICANT: Kuriyan, John
/ TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
/ TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
/ FILE REFERENCE: 22221/1030
/ CURRENT APPLICATION NUMBER: US/10/671,412
/ CURRENT FILING DATE: 2003-09-25
/ PRIOR APPLICATION NUMBER: US/09/716,964A
/ PRIOR FILING DATE: 2000-11-21
/ PRIOR APPLICATION NUMBER: 60/143,202
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 08/823,407
/ PRIOR FILING DATE: 1997-04-08
/ PRIOR APPLICATION NUMBER: 09/057,416
/ PRIOR FILING DATE: 1998-04-08
/ NUMBER OF SEQ ID NOS: 212
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 210
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-412-210

Query Match 30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGYL 10
| | | | |
Db 7 HGYL 11

RESULT 38

```
US-10-671-859-210
; Sequence 210, Application US/10671859
; Publication No. US20050112580A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Yurileva, Olga
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kurlyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/671,859
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: US/09/716,964A
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-859-210

Query Match          30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
       |||||
Db      7 HGYYL 11

RESULT 39
US-10-671-106-210
; Sequence 210, Application US/10671106
; Publication No. US20050153299A1
; GENERAL INFORMATION:
; APPLICANT: O'Donnell, Michael E.
; APPLICANT: Yuzhakov, Alexander
; APPLICANT: Jeruzalmi, David
; APPLICANT: Bruck, Irina
; APPLICANT: Kurlyan, John
; TITLE OF INVENTION: ENZYMES DERIVED FROM THERMOPHILIC ORGANISMS THAT
; TITLE OF INVENTION: FUNCTION AS A CHROMOSOMAL REPLICASE, PREPARATION AND
; FILE REFERENCE: 22221/1030
; CURRENT APPLICATION NUMBER: US/10/671,106
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: US/09/716,964B
; PRIOR FILING DATE: 2000-11-21
; PRIOR APPLICATION NUMBER: 60/143,202
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 08/823,407
; PRIOR FILING DATE: 1997-04-08
; PRIOR APPLICATION NUMBER: 09/057,416
; PRIOR FILING DATE: 1998-04-08
; NUMBER OF SEQ ID NOS: 212
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 210
; LENGTH: 11
; TYPE: PRT
```

```
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: polypeptide
US-10-671-106-210

Query Match          30.2%; Score 29; DB 5; Length 11;
Best Local Similarity 100.0%; Pred. No. 7.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      6 HGYYL 10
       |||||
Db      7 HGYYL 11

RESULT 40
US-09-932-161-4
; Sequence 4, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
; APPLICANT: Clivelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-932-161-4

Query Match          30.2%; Score 29; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY      5 PHGYLLTAIV 14
       |||||
Db      1 PHGYMNTVSV 10

RESULT 41
US-09-932-161-12
; Sequence 12, Application US/09932161
; Patent No. US20020037533A1
; GENERAL INFORMATION:
; APPLICANT: Clivelli, Olivier
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Screening and Therapeutic Methods For
; TITLE OF INVENTION: Promoting Wakefulness and Sleep
; FILE REFERENCE: P-UC 4679
; CURRENT APPLICATION NUMBER: US/09/932,161
; CURRENT FILING DATE: 2001-08-17
; PRIOR APPLICATION NUMBER: US 09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: human GPR10 variant
US-09-932-161-12

Query Match          30.2%; Score 29; DB 3; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.6e+02;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

Oy 5 PHGYLLTAAY 14
 ||| : |
 Db 1 PHGQNTVSV 10

```

RESULT 42
US-10-096-777-4
; Sequence 4, Application US/10096777
; Publication No. US20030171270A1
; GENERAL INFORMATION:
; APPLICANT: Civeili, Oliver
; APPLICANT: Lin, Steven
; TITLE OF INVENTION: Therapeutic Compositions and Methods
; TITLE OF INVENTION: Relating to Prolactin Releasing Peptide (PRRP)
; FILE REFERENCE: P-UC 3534
; CURRENT APPLICATION NUMBER: US/10/096,777
; CURRENT FILING DATE: 2002-03-12
; PRIOR APPLICATION NUMBER: US/09/560,915
; PRIOR FILING DATE: 2000-04-28
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 12
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-096-777-4

```

Query Match	30.2%	Score	29	DB	4	Length	12
Best Local Similarity	50.0%	Pred	No.	6.6e+02			
Matches	5	Conservative	2	Mismatches	3	Indels	0
						Gaps	0

```

Qy      5 PHGYLLTAAY 14
          ||| :| :|
Db      1 PHGQNMIVSV 10

```

```

RESULT 43
US-10-096-777-12
/ Sequence 12, Application US/10096777
/ Publication No. US20030171270A1
/ GENERAL INFORMATION:
/ APPLICANT: Cliveall, Oliver
/ APPLICANT: Lin, Steven
/ TITLE OF INVENTION: Therapeutic Compositions and Methods
/ TITLE OF INVENTION: Relating To Prolectin Releasing Peptide (P-RP)
/ FILE REFERENCE: P-UC 354
/ CURRENT APPLICATION NUMBER: US/10/096,777
/ CURRENT FILING DATE: 2002-03-12
/ PRIOR APPLICATION NUMBER: US/09/560,915
/ PRIOR FILING DATE: 2000-04-28
/ NUMBER OF SEQ ID NOS: 24
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURES:
/ OTHER INFORMATION: human GPR10 variant
/ US-10-096-777-12

```

Query Match	30.2%	Score 29;	DB 4;	Length 12;
Best Local Similarity	50.0%	Pred. No.	8.6e+02;	
Matches	5;	Conservative	2;	Mismatches 3;
				Indels 0;
				Gaps 0;

Qy 5 PHGYLLTAAY 14
||| : | : |
Db 1 PHGQNMIVSV 10

RESULT 44
US-09-747-287-205
; Sequence 205, Application US/09747287
; Publication No. US20030207264A1

```

GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
APPLICANT: PACKARD, BEVERLY S.
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
TITLE OF INVENTION: ACTIVITY IN BIOLOGICAL SAMPLES
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287
CURRENT FILING DATE: 2000-12-22
PRIORITY APPLICATION NUMBER: US 09/349,019
PRIORITY FILING DATE: 1999-09-10
PRIORITY APPLICATION NUMBER: US08/802,981
PRIORITY FILING DATE: 1997-02-20
PRIORITY APPLICATION NUMBER: PCT/US00/24882
PRIORITY FILING DATE: 2000-09-11
NUMBER OF SEQ ID NOS: 242
SOFTWARE: PatentIn version 3.2
SEQ ID NO 205
LENGTH: 16
TYPE: PRP
ORGANISM: Artificial
FEATURES:
OTHER INFORMATION: Synthetic peptide.
FEATURES:
NAME/KEY: misc feature
LOCATION: (4)..(4)
OTHER INFORMATION: Xaa can be any naturally occurring amino acid
US-09-747-287-205

```

Query Match	30.24	Score	29	DB	3	Length	16
Best Local Similarity	42.94	Score	No. 1.2e+03				
Matches	6	Conservative	2	Mismatches	6	Indels	0
						Gaps	0

QY 4 BPHGYLLTAAVSPG 17
: |||: | | |
Db 2 DPXGYVHDAPVPRKG 15

```

RESULT 45
US-10-300-694A-114
Sequence 114, Application US/10300694A
Publication No. US20030185870A1
GENERAL INFORMATION:
APPLICANT: Duke University
APPLICANT: Grinstaff, Mark W.
APPLICANT: Kenan, Daniel J.
APPLICANT: Walsh, Elisabeth B.
APPLICANT: Middleton, Ciyshan
TITLE OF INVENTION: INTERFACIAL BIOMATERIALS
FILE REFERENCE: 180/143/2
CURRENT APPLICATION NUMBER: US/10/300,694A
CURRENT FILING DATE: 2003-05-07
PRIOR APPLICATION NUMBER: US 60/331,843
PRIOR FILING DATE: 2001-11-20
NUMBER OF SEQ ID NOS: 117
SOFTWARE: PatentIn version 3.2
SEQ ID NO 114
LENGTH: 19
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Nylon suture-binding peptide 114d
US-10-300-694A-114

```

Query Match	30.2%	Score 29;	DB 4;	Length 19;
Best Local Similarity	62.5%;	Pred. No. 1.4e+03;		
Matches	5;	Conservative	0;	Mismatches 3;
			Indels	0;
			Gaps	0;

Qy	1	DAFBPHGY	8
Db	3	DFPNRHGY	10

RESULT 46

US-10-918-015A-15
; Sequence 15, Application US/10918015A
; Publication No. US20050106653A1
; GENERAL INFORMATION:
; APPLICANT: Aventis Pharma Deutschland GmbH
; APPLICANT: TENNASELS, Norbert
; APPLICANT: ECKEL, Jürgen
; APPLICANT: METZGER, Sabine
; APPLICANT: SOMMERFELD, Mark
; TITLE OF INVENTION: A METHOD FOR THE IDENTIFICATION OF IRS PROTEIN KINASE INHIBITORS
; FILE REFERENCE: DE4V2003/0061 US NP
; CURRENT APPLICATION NUMBER: US/10/918,015A
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: 60/535,139
; PRIOR FILING DATE: 2004-01-08
; PRIOR APPLICATION NUMBER: 03018517.7
; PRIOR FILING DATE: 2003-08-16
; NUMBER OF SEQ ID NOS: 17
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 15
; LENGTH: 16
; TYPE: PRT
; ORGANISM: artificial sequence
; FEATURE:
; OTHER INFORMATION: Rat IRS-1 fragment
US-10-918-015A-15

Query Match 29.7%; Score 28.5; DB 5; Length 16;
Best Local Similarity 40.0%; Pred. No. 1.4e+03;
Matches 6; Conservative 5; Mismatches 1; Indels 3; Gaps 1;

QY 4 BPHGYLL--TAAVS 15
DB 2 DPGYMMSPSAAS 16

RESULT 47
US-10-699-088-232
; Sequence 232, Application US/10699088
; Publication No. US20040209282A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Ackinson
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
; FILE REFERENCE: 25885-1754
; CURRENT APPLICATION NUMBER: US/10/699,088
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-088-232

Query Match 29.2%; Score 28; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8
DB 1 PHGY 4

RESULT 48

US-10-699-088-240
; Sequence 240, Application US/10699088
; Publication No. US20040209282A1
; GENERAL INFORMATION:
; APPLICANT: Dana Ault-Riche
; APPLICANT: Bruce Ackinson
; TITLE OF INVENTION: METHODS FOR PRODUCING POLYPEPTIDE-TAGGED COLLECTIONS AND CAPTURE
; FILE REFERENCE: 25885-1754
; CURRENT APPLICATION NUMBER: US/10/699,088
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/422,923
; PRIOR FILING DATE: 2002-10-30
; PRIOR APPLICATION NUMBER: 60/423,018
; PRIOR FILING DATE: 2002-10-30
; NUMBER OF SEQ ID NOS: 1094
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 240
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-088-240

Query Match 29.2%; Score 28; DB 4; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8
DB 1 PHGY 4

RESULT 49
US-10-699-113-232
; Sequence 232, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:
; APPLICANT: Ault-Riche, Dana
; APPLICANT: Kumble, Krishnanand
; APPLICANT: Schulz, Rainer
; APPLICANT: Schulz, Kenneth
; TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
; FILE REFERENCE: 25885-1755
; CURRENT APPLICATION NUMBER: US/10/699,113
; PRIOR FILING DATE: 2003-10-30
; PRIOR APPLICATION NUMBER: 60/446,687
; PRIOR FILING DATE: 2003-02-10
; NUMBER OF SEQ ID NOS: 948
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 232
; LENGTH: 6
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: synthetic peptide
US-10-699-113-232

Query Match 29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8
DB 1 PHGY 4

RESULT 50
US-10-699-113-240
; Sequence 240, Application US/10699113
; Publication No. US20040241748A1
; GENERAL INFORMATION:

```
/ APPLICANT: Ault-Riche, Dana
/ APPLICANT: Kumble, Krishnamand
/ APPLICANT: Schult, Rainer
/ APPLICANT: Schult, Kenneth
/ TITLE OF INVENTION: Self-Assembling Arrays and Uses Thereof
/ FILE REFERENCE: 25885-1755
/ CURRENT APPLICATION NUMBER: US/10/699,113
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/446,687
/ NUMBER OF SEQ ID NOS: 948
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 240
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-113-240
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 51
US-10-699-114-232
/ Sequence 233, Application US/10699114
/ Publication No. US20050042623A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
/ APPLICANT: Bruce Atkinson
/ APPLICANT: Krishnamand Kumble
/ APPLICANT: Lynne Jersaltis
/ APPLICANT: Gizette Sperinde
/ TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND MET
/ FILE REFERENCE: 25885-1759
/ CURRENT APPLICATION NUMBER: US/10/699,114
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 232
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-114-232
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 52
US-10-699-114-240
/ Sequence 240, Application US/10699114
/ Publication No. US20050042623A1
/ GENERAL INFORMATION:
/ APPLICANT: Dana Ault-Riche
```

```
/ APPLICANT: Bruce Atkinson
/ APPLICANT: Krishnamand Kumble
/ APPLICANT: Lynne Jersaltis
/ APPLICANT: Gizette Sperinde
/ TITLE OF INVENTION: SYSTEMS FOR CAPTURE AND ANALYSIS OF BIOLOGICAL PARTICLES AND MET
/ FILE REFERENCE: 25885-1759
/ CURRENT APPLICATION NUMBER: US/10/699,114
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/423,018
/ PRIOR FILING DATE: 2002-10-30
/ PRIOR APPLICATION NUMBER: 60/422,923
/ PRIOR FILING DATE: 2002-10-30
/ NUMBER OF SEQ ID NOS: 1094
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 240
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-699-114-240
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 53
US-10-806-924-195
/ Sequence 195, Application US/10806924
/ Publication No. US20050095648A1
/ GENERAL INFORMATION:
/ APPLICANT: Geyzen, H. Mario
/ APPLICANT: Ault-Riche, Dana
/ TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
/ FILE REFERENCE: 25885-1760
/ CURRENT APPLICATION NUMBER: US/10/806,924
/ PRIOR FILING DATE: 2004-03-22
/ NUMBER OF SEQ ID NOS: 911
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 195
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-806-924-195
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 5 PHGY 8
    ||||
Db 1 PHGY 4
```

```
RESULT 54
US-10-806-924-203
/ Sequence 203, Application US/10806924
/ Publication No. US20050095648A1
/ GENERAL INFORMATION:
/ APPLICANT: Geyzen, H. Mario
/ APPLICANT: Ault-Riche, Dana
/ TITLE OF INVENTION: Method for designing linear epitopes and algorithm therefor
/ FILE REFERENCE: 25885-1760
```

```
/ CURRENT APPLICATION NUMBER: US/10/806,924
/ CURRENT FILING DATE: 2004-03-22
/ NUMBER OF SEQ ID NOS: 911
/ SOFTWARE: PatSeq for Windows Version 4.0
/ SEQ ID NO 203
/ LENGTH: 6
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: synthetic peptide
US-10-806-924-203
```

```
Query Match          29.2%; Score 28; DB 5; Length 6;
Best Local Similarity 100.0%; Pred. No. 1.7e+06;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      5 PHGY 8
       ||||
Db      1 PHGY 4
```

```
RESULT 55
US-10-862-195-1482
/ Sequence 1482, Application US/10862195
/ Publication No. US20050164324A1
/ GENERAL INFORMATION:
/ APPLICANT: GYGI, STEVEN P.
/ TITLE OF INVENTION: SYSTEMS, METHODS AND KITS FOR CHARACTERIZING PHOSPHOPROTEOMES
/ FILE REFERENCE: 58890(70207)
/ CURRENT APPLICATION NUMBER: US/10/862,195
/ CURRENT FILING DATE: 2004-06-04
/ PRIOR APPLICATION NUMBER: 60/476,010
/ PRIOR FILING DATE: 2003-06-04
/ NUMBER OF SEQ ID NOS: 2245
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 1482
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Homo sapiens
/ FEATURE:
/ OTHER INFORMATION: See specification as filed for preferred embodiments
/ OTHER INFORMATION: and description of phosphorylation sites
US-10-862-195-1482
```

```
Query Match          29.2%; Score 28; DB 5; Length 13;
Best Local Similarity 62.5%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 TAAVSPGK 18
       |||||
Db      6 STRLSPGK 13
```

```
RESULT 56
US-09-906-179A-203
/ Sequence 203, Application US/09906179A
/ Publication No. US20030219737A1
/ GENERAL INFORMATION:
/ APPLICANT: Bullard, James M.
/ APPLICANT: Janjic, Nedoljca
/ APPLICANT: McHenry, Charles S.
/ TITLE OF INVENTION: NOVEL DNA POLYMERASE III HOLOENZYME DELTA SUBUNIT
/ TITLE OF INVENTION: NUCLEIC ACID MOLECULES AND PROTEINS
/ FILE REFERENCE: RD1N03
/ CURRENT APPLICATION NUMBER: US/09/906,179A
/ CURRENT FILING DATE: 2001-07-16
/ PRIOR APPLICATION NUMBER: 60/218,246
/ PRIOR FILING DATE: 2000-07-14
/ PRIOR APPLICATION NUMBER: 09/818,780
/ PRIOR FILING DATE: 2001-03-28
/ PRIOR APPLICATION NUMBER: 60/192,736
/ PRIOR FILING DATE: 2000-03-28
/ NUMBER OF SEQ ID NOS: 230
```

```
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 203
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: Consensus
/ NAME/KEY: UNSURE
/ LOCATION: (1)..(14)
/ OTHER INFORMATION: Xaa at position 14 is Thr or Ser
US-09-906-179A-203
```

```
Query Match          29.2%; Score 28; DB 3; Length 14;
Best Local Similarity 38.5%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
Qy      6 HGYLTTAAVSPGK 18
       |||||
Db      1 HAYLFGKXGXGK 13
```

```
RESULT 57
US-10-447-161-1
/ Sequence 1, Application US/10447161
/ Publication No. US20040023314A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Rong-fu
/ TITLE OF INVENTION: Mutant Fibronectin and Tumor Metastasis
/ FILE REFERENCE: HO-P02484US1
/ CURRENT APPLICATION NUMBER: US/10/447,161
/ CURRENT FILING DATE: 2003-05-28
/ PRIOR APPLICATION NUMBER: 60/383,530
/ PRIOR FILING DATE: 2002-05-28
/ NUMBER OF SEQ ID NOS: 148
/ SOFTWARE: PatentIn version 3.1
/ SEQ ID NO 1
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Human
US-10-447-161-1
```

```
Query Match          29.2%; Score 28; DB 4; Length 14;
Best Local Similarity 55.6%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy      3 FBPHGYLLT 11
       |||||
Db      3 FEKHGFRRT 11
```

```
RESULT 58
US-10-103-395-176
/ Sequence 176, Application US/10103395
/ Publication No. US20020160019A1
/ GENERAL INFORMATION:
/ APPLICANT: EPRIMUNE, Inc.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
/ TITLE OF INVENTION: RESTRICTED EPITOPES
/ FILE REFERENCE: 39963-20016.01
/ CURRENT APPLICATION NUMBER: US/10/103,395
/ CURRENT FILING DATE: 2003-01-03
/ PRIOR APPLICATION NUMBER: US 09/009,953
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: PCT/US98/01373
/ PRIOR FILING DATE: 1998-01-23
/ PRIOR APPLICATION NUMBER: US 60/036,713
/ PRIOR FILING DATE: 1997-01-23
/ PRIOR APPLICATION NUMBER: US 60/037,432
/ PRIOR FILING DATE: 1997-02-07
```



```
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 176
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-103-395-176
```

```
Query Match          29.2%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 9 LPTAAVSPG 17
    |||:|
Db 6 LPTAIIISP 14
```

```
RESULT 59
US-10-103-395-183
/ Sequence 183, Application US/10103395
/ Publication No. US20020160019A1
/ GENERAL INFORMATION:
/ APPLICANT: EPIMUNE, Inc.
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ TITLE OF INVENTION: IDENTIFICATION OF BROADLY REACTIVE DR
/ TITLE OF INVENTION: RESTRICTED EPITOPES
/ FILE REFERENCE: 39963-20016.01
/ CURRENT APPLICATION NUMBER: US/10/103,395
/ PRIOR FILING DATE: 2003-01-03
/ PRIOR APPLICATION NUMBER: US 09/009,953
/ PRIOR FILING DATE: 1998-01-21
/ PRIOR APPLICATION NUMBER: PCT/US98/01373
/ PRIOR FILING DATE: 1998-01-23
/ PRIOR APPLICATION NUMBER: US 60/036,713
/ PRIOR FILING DATE: 1997-01-23
/ PRIOR APPLICATION NUMBER: US 60/037,432
/ PRIOR FILING DATE: 1997-02-07
/ NUMBER OF SEQ ID NOS: 274
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 183
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-103-395-183
```

```
Query Match          29.2%; Score 28; DB 4; Length 15;
Best Local Similarity 66.7%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 9 LPTAAVSPG 17
    |||:|
Db 3 LPTAIIISP 11
```

```
RESULT 60
US-10-203-915A-174
/ Sequence 174, Application US/10203915A
/ Publication No. US20040106159A1
/ GENERAL INFORMATION:
/ APPLICANT: Kern, Florian
/ TITLE OF INVENTION: Method for Antigen-Specific Stimulation of T
/ TITLE OF INVENTION: Lymphocytes with synthetic Peptide Libraries
/ FILE REFERENCE: 010266w/JH/ml
/ CURRENT APPLICATION NUMBER: US/10/203,915A
/ CURRENT FILING DATE: 2002-08-15
/ NUMBER OF SEQ ID NOS: 260
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 174
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
```

```
/ FEATURE:
/ OTHER INFORMATION: Description of Artificial Sequence: HCMV pp65
/ OTHER INFORMATION: Fragment
US-10-203-915A-174
```

```
Query Match          29.2%; Score 28; DB 4; Length 15;
Best Local Similarity 46.7%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 4 EPHGYLLTAAVSPGK 18
    |||:|
Db 1 EPDVYTTSAFVFPTK 15
```

```
RESULT 61
US-10-886-773-49
/ Sequence 49, Application US/10886773
/ Publication No. US20050054107A1
/ GENERAL INFORMATION:
/ APPLICANT: Chulay, Jeffrey D.
/ APPLICANT: Dryga, Sergey A.
/ APPLICANT: Reap, Elizabeth A.
/ APPLICANT: Morris, John S.
/ APPLICANT: Olmsted, Robert A.
/ TITLE OF INVENTION: ALPHAVIRUS-BASED CYTOMEGALOVIRUS VACCINES
/ FILE REFERENCE: 9368-7
/ CURRENT APPLICATION NUMBER: US/10/886,773
/ CURRENT FILING DATE: 2004-07-08
/ PRIOR APPLICATION NUMBER: US 60/486,501
/ PRIOR FILING DATE: 2003-07-11
/ NUMBER OF SEQ ID NOS: 262
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 49
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Human cytomegalovirus
US-10-886-773-49
```

```
Query Match          29.2%; Score 28; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 4 EPHGYLLTAAVSPGK 18
    |||:|
Db 1 EPDVYTTSAFVFPTK 15
```

```
RESULT 62
US-10-414-522-25
/ Sequence 25, Application US/10414522
/ Publication No. US20050170433A1
/ GENERAL INFORMATION:
/ APPLICANT: The Procter & Gamble Company
/ APPLICANT: Mieling, Glen
/ APPLICANT: Bush, Rodney
/ APPLICANT: Colson, Amy-Odile
/ TITLE OF INVENTION: Three Dimensional Coordinates of Melanin-Concentrating Hormone
/ FILE REFERENCE: 9208
/ CURRENT APPLICATION NUMBER: US/10/414,522
/ CURRENT FILING DATE: 2003-04-15
/ NUMBER OF SEQ ID NOS: 25
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 25
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-414-522-25
```

```
Query Match          29.2%; Score 28; DB 5; Length 15;
Best Local Similarity 60.0%; Pred. No. 1.6e+03;
Matches 6; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

QY 8 YLTTAAVSPG 17
|||:
Db 1 YLYNAAISLG 10

RESULT 63

US-10-505-929-202
Sequence 202, Application US/10505929
Publication No. US20050221381A1
GENERAL INFORMATION:
APPLICANT: KLADE, CHRISTOF
APPLICANT: SCHALICH, JULIANE
APPLICANT: VYTVYTSKA, ORESTA
APPLICANT: AICHINGER, GERALD
APPLICANT: OTAVA, ALEXANDER
APPLICANT: MATTERN, FRANK
TITLE OF INVENTION: METHOD FOR ISOLATING LIGANDS
FILE REFERENCE: SONN:05505
CURRENT APPLICATION NUMBER: US/10/505,929
PRIOR FILING DATE: 2004-08-27
PRIOR APPLICATION NUMBER: PCT/EP03/02005
PRIOR FILING DATE: 2003-02-27
PRIOR APPLICATION NUMBER: A 316/2002
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: A 1376/2002
PRIOR FILING DATE: 2002-09-13
NUMBER OF SEQ ID NOS: 584
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 202
LENGTH: 15
TYPE: PRT
ORGANISM: Cycomegaloivirus
US-10-505-929-202

Query Match 29.2%; Score 28; DB 5; Length 15;
Best Local Similarity 46.7%; Pred. No. 1.6e+03;
Matches 7; Conservative 1; Mismatches 7; Indels 0; Gaps 0;

QY 4 BPHGYLTTAAVSPGX 18
|||:
Db 1 BPDVYTTSAFVPTK 15

RESULT 64

US-10-083-446-188
Sequence 188, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452

INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:

LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:

US-10-083-446-188

Query Match 29.2%; Score 28; DB 4; Length 18;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSPG 17
|||:
Db 1 YVIEGRISPG 10

RESULT 65

US-10-083-446-189
Sequence 189, Application US/10083446
Publication No. US20030185790A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Braford-Goldberg, Sarah R.
Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
Thomas, John W.

TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant (IL-3) Hematopoiesis Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: S. Christopher Bauer, Pharmacia Corporation
Corporate Patent Dept., Mail Zone 04E
STREET: 800 N. Lindbergh
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63167

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/083,446
FILING DATE: 26-Feb-2002
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: S. Christopher Bauer
REGISTRATION NUMBER: 42,305
REFERENCE/DOCKET NUMBER: C-2790/6
TELECOMMUNICATION INFORMATION:
TELEPHONE: (636)737-6257
TELEFAX: (636)737-5452
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-10-083-446-189

Query Match 29.2%; Score 28; DB 4; Length 18;
Best Local Similarity 40.0%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTLAAVSPG 17
|:::|
Db 1 YVIEGRISPG 10

RESULT 66
US-10-948-576-188
Sequence 188, Application US/10948576
Publication No. US20050059149A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Bratford-Goldberg, Sarah R.
Caparon, Maïre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoietic Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol M. Nielsen, Winstead Sechrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-SEP-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
FILING DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325

FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 188:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 188:
US-10-948-576-188

Query Match 29.2%; Score 28; DB 5; Length 18;
Best Local Similarity 40.0%; Pred. No. 2e+03; 3; Indels 0; Gaps 0;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTLAAVSPG 17
|:::|
Db 1 YVIEGRISPG 10

RESULT 67
US-10-948-576-189
Sequence 189, Application US/10948576
Publication No. US20050059149A1
GENERAL INFORMATION:
APPLICANT: Abrams, Mark A.
Bauer, S. C.
Bratford-Goldberg, Sarah R.
Caparon, Maïre H.
Easton, Alan M.
Klein, Barbara K.
McKearn, John P.
Olins, Peter O.
Paik, Kumman
Thomas, John W.
TITLE OF INVENTION: Methods Of Ex-Vivo Expansion Of Hematopoietic Cells
Using Multivariant IL-3 Hematopoietic Chimera Proteins
NUMBER OF SEQUENCES: 197
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol M. Nielsen, Winstead Sechrest & Minick P.C.
STREET: P.O. Box 50784
CITY: Dallas
STATE: Texas
COUNTRY: USA
ZIP: 75201
COMPUTER READABLE FORM:
MEDIUM TYPE: CD
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/948,576
FILING DATE: 22-SEP-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 10/083,446
FILING DATE: 22-FEB-2002
APPLICATION NUMBER: 08/762,227
FILING DATE: 09-DEC-1996
APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
ATTORNEY/AGENT INFORMATION:

NAME: Carol M. Nielsen
REGISTRATION NUMBER: 37,676
REFERENCE/DOCKET NUMBER: 2790/7 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-650-2722
TELEFAX: 214-745-5390
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 189:
US-10-948-576-189

Query Match 29.2%; Score 28; DB 5; Length 18;
Best Local Similarity 40.0%; Pred. No. 2e+03;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLLTAVSPG 17
|::|||
Db 1 YVLEKISPG 10

RESULT 68
US-09-863-054-18
Sequence 18, Application US/09863054
Publication No. US20030021809A1
GENERAL INFORMATION:
APPLICANT: Chisari, Francis V.
TITLE OF INVENTION: Peptides for Inducing Cytotoxic T
Lymphocyte Responses to Hepatitis B Virus
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/863,054
FILING DATE: 21-May-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/935,898
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 08/024,120
FILING DATE: 26-FEB-1993
APPLICATION NUMBER: US 08/396,283
FILING DATE: 27-FEB-1995
APPLICATION NUMBER: US 08/463,486
FILING DATE: 05-JUN-1995
ATTORNEY/AGENT INFORMATION:
NAME: Lockyer, Jean M.
REGISTRATION NUMBER: 44,879
REFERENCE/DOCKET NUMBER: 014740-000421US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 18:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide

SEQUENCE DESCRIPTION: SEQ ID NO: 18:
US-09-863-054-18

Query Match 29.2%; Score 28; DB 3; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHSYLLTAAV 14
|::|||
Db 1 PHSYLLTAAV 10

RESULT 69
US-10-128-711-101
Sequence 101, Application US/10128711
Publication No. US2003009634A1
GENERAL INFORMATION:
APPLICANT: VITIELLO, Maria A.
CHESTNUT, Robert W.
SETTE, Alessandro D.
CELIS, Betsan
GRAY, Howard
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR ELICITING
CTL IMMUNITY
NUMBER OF SEQUENCES: 153
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Kourile and Crew
STREET: Stewart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/128,711
FILING DATE: 22-Apr-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/197,484
FILING DATE: 16-FEB-1994
APPLICATION NUMBER: US 07/935,811
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
APPLICATION NUMBER: US 07/749,568
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEFAX: (206) 623-6793
INFORMATION FOR SEQ ID NO: 101:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 1..20
OTHER INFORMATION: /note= "HTI-inducing peptide
specific for HBV/ HBc50-69"
SEQUENCE DESCRIPTION: SEQ ID NO: 101:
US-10-128-711-101

Query Match 29.2% Score 28; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
| | | | |
| | | | |
Db 1 PHHYALRQAI 10

RESULT 70
US-10-359-431-7
; Sequence 7, Application US/10359431
; Publication No. US2003017538A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for inducing cytotoxic T
; Lymphocyte Responses to Hepatitis B Virus
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Townsend and Townsend and Crew LLP
; STREET: Two Embarcadero Center, Eighth Floor
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/359,431
; FILING DATE: 05-Feb-2003
; CLASSIFICATION: <Unknown>
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/749,540
; FILING DATE: 26-AUG-1991
; APPLICATION NUMBER: US 07/935,898
; FILING DATE: 26-AUG-1992
; APPLICATION NUMBER: US 08/100,870
; FILING DATE: 02-AUG-1993
; APPLICATION NUMBER: WO PCT/US94/08685
; FILING DATE: 01-AUG-1994
; APPLICATION NUMBER: US 08/591,502
; FILING DATE: 20-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Lockyer, Jean M.
; REGISTRATION NUMBER: 44,879
; REFERENCE/DOCKET NUMBER: 014740-000231US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 576-0200
; TELEFAX: (415) 576-0300
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
; MOLECULAR TYPE: peptide
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-10-359-431-7

Query Match 29.2% Score 28; DB 4; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
| | | | |
| | | | |
Db 1 PHHYALRQAI 10

RESULT 71

US-10-397-411-13
; Sequence 13, Application US/10397411
; Publication No. US2003018622A1
; GENERAL INFORMATION:
; APPLICANT: Immune systems
; TITLE OF INVENTION: CD4+ T-LYMPHOCYTE-SPECIFIC HEPATITIS C VIRUS-EPITOPES
; FILE REFERENCE: 029474-5011
; CURRENT APPLICATION NUMBER: US/10/397,411
; CURRENT FILING DATE: 2003-03-26
; PRIOR APPLICATION NUMBER: PCT/EP01/11263
; PRIOR FILING DATE: 2001-09-28
; PRIOR APPLICATION NUMBER: EP 00121138.2
; PRIOR FILING DATE: 2000-09-28
; NUMBER OF SEQ ID NOS: 21
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 13
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-397-411-13

Query Match 29.2% Score 28; DB 4; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LRTAAVSPG 17
| | | | |
| | | | |
Db 8 LRPALISPG 16

RESULT 72
US-10-776-013-250
; Sequence 250, Application US/10776013
; Publication No. US20040226056A1
; GENERAL INFORMATION:
; APPLICANT: MYRIAD GENETICS, INC.
; APPLICANT: Roch, Jean-Marc
; APPLICANT: Bartel, Paul
; APPLICANT: Heichman, Karen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATING NEUROLOGICAL DISORDERS AND
; FILE REFERENCE: 1600.24
; CURRENT APPLICATION NUMBER: US/10/776,013
; CURRENT FILING DATE: 2004-02-09
; PRIOR APPLICATION NUMBER: 09/948904
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 09/466139
; PRIOR FILING DATE: 1999-12-21
; PRIOR APPLICATION NUMBER: 60/113534
; PRIOR FILING DATE: 1998-12-22
; PRIOR APPLICATION NUMBER: 60/124120
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/141243
; PRIOR FILING DATE: 1999-06-30
; PRIOR APPLICATION NUMBER: 09/975072
; PRIOR FILING DATE: 2001-10-12
; PRIOR APPLICATION NUMBER: 60/240790
; PRIOR FILING DATE: 2000-10-17
; PRIOR APPLICATION NUMBER: 10/194967
; PRIOR FILING DATE: 2002-07-15
; PRIOR APPLICATION NUMBER: 60/304775
; PRIOR FILING DATE: 2001-07-13
; NUMBER OF SEQ ID NOS: 695
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 250
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-776-013-250

Query Match 29.2% Score 28; DB 5; Length 20;
Best Local Similarity 41.7%; Pred. No. 2.2e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 5 PHGYLTAASP 16
| | | | |
DB 2 PRRYTAALLSP 13

RESULT 73
US-10-453-18
; Sequence 18, Application US/10881453
; Publication No. US20040241143A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T Lymphocyte Responses to
; FILE REFERENCE: EPI-T101D5
; CURRENT APPLICATION NUMBER: US/10/881,453
; PRIOR FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 09/863,054
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 08/463,486
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/396,283
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: 08/024,120
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/935,898
; PRIOR FILING DATE: 1992-08-26
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: HBC50-69
US-10-881-453-18

Query Match 29.2%; Score 28; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAASP 14
| | | | |
DB 1 PHHYALRQAI 10

RESULT 74
US-10-621-675-446
; Sequence 446, Application US/10621675
; Publication No. US20050049398A1
; GENERAL INFORMATION:
; APPLICANT: De Levy, Robert
; TITLE OF INVENTION: PROCESS FOR THE DETERMINATION OF PEPTIDES CORRESPONDING
; TITLE OF INVENTION: TO IMMUNOLOGICALLY IMPORTANT EPITOPES AND THEIR USE IN
; TITLE OF INVENTION: A PROCESS FOR DETERMINATION OF ANTIBODIES OF
; TITLE OF INVENTION: BIOTINYLATED PEPTIDES CORRESPONDING TO IMMUNOLOGICALLY IMPORTANT
; TITLE OF INVENTION: EPITOPES, A PROCESS FOR PREPARING THEM AND COMPOSITIONS
; FILE REFERENCE: 2752-11
; CURRENT APPLICATION NUMBER: US/10/621,675
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US/09/576,824A
; PRIOR FILING DATE: 08/723,425
; PRIOR APPLICATION NUMBER: 1996-09-30
; PRIOR FILING DATE: 1996-09-30
; PRIOR APPLICATION NUMBER: 09/146,028
; PRIOR FILING DATE: 1993-11-22
; PRIOR APPLICATION NUMBER: PCT/EP93/00517
; PRIOR FILING DATE: 1993-03-08
; PRIOR APPLICATION NUMBER: EP 92400598.6
; PRIOR FILING DATE: 1992-03-06
; NUMBER OF SEQ ID NOS: 600
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 446

; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis C virus
US-10-621-675-446

Query Match 29.2%; Score 28; DB 5; Length 20;
Best Local Similarity 66.7%; Pred. No. 2.2e+03;
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LITAAVSPG 17
| | | | |
DB 10 LLPALISPG 18

RESULT 75
US-10-931-566-22
; Sequence 22, Application US/10931566
; Publication No. US20050106137A1
; GENERAL INFORMATION:
; APPLICANT: Apton Corporation
; APPLICANT: Grimes, Stephen
; TITLE OF INVENTION: Chimeric Peptide Immunogens
; FILE REFERENCE: 1102865-0047CIP
; CURRENT APPLICATION NUMBER: US/10/931,566
; CURRENT FILING DATE: 2004-08-31
; PRIOR APPLICATION NUMBER: 09/848,834
; PRIOR FILING DATE: 2001-05-04
; PRIOR APPLICATION NUMBER: 60/202,328
; PRIOR FILING DATE: 2000-05-05
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 22
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Hepatitis B virus
US-10-931-566-22

Query Match 29.2%; Score 28; DB 5; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAASP 14
| | | | |
DB 1 PHHYALRQAI 10

RESULT 76
US-11-068-710-18
; Sequence 18, Application US/11068710
; Publication No. US20050232935A1
; GENERAL INFORMATION:
; APPLICANT: Chisari, Francis V.
; TITLE OF INVENTION: Peptides for Inducing Cytotoxic T Lymphocyte Responses to
; TITLE OF INVENTION: Hepatitis B Virus
; FILE REFERENCE: EPI-T101D5
; CURRENT APPLICATION NUMBER: US/11/068,710
; CURRENT FILING DATE: 2005-02-28
; PRIOR APPLICATION NUMBER: US/10/861,453
; PRIOR FILING DATE: 2004-06-29
; PRIOR APPLICATION NUMBER: 09/863,054
; PRIOR FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 08/463,486
; PRIOR FILING DATE: 1995-06-05
; PRIOR APPLICATION NUMBER: 08/396,283
; PRIOR FILING DATE: 1995-02-27
; PRIOR APPLICATION NUMBER: 08/024,120
; PRIOR FILING DATE: 1993-02-26
; PRIOR APPLICATION NUMBER: 07/935,898
; PRIOR FILING DATE: 1992-08-26
; NUMBER OF SEQ ID NOS: 57
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 18
; LENGTH: 20

TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: HBC50-69
US-11-068-710-18

Query Match 29.2%; Score 28; DB 6; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAY 14
DB 1 PHHYALRQAI 10

RESULT 77
US-10-461-864-5
Sequence 5, Application US/10461864
Publication No. US20040208919A1
GENERAL INFORMATION:
APPLICANT: Nicotian, Yves Claude
TITLE OF INVENTION: Vaccination Against Prion Diseases
FILE REFERENCE: 49918-0123 (49918-286753)
CURRENT APPLICATION NUMBER: US/10/461,864
CURRENT FILING DATE: 2003-06-13
PRIOR APPLICATION NUMBER: US 60/388,795
PRIOR FILING DATE: 2002-06-13
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.1
SEQ ID NO 5
LENGTH: 9
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic
US-10-461-864-5

Query Match 28.1%; Score 27; DB 4; Length 9;
Best Local Similarity 55.6%; Pred. No. 1.7e+06;
Matches 5; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLTAAYS 15
DB 1 GYMLGSAMS 9

RESULT 78
US-09-747-287-215
Sequence 215, Application US/09747287
Publication No. US20030207264A1
GENERAL INFORMATION:
APPLICANT: KOMORIYA, AKIRA
TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
FILE REFERENCE: 300-948600US
CURRENT APPLICATION NUMBER: US/09/747,287
CURRENT FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: US 09/349,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US08/802,981
PRIOR FILING DATE: 1997-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11
SOFTWARE: PatentIn version 3.2
SEQ ID NO 215
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Synthetic peptide. Artificial protease substrate.
US-09-747-287-215

Query Match 28.1%; Score 27; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 4 DGIIDPKGY 11

RESULT 79
US-09-874-350A-186
Sequence 186, Application US/09874350A
Publication No. US20040096926A1
GENERAL INFORMATION:
APPLICANT: Oncolimmunin, Inc.
APPLICANT: Komoriya, Akira
TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL
FILE REFERENCE: 300-903840US
CURRENT APPLICATION NUMBER: US/09/874,350A
CURRENT FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: PCT/US98/00300
PRIOR FILING DATE: 1998-02-20
PRIOR APPLICATION NUMBER: PCT/US00/24882
PRIOR FILING DATE: 2000-09-11
PRIOR APPLICATION NUMBER: US 09/394,019
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 08/802,981
PRIOR FILING DATE: 1997-02-20
NUMBER OF SEQ ID NOS: 221
SOFTWARE: PatentIn version 3.0
SEQ ID NO 186
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Synthetic peptide substrate
NAME/KEY: misc feature
OTHER INFORMATION: Artificial = synthetic protease indicator
NAME/KEY: MOD_RES
LOCATION: (9)-(9)
OTHER INFORMATION: K is derivatized with fluorophore
NAME/KEY: MOD_RES
LOCATION: (1)-(1)
OTHER INFORMATION: D is derivatized with fluorophore
US-09-874-350A-186

Query Match 28.1%; Score 27; DB 3; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 4 DGIIDPKGY 11

RESULT 80
US-10-014-340-731
Sequence 731, Application US/10014340
Publication No. US20030064411A1
GENERAL INFORMATION:
APPLICANT: Herath, et al
TITLE OF INVENTION: Nucleic Acid Molecules, Polypeptides and Uses Therefor, Including
FILE REFERENCE: 9195-078
CURRENT APPLICATION NUMBER: US/10/014,340
CURRENT FILING DATE: 2001-12-10
NUMBER OF SEQ ID NOS: 823
SOFTWARE: PatentIn version 3.0
SEQ ID NO 731
LENGTH: 11

TYPE: PRT
ORGANISM: Homo sapiens
US-10-014-340-731

Query Match 28.1%; Score 27; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEBPGYL 10
DB 2 FIPHGLIM 9

RESULT 81
US-10-285-394-364
Sequence 364, Application US/10285394
Publication No. US20030228583A1
GENERAL INFORMATION:
APPLICANT: AMACHER, DAVID E.
APPLICANT: PASULO, LISA M.
APPLICANT: HERATH, HERATH MUDIYANSELAGE ATHULA CHANDRASIRI
APPLICANT: HOLT, GORDON DUANE
APPLICANT: STIGER, THOMAS R.
TITLE OF INVENTION: BIOMARKERS OF LIVER RESPONSE
FILE REFERENCE: POA-003.01
CURRENT APPLICATION NUMBER: US/10/285,394
CURRENT FILING DATE: 2003-02-07
PRIOR APPLICATION NUMBER: 60/335,964
PRIOR FILING DATE: 2001-10-31
NUMBER OF SEQ ID NOS: 412
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 364
LENGTH: 11
TYPE: PRT
ORGANISM: Homo sapiens
US-10-285-394-364

Query Match 28.1%; Score 27; DB 4; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.7e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEBPGYL 10
DB 2 FIPHGLIM 9

RESULT 82
US-10-468-543-79
Sequence 79, Application US/10468543
Publication No. US20040091938A1
GENERAL INFORMATION:
APPLICANT: Irimura, Tetsuro
APPLICANT: Matsumoto, Mariko
APPLICANT: Yam, Mijung
APPLICANT: Ono, Takashi
TITLE OF INVENTION: Lectins for Analyzing Sugar Chains and Method of Using the Same
FILE REFERENCE: 03-786
CURRENT APPLICATION NUMBER: US/10/468,543
CURRENT FILING DATE: 2003-08-20
PRIOR APPLICATION NUMBER: JP 2001-044221
PRIOR FILING DATE: 2001-02-20
NUMBER OF SEQ ID NOS: 95
SOFTWARE: PatentIn version 3.1
SEQ ID NO 79
LENGTH: 11
TYPE: PRT
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Generated from randomly recombinant DNA part of MAH.
US-10-468-543-79

Query Match 28.1%; Score 27; DB 4; Length 11;
Best Local Similarity 57.1%; Pred. No. 1.7e+03;

Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPHG 7
DB 1 DTYLPHG 7

RESULT 83
US-09-486-734A-28
Sequence 28, Application US/09486734A
Patent No. US20020164732A1
GENERAL INFORMATION:
APPLICANT: Chopin, Marie-Christine
APPLICANT: Clier, Florence
APPLICANT: Erlich, S. Dusko
APPLICANT: Gautier, Michel
APPLICANT: Schouler, Catherine
TITLE OF INVENTION: Institut National de la Recherche Agronomique
TITLE OF INVENTION: Resistance Mechanisms to ic Type R/M
FILE REFERENCE: 33339/196048
CURRENT APPLICATION NUMBER: US/09/486,734A
CURRENT FILING DATE: 2000-05-03
PRIOR APPLICATION NUMBER: PCT/FR98/01873
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: FR 97/10885
PRIOR FILING DATE: 1997-09-02
NUMBER OF SEQ ID NOS: 40
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 28
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Hcdm subunit
US-09-486-734A-28

Query Match 28.1%; Score 27; DB 3; Length 12;
Best Local Similarity 55.6%; Pred. No. 1.8e+03;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTTAA 13
DB 2 PHGVLPFGA 10

RESULT 84
US-09-929-266-13
Sequence 13, Application US/09929266
Publication No. US20030045594A1
GENERAL INFORMATION:
APPLICANT: Brian T. Chait
APPLICANT: Datin R. Latimer
APPLICANT: Paul M. Lizaradi
APPLICANT: Eric R. Kershner
APPLICANT: Jon S. Morrow
APPLICANT: Matthew E. Roch
APPLICANT: Martin J. McConnell
TITLE OF INVENTION: ULTRA-SENSITIVE DETECTION SYSTEMS
FILE REFERENCE: 01173_0003U2
CURRENT APPLICATION NUMBER: US/09/929,266
CURRENT FILING DATE: 2001-08-13
PRIOR APPLICATION NUMBER: 60/224,939
PRIOR FILING DATE: 2000-08-11
PRIOR APPLICATION NUMBER: 60/283,498
PRIOR FILING DATE: 2000-04-12
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 13
LENGTH: 12
TYPE: PRT
ORGANISM: Artificial Sequence


```
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 40
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-40
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : | | |
DB      6 DGDIDPKGY 13
```

```
RESULT 89
US-09-747-287-41
/ Sequence 41, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 41
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-41
```

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Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : | | |
DB      6 DGDIDPKGY 13
```

```
RESULT 90
US-09-747-287-44
/ Sequence 44, Application US/09747287
```

```
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 44
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-44
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : | | |
DB      6 DGDIDPKGY 13
```

```
RESULT 91
US-09-747-287-50
/ Sequence 50, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 50
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-50
```

```
Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      1 DAFEPHGY 8
      | : | | |
DB      6 DGDIDPKGY 13
```

```
RESULT 92
US-09-747-287-224
```

```
/ Sequence 224, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 224
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-224
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPPHY 8
DB 6 DGIIDPKGY 13
```

```
RESULT 93
US-09-747-287-225
/ Sequence 225, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 225
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-225
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPPHY 8
DB 6 DGIIDPKGY 13
```

RESULT 94

```
US-09-747-287-229
/ Sequence 229, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 229
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-229
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPPHY 8
DB 6 DGIIDPKGY 13
```

```
RESULT 95
US-09-747-287-230
/ Sequence 230, Application US/09747287
/ Publication No. US20030207264A1
/ GENERAL INFORMATION:
/ APPLICANT: KOMORIYA, AKIRA
/ APPLICANT: PACKARD, BEVERLY S.
/ TITLE OF INVENTION: HOMO-DOUBLY LABELED COMPOSITIONS FOR THE DETECTION OF ENZYME
/ FILE REFERENCE: 300-948600US
/ CURRENT APPLICATION NUMBER: US/09/747,287
/ PRIOR FILING DATE: 2000-12-22
/ PRIOR APPLICATION NUMBER: US 09/349,019
/ PRIOR FILING DATE: 1999-09-10
/ PRIOR APPLICATION NUMBER: US08/802,981
/ PRIOR FILING DATE: 1997-02-20
/ PRIOR APPLICATION NUMBER: PCT/US00/24882
/ PRIOR FILING DATE: 2000-09-11
/ NUMBER OF SEQ ID NOS: 242
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 230
/ LENGTH: 13
/ TYPE: PRT
/ ORGANISM: Artificial
/ FEATURE:
/ OTHER INFORMATION: Synthetic peptide.
US-09-747-287-230
```

```
Query Match      28.1% Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY 1 DAEPPHY 8
DB 6 DGIIDPKGY 13
```

```
RESULT 96
US-09-874-350A-6
; Sequence 6, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 6
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb or Pro
US-09-874-350A-6

Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DAFEPHGY 8
DB      6 DGIIDPKGY 13

RESULT 97
US-09-874-350A-7
; Sequence 7, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 7
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: Synthetic peptide substrate
US-09-874-350A-7
```

```
; LOCATION: (4)..(4)
; OTHER INFORMATION: X is Alb or Pro
US-09-874-350A-7

Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DAFEPHGY 8
DB      6 DGIIDPKGY 13

RESULT 98
US-09-874-350A-10
; Sequence 10, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
; PRIOR FILING DATE: 1998-02-20
; PRIOR APPLICATION NUMBER: PCT/US00/24882
; PRIOR FILING DATE: 2000-09-11
; PRIOR APPLICATION NUMBER: US 09/394,019
; PRIOR FILING DATE: 1999-09-10
; PRIOR APPLICATION NUMBER: US 08/802,981
; PRIOR FILING DATE: 1997-02-20
; NUMBER OF SEQ ID NOS: 221
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: MOD_RES
; LOCATION: (1)..(1)
; OTHER INFORMATION: BLOCKED with Fmoc
; NAME/KEY: MOD_RES
; LOCATION: (3)..(3)
; OTHER INFORMATION: X is Alb or Pro
US-09-874-350A-10

Query Match      28.1%; Score 27; DB 3; Length 13;
Best Local Similarity 50.0%; Pred. No. 2e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY      1 DAFEPHGY 8
DB      6 DGIIDPKGY 13

RESULT 99
US-09-874-350A-16
; Sequence 16, Application US/09874350A
; Publication No. US20040096926A1
; GENERAL INFORMATION:
; APPLICANT: Oncoimmunin, Inc.
; APPLICANT: Komoriya, Akira
; APPLICANT: Packard, Beverly
; TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
; FILE REFERENCE: 300-903840US
; CURRENT APPLICATION NUMBER: US/09/874,350A
; PRIOR FILING DATE: 2001-06-04
; PRIOR APPLICATION NUMBER: PCT/US98/00300
```

/ PRIOR FILING DATE: 1998-02-20
 / PRIOR APPLICATION NUMBER: PCT/US00/24882
 / PRIOR FILING DATE: 2000-09-11
 / PRIOR APPLICATION NUMBER: US 09/394,019
 / PRIOR FILING DATE: 1999-09-10
 / PRIOR APPLICATION NUMBER: US 08/802,981
 / PRIOR FILING DATE: 1997-02-20
 / NUMBER OF SEQ ID NOS: 221
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 16
 / LENGTH: 13
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Synthetic peptide substrate
 / NAME/KEY: MOD_RES
 / LOCATION: (1)..(11)
 / OTHER INFORMATION: BLOCKED with Fmoc
 US-09-874-350A-16

Query Match 28.1%; Score 27; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHGY 8
 Db 6 DGIDPKGY 13

RESULT 100
 US-09-874-350A-195
 / Sequence 195, Application US/09874350A
 / Publication No. US20040096926A1
 / GENERAL INFORMATION:
 / APPLICANT: Oncolimmunin, Inc.
 / APPLICANT: Komoriya, Akira
 / APPLICANT: Packard, Beverly
 / TITLE OF INVENTION: COMPOSITIONS FOR THE DETECTION OF ENZYME ACTIVITY IN BIOLOGICAL S
 / TITLE OF INVENTION: AND METHODS OF USE THEREOF
 / FILE REFERENCE: 300-903840US
 / CURRENT APPLICATION NUMBER: US/09/874,350A
 / CURRENT FILING DATE: 2001-06-04
 / PRIOR APPLICATION NUMBER: PCT/US98/00300
 / PRIOR FILING DATE: 1998-02-20
 / PRIOR APPLICATION NUMBER: PCT/US00/24882
 / PRIOR FILING DATE: 2000-09-11
 / PRIOR APPLICATION NUMBER: US 09/394,019
 / PRIOR FILING DATE: 1999-09-10
 / PRIOR APPLICATION NUMBER: US 08/802,981
 / PRIOR FILING DATE: 1997-02-20
 / NUMBER OF SEQ ID NOS: 221
 / SOFTWARE: PatentIn version 3.0
 / SEQ ID NO 195
 / LENGTH: 13
 / TYPE: PRT
 / ORGANISM: Artificial Sequence
 / FEATURE:
 / OTHER INFORMATION: Synthetic peptide substrate
 / NAME/KEY: misc feature
 / OTHER INFORMATION: ARTIFICIAL/UNKNOWN = synthetic protease indicator
 / NAME/KEY: MOD_RES
 / LOCATION: (1)..(11)
 / OTHER INFORMATION: K 1s blocked with Fmoc
 / OTHER INFORMATION: K 1s derivatized with fluorophore
 US-09-874-350A-195

Query Match 28.1%; Score 27; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2e+03;
 Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 1 DAFEPHGY 8

Db 6 DGIDPKGY 13

Search completed: January 20, 2006, 19:45:43
 Job time : 66.9038 secs

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OM protein - protein search, using sw model

Run on: January 20, 2006, 19:12:21 Search time 7.26923 Seconds
(without alignments)
25.093 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96

Sequence: 1 DAFEPHYLTAVSPEK 18

Scoring table: BLOSUM62

Gapop 10.0, Gapept 0.5

Searched: 70606 seqs, 10133881 residues

Total number of hits satisfying chosen parameters: 34662

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database:

Published Applications AA New:
1: /cgn2_6/prodata/1/pubpaa/US08_NEW_PUB.pep:*
2: /cgn2_6/prodata/1/pubpaa/US06_NEW_PUB.pep:*
3: /cgn2_6/prodata/1/pubpaa/US07_NEW_PUB.pep:*
4: /cgn2_6/prodata/1/pubpaa/PCT_NEW_PUB.pep:*
5: /cgn2_6/prodata/1/pubpaa/US09_NEW_PUB.pep:*
6: /cgn2_6/prodata/1/pubpaa/US10_NEW_PUB.pep:*
7: /cgn2_6/prodata/1/pubpaa/US11_NEW_PUB.pep:*
8: /cgn2_6/prodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	31	32.3	18	6	US-10-939-890-133
2	28	29.2	16	7	US-11-134-046-10
3	27	28.1	19	6	US-10-503-575-224
4	26	27.1	14	7	US-11-054-515-2400
5	26	27.1	14	7	US-11-054-515-2477
6	26	27.1	14	7	US-11-144-630-33
7	25.5	26.6	15	7	US-11-045-024-13324
8	25.5	26.6	15	7	US-11-045-024-13327
9	25	26.0	8	7	US-11-062-186-2
10	25	26.0	9	7	US-11-045-024-3531
11	25	26.0	9	7	US-11-045-024-10473
12	25	26.0	9	7	US-11-045-024-12303
13	25	26.0	10	7	US-11-045-024-3546
14	25	26.0	10	7	US-11-045-024-10479
15	25	26.0	11	7	US-11-045-024-12307
16	25	26.0	11	7	US-11-045-024-3559
17	25	26.0	11	7	US-11-045-024-10483
18	25	26.0	11	7	US-11-045-024-12311
19	25	26.0	15	7	US-11-041-893-2
20	25	26.0	15	7	US-11-041-893-13
21	25	26.0	20	6	US-10-939-890-138
22	25	26.0	20	6	US-10-623-155-247
23	25	26.0	20	7	US-11-022-562-292
24	25	26.0	20	7	US-11-022-562-293
25	25	26.0	20	7	US-11-043-542-42

26	24	25.0	9	7	US-11-152-747-35	Sequence 35, App1
27	24	25.0	11	7	US-11-054-515-3192	Sequence 3192, App
28	24	25.0	11	7	US-11-158-723-7	Sequence 7, App1
29	24	25.0	12	6	US-10-507-662-53	Sequence 53, App1
30	24	25.0	14	7	US-11-054-515-2602	Sequence 2602, App
31	24	25.0	15	7	US-11-054-515-2909	Sequence 2909, App
32	24	25.0	16	6	US-10-467-657-9074	Sequence 9074, App
33	24	25.0	16	6	US-10-467-657-9075	Sequence 9075, App
34	24	25.0	20	7	US-11-022-562-176	Sequence 176, App
35	24	25.0	20	7	US-11-128-900-1118	Sequence 118, App
36	24	25.0	20	7	US-11-128-900-1119	Sequence 119, App
37	24	25.0	20	7	US-11-128-900-121	Sequence 121, App
38	24	25.0	20	7	US-11-128-900-122	Sequence 122, App
39	24	25.0	20	7	US-11-128-900-123	Sequence 123, App
40	24	25.0	20	7	US-11-128-900-124	Sequence 124, App
41	24	25.0	20	7	US-11-128-900-125	Sequence 125, App
42	23	24.0	8	6	US-10-859-643-31	Sequence 31, App1
43	23	24.0	9	6	US-10-859-643-31	Sequence 31, App1
44	23	24.0	9	6	US-10-859-643-115	Sequence 115, App
45	23	24.0	9	6	US-10-859-643-698	Sequence 698, App
46	23	24.0	9	7	US-11-097-864-31	Sequence 31, App1
47	23	24.0	9	7	US-11-097-864-115	Sequence 115, App
48	23	24.0	9	7	US-11-097-864-698	Sequence 698, App
49	23	24.0	9	7	US-11-097-812-31	Sequence 31, App1
50	23	24.0	9	7	US-11-097-812-115	Sequence 115, App
51	23	24.0	9	7	US-11-097-812-698	Sequence 698, App
52	23	24.0	10	6	US-10-859-643-100	Sequence 100, App
53	23	24.0	10	6	US-10-859-643-433	Sequence 433, App
54	23	24.0	10	6	US-10-859-643-619	Sequence 619, App
55	23	24.0	10	7	US-11-097-864-100	Sequence 100, App
56	23	24.0	10	7	US-11-097-864-433	Sequence 433, App
57	23	24.0	10	7	US-11-097-864-619	Sequence 619, App
58	23	24.0	10	7	US-11-097-912-100	Sequence 100, App
59	23	24.0	10	7	US-11-097-912-433	Sequence 433, App
60	23	24.0	10	7	US-11-097-912-619	Sequence 619, App
61	23	24.0	13	6	US-10-511-559-637	Sequence 637, App
62	23	24.0	14	7	US-10-866-671-14	Sequence 14, App
63	23	24.0	14	7	US-11-054-515-2916	Sequence 2916, App
64	23	24.0	14	7	US-11-073-347-116	Sequence 116, App
65	23	24.0	15	7	US-11-022-562-35	Sequence 35, App1
66	23	24.0	15	7	US-11-073-347-110	Sequence 110, App
67	23	24.0	15	7	US-11-045-024-13033	Sequence 13033, App
68	23	24.0	15	7	US-11-045-024-13034	Sequence 13034, App
69	23	24.0	15	7	US-11-045-024-13046	Sequence 13046, App
70	23	24.0	15	7	US-11-045-024-14210	Sequence 14210, App
71	23	24.0	15	7	US-11-045-024-14400	Sequence 14400, App
72	23	24.0	15	7	US-11-045-024-14417	Sequence 14417, App
73	23	24.0	15	7	US-11-045-024-14477	Sequence 14477, App
74	23	24.0	15	7	US-11-033-039-581	Sequence 581, App
75	23	24.0	15	7	US-11-041-893-176	Sequence 176, App
76	23	24.0	16	7	US-11-033-039-839	Sequence 839, App
77	23	24.0	17	7	US-11-073-347-118	Sequence 118, App
78	23	24.0	18	7	US-11-033-039-993	Sequence 993, App
79	23	24.0	18	7	US-11-033-039-1048	Sequence 1048, App
80	23	24.0	19	7	US-11-054-515-3036	Sequence 3036, App
81	23	24.0	20	7	US-11-022-562-286	Sequence 286, App
82	23	24.0	20	7	US-11-022-562-287	Sequence 287, App
83	22.5	23.4	11	7	US-11-045-024-3558	Sequence 3558, App
84	22.5	23.4	11	7	US-11-045-024-10541	Sequence 10541, App
85	22.5	23.4	11	7	US-11-045-024-12349	Sequence 12349, App
86	22.5	23.4	15	7	US-11-045-024-13314	Sequence 13314, App
87	22.5	23.4	19	6	US-10-503-575-197	Sequence 197, App
88	22	22.9	8	7	US-11-045-024-1035	Sequence 1035, App
89	22	22.9	8	7	US-11-045-024-3518	Sequence 3518, App
90	22	22.9	8	7	US-11-045-024-4007	Sequence 4007, App
91	22	22.9	8	7	US-11-045-024-6362	Sequence 6362, App
92	22	22.9	8	7	US-11-045-024-10522	Sequence 10522, App
93	22	22.9	8	7	US-11-045-024-12335	Sequence 12335, App
94	22	22.9	8	7	US-11-045-024-12616	Sequence 12616, App
95	22	22.9	8	7	US-11-116-144-73	Sequence 73, App1
96	22	22.9	9	6	US-10-999-866-60	Sequence 60, App1
97	22	22.9	9	7	US-11-045-024-1138	Sequence 1138, App
98	22	22.9	9	7	US-11-045-024-3530	Sequence 3530, App

99 22 22.9 9 7 US-11-045-024-4061 Sequence 4061, Ap
100 22 22.9 9 7 US-11-045-024-5639 Sequence 5639, Ap

ALIGNMENTS

RESULT 1

US-10-939-890-133
Sequence 133, Application US/10939890
Publication No. US20050250700A1
GENERAL INFORMATION:
APPLICANT: Sato, Aaron K.
APPLICANT: Sexton, Daniel J.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Ladner, Robert C.
APPLICANT: Arbogast, Christophe
APPLICANT: Bussat, Philippe
APPLICANT: Fan, Hong
APPLICANT: Khurana, Sudha
APPLICANT: Linder, Karen B.
APPLICANT: Marinelli, Edmund R.
APPLICANT: Nanjappa, Palaniappa
APPLICANT: Nunn, Adrian D.
APPLICANT: Pillai, Radhakrishna
APPLICANT: Pochon, Sibylle
APPLICANT: Ramalingam, Kondareddiar
APPLICANT: Shrivastava, Ajay
APPLICANT: Song, Bo
APPLICANT: Swenson, Rolf E.
APPLICANT: Von Wronski, Mathew A.
TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
FILE REFERENCE: D0617,70014US00
CURRENT APPLICATION NUMBER: US/10/939,890
CURRENT FILING DATE: 2004-09-13
PRIOR APPLICATION NUMBER: US 10/661,156
PRIOR FILING DATE: 2003-09-11
PRIOR APPLICATION NUMBER: US 10/382,082
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: PCT/US03/06731
PRIOR FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/440,411
PRIOR FILING DATE: 2003-01-15
PRIOR APPLICATION NUMBER: US 60/360,851
PRIOR FILING DATE: 2002-03-01
NUMBER OF SEQ ID NOS: 883
SOFTWARE: PatSeq for Windows Version 4.0
SEQ ID NO 133
LENGTH: 18
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Library Isolate
US-10-939-890-133

Query Match 32.3%; Score 31; DB 6; Length 18;

Best Local Similarity 55.6%; Pred. No. 19;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEBHYLLT 11
:|:|:|

Db 6 YEDHTYMLT 14

RESULT 2

US-11-134-046-10
Sequence 10, Application US/11134046
Publication No. US20050266467A1
GENERAL INFORMATION:
APPLICANT: Roy, Susmita
TITLE OF INVENTION: BLOWMARRERS FOR MULTIPLE SCLEROSIS AND METHODS OF USE THEREOF
FILE REFERENCE: 4220-103
CURRENT APPLICATION NUMBER: US/11/134,046

CURRENT FILING DATE: 2005-05-19
PRIOR APPLICATION NUMBER: 60/572,655
PRIOR FILING DATE: 2004-05-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn version 3.3
SEQ ID NO 10
LENGTH: 16
TYPE: PRT
ORGANISM: Homo sapiens
US-11-134-046-10

Query Match 29.2%; Score 28; DB 7; Length 16;

Best Local Similarity 42.9%; Pred. No. 52;
Matches 6; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 5 PHGYLLTAVSPGK 18
:|:|:|:|

Db 2 PYSYSTAVVTNPK 15

RESULT 3

US-10-503-575-224
Sequence 224, Application US/10503575
Publication No. US20050244823A1
GENERAL INFORMATION:
APPLICANT: Driffohout, Jan Mouter
APPLICANT: van Veele, Petrus Antonius
APPLICANT: Konig, Frits
TITLE OF INVENTION: NOVEL EPTTOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
FILE REFERENCE: 2799/72843-PCT-US
CURRENT APPLICATION NUMBER: US/10/503,575
CURRENT FILING DATE: 2004-08-04
PRIOR APPLICATION NUMBER: PCT/NL03/00077
PRIOR FILING DATE: 2003-02-04
PRIOR APPLICATION NUMBER: EP 02075456.0
PRIOR FILING DATE: 2002-02-04
NUMBER OF SEQ ID NOS: 340
SOFTWARE: PatentIn version 3.1
SEQ ID NO 224
LENGTH: 19
TYPE: PRT
ORGANISM: Homo sapiens
US-10-503-575-224

Query Match 28.1%; Score 27; DB 6; Length 19;

Best Local Similarity 50.0%; Pred. No. 93;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 BPHGYLLT 11
:|:|:|:|

Db 1 BEYGYIVT 8

RESULT 4

US-11-054-515-2400
Sequence 2400, Application US/11054515
Publication No. US20050255532A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
FILE REFERENCE: PFS2393
CURRENT APPLICATION NUMBER: US/11/054,515
CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11
PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418
PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817


```
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2400
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2400
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```
Query Match      27.1% Score 26; DB 7; Length 14;
Best Local Similarity 83.3%; Pred. No. 97;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 PHGYL 10
      |||||
Db      8 PHGPL 13
```

```
RESULT 5
US-11-054-515-2477
/ Sequence 2477, Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
/ FILE REFERENCE: PF523P3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ CURRENT FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2477
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-2477
```

```
Query Match      27.1% Score 26; DB 7; Length 14;
Best Local Similarity 80.0%; Pred. No. 97;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      5 PHGYL 9
      |||||
Db      8 PHSYL 12
```

```
RESULT 6
US-11-144-630-33
/ Sequence 33, Application US/11144630
/ Publication No. US20060010517A1
/ GENERAL INFORMATION:
/ APPLICANT: KALEEN, ZHONGYILI
/ APPLICANT: MORELL, MATTHEW
/ APPLICANT: RAHMAN, SADEOUR
/ TITLE OF INVENTION: REGULATION OF GENE EXPRESSION IN PLANTS
/ FILE REFERENCE: 054270/0126
/ CURRENT APPLICATION NUMBER: US/11/144,630
/ CURRENT FILING DATE: 2005-06-06
/ PRIOR APPLICATION NUMBER: US/09/508,377
/ PRIOR FILING DATE: 2000-06-09
/ PRIOR APPLICATION NUMBER: AU PP 2509
/ PRIOR FILING DATE: 1998-03-20
/ PRIOR APPLICATION NUMBER: PCT/AU98/00743
/ PRIOR FILING DATE: 1998-09-11
/ PRIOR APPLICATION NUMBER: AU PP 9108
/ PRIOR FILING DATE: 1997-09-12
/ NUMBER OF SEQ ID NOS: 71
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 33
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Trifolium trautschii
US-11-144-630-33
```

```
Query Match      27.1% Score 26; DB 7; Length 20;
Best Local Similarity 83.3%; Pred. No. 1,4e+02;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      13 AVSPGK 18
      |||||
Db      1 AASPGK 6
```

```
RESULT 7
US-11-045-024-13324
/ Sequence 13324, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Bastejan
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060,0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
```

```

; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13324
; LENGTH: 15
; TYPE: PRF
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13324
```

```

Query Match          26.6%; Score 25.5; DB 7; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      8 YL-LTPAASPK 18
      |||||:|
DB      4 YLALTLALIKPK 15
```

RESULT 8

```

US-11-045-024-13327
; Sequence 13327, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 13327
; LENGTH: 15
; TYPE: PRF
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13327
```

```

Query Match          26.6%; Score 25.5; DB 7; Length 15;
Best Local Similarity 58.3%; Pred. No. 1.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      8 YL-LTPAASPK 18
      |||||:|
DB      3 YLALTLALIKPK 14
```

RESULT 9

```

US-11-062-186-2
; Sequence 2, Application US/11062186
; Publication No. US20050272097A1
; GENERAL INFORMATION:
; APPLICANT: CALENOFF, EMANUEL
; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR DETECTING AND TREATING
; FILE REFERENCE: 21417-98470
; CURRENT APPLICATION NUMBER: US/11/062,186
; CURRENT FILING DATE: 2005-02-18
; PRIOR APPLICATION NUMBER: 60/546,062
; PRIOR FILING DATE: 2004-02-18
; PRIOR APPLICATION NUMBER: 60/545,980
; PRIOR FILING DATE: 2004-02-18
; NUMBER OF SEQ ID NOS: 172
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 2
; LENGTH: 8
; TYPE: PRF
; ORGANISM: Homo sapiens
US-11-062-186-2
```

```

Query Match          26.0%; Score 25; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      14 VSPGK 18
      :|||
DB      1 ISPGK 5
```

RESULT 10

```

US-11-045-024-3531
; Sequence 3531, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Esceban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3531
; LENGTH: 9
; TYPE: PRF
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

US-11-045-024-3531

Query Match 26.0%; Score 25; DB 7; Length 9;
 Best Local Similarity 55.6%; Pred. No. 5.5e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LTAASPGK 18
 |||:|
 Db 1 LTAALPKKK 9

RESULT 11

US-11-045-024-10473
 ; Sequence 10473, Application US/11045024
 ; Publication NO. US20050271676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Baker, Denise Marie
 ; APPLICANT: Kubo, Ralph
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Bpimmune Inc.
 ; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 ; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 ; FILE REFERENCE: 2060.0040007
 ; CURRENT APPLICATION NUMBER: US/11/045,024
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: US 09/412,863
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/159,339
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; NUMBER OF SEQ ID NOS: 14528
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 10473
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-10473

Query Match 26.0%; Score 25; DB 7; Length 9;
 Best Local Similarity 55.6%; Pred. No. 5.5e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LTAASPGK 18
 |||:|
 Db 1 LTAALPKKK 9

RESULT 12

US-11-045-024-12303
 ; Sequence 12303, Application US/11045024
 ; Publication NO. US20050271676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert
 ; APPLICANT: Baker, Denise Marie
 ; APPLICANT: Celis, Bastejan
 ; APPLICANT: Kubo, Ralph
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Bpimmune Inc.

US-11-045-024-12303
 ; Sequence 3546, Application US/11045024
 ; Publication NO. US20050271676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Baker, Denise Marie
 ; APPLICANT: Kubo, Ralph
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Bpimmune Inc.
 ; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 ; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 ; FILE REFERENCE: 2060.0040007
 ; CURRENT APPLICATION NUMBER: US/11/045,024
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: US 09/412,863
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/159,339
 ; PRIOR FILING DATE: 1993-11-29
 ; PRIOR APPLICATION NUMBER: US 08/205,713
 ; PRIOR FILING DATE: 1994-03-04
 ; PRIOR APPLICATION NUMBER: US 08/347,610
 ; PRIOR FILING DATE: 1994-12-01
 ; NUMBER OF SEQ ID NOS: 14528
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 12303
 ; LENGTH: 9
 ; TYPE: PRT
 ; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-12303

Query Match 26.0%; Score 25; DB 7; Length 9;
 Best Local Similarity 55.6%; Pred. No. 5.5e+04;
 Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 10 LTAASPGK 18
 |||:|
 Db 1 LTAALPKKK 9

RESULT 13

US-11-045-024-3546
 ; Sequence 3546, Application US/11045024
 ; Publication NO. US20050271676A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Sette, Alessandro
 ; APPLICANT: Sidney, John
 ; APPLICANT: Southwood, Scott
 ; APPLICANT: Livingston, Brian
 ; APPLICANT: Chesnut, Robert
 ; APPLICANT: Baker, Denise Marie
 ; APPLICANT: Kubo, Ralph
 ; APPLICANT: Grey, Howard M.
 ; APPLICANT: Bpimmune Inc.
 ; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 ; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 ; FILE REFERENCE: 2060.0040007
 ; CURRENT APPLICATION NUMBER: US/11/045,024
 ; CURRENT FILING DATE: 2005-01-28
 ; PRIOR APPLICATION NUMBER: US 09/412,863
 ; PRIOR FILING DATE: 1999-10-05
 ; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIOR APPLICATION NUMBER: US 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: US 08/159,184

```

; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3546
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3546
```

```
Query Match          26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          10 LTRAAVSPK 18
            |||:|
Db          2 LTRALIKPKK 10
```

```
RESULT 14
US-11-045-024-10479
; Sequence 10479, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10479
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10479
```

```
Query Match          26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY          10 LTRAAVSPK 18
```

```
Db          2 LTRALIKPKK 10
            |||:|
```

```
RESULT 15
US-11-045-024-12307
; Sequence 12307, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 12307
; LENGTH: 10
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12307
```

```
Query Match          26.0%; Score 25; DB 7; Length 10;
Best Local Similarity 55.6%; Pred. No. 98;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY          10 LTRAAVSPK 18
            |||:|
Db          2 LTRALIKPKK 10
```

```
RESULT 16
US-11-045-024-3559
; Sequence 3559, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chennut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Epiimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
```

```
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3559
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3559

Query Match          26.0%; Score 25; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSPGK 18
        |||:|
        3 LTRALPKPK 11

DB
```

```
RESULT 17
US-11-045-024-10483
/ Sequence 10483, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
```

```
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10483
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10483
```

```
Query Match          26.0%; Score 25; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSPGK 18
        |||:|
        3 LTRALPKPK 11

DB
```

```
RESULT 18
US-11-045-024-12311
/ Sequence 12311, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Betteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: EpiImmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12311
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12311
```

```
Query Match          26.0%; Score 25; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.1e+02;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSPGK 18
        |||:|
        3 LTRALPKPK 11

DB
```

```
RESULT 19
US-11-041-893-2
/ Sequence 2, Application US/11041893
```

```
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahairas, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ PRIOR FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 2
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Mycobacterium leprae
US-11-041-893-2
```

```
Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 TAAVSPG 17
        |||:|
Db      6 TAAISAG 12
```

```
RESULT 20
US-11-041-893-13
/ Sequence 13, Application US/11041893
/ Publication No. US20060002941A1
/ GENERAL INFORMATION:
/ APPLICANT: Mahairas, Gregory G.
/ TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
/ FILE REFERENCE: 100123.401
/ CURRENT APPLICATION NUMBER: US/11/041,893
/ PRIOR FILING DATE: 2005-01-24
/ PRIOR APPLICATION NUMBER: US 60/616,855
/ PRIOR FILING DATE: 2004-10-06
/ PRIOR APPLICATION NUMBER: US 60/538,713
/ NUMBER OF SEQ ID NOS: 295
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 13
/ LENGTH: 15
/ TYPE: PRT
/ ORGANISM: Mycobacterium tuberculosis
US-11-041-893-13
```

```
Query Match      26.0%; Score 25; DB 7; Length 15;
Best Local Similarity 71.4%; Pred. No. 1.5e+02;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      11 TAAVSPG 17
        |||:|
Db      6 TAAISAG 12
```

```
RESULT 21
US-10-939-890-138
/ Sequence 138, Application US/10939890
/ Publication No. US20050250700A1
/ GENERAL INFORMATION:
/ APPLICANT: Sato, Aaron K.
/ APPLICANT: Sexton, Daniel J.
/ APPLICANT: Dransfield, Daniel T.
/ APPLICANT: Ladner, Robert C.
/ APPLICANT: Arbogast, Christophe
/ APPLICANT: Bueset, Philippe
/ APPLICANT: Fan, Hong
```

```
/ APPLICANT: Khurana, Sudha
/ APPLICANT: Linder, Karen B.
/ APPLICANT: Marinelli, Edmund R.
/ APPLICANT: Nanjappan, Palaniappa
/ APPLICANT: Nunn, Adrian D.
/ APPLICANT: Pillai, Radhakrishna
/ APPLICANT: Pochon, Sibylle
/ APPLICANT: Ramalingam, Kondareddat
/ APPLICANT: Shrivastava, Ajay
/ APPLICANT: Song, Bo
/ APPLICANT: Swenson, Rolf E.
/ APPLICANT: Von Wronski, Mathew A.
/ TITLE OF INVENTION: KDR AND VEGF/KDR BINDING PEPTIDES
/ FILE REFERENCE: D0647.70014US00
/ CURRENT APPLICATION NUMBER: US/10/939,890
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: US 10/661,156
/ PRIOR FILING DATE: 2003-09-11
/ PRIOR APPLICATION NUMBER: US 10/382,082
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: PCT/US03/06731
/ PRIOR FILING DATE: 2003-03-03
/ PRIOR APPLICATION NUMBER: US 60/440,411
/ PRIOR FILING DATE: 2003-01-15
/ PRIOR APPLICATION NUMBER: US 60/360,851
/ PRIOR FILING DATE: 2002-03-01
/ NUMBER OF SEQ ID NOS: 883
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 138
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Artificial Sequence
/ FEATURE:
/ OTHER INFORMATION: Library Isolate
US-10-939-890-138
```

```
Query Match      26.0%; Score 25; DB 6; Length 20;
Best Local Similarity 80.0%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
```

```
Qy      4 EPHGY 8
        |||
Db      1 EPEGY 5
```

```
RESULT 22
US-10-623-155-247
/ Sequence 247, Application US/10623155
/ Publication No. US20050261166A1
/ GENERAL INFORMATION:
/ APPLICANT: Wang, Tonglong
/ APPLICANT: Peckham, David W.
/ APPLICANT: Retter, Marc W.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
/ FILE REFERENCE: 210121.455C20
/ CURRENT APPLICATION NUMBER: US/10/623,155
/ PRIOR FILING DATE: 2003-07-17
/ NUMBER OF SEQ ID NOS: 560
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 247
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-623-155-247
```

```
Query Match      26.0%; Score 25; DB 6; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
```

```
Qy      5 PHGYLLTAAVSPG 17
        ||::|||
```

Db 4 PHEPMIVANVKG 16

```
RESULT 23
US-11-022-562-292
; Sequence 292, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 292
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-292
```

```
Query Match 26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 2 APEPHGYLTAAVSPG 17
Db 3 APEPEVIMPSALSEG 18
```

```
RESULT 24
US-11-022-562-293
; Sequence 293, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; APPLICANT: Shisong, Jiang
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DEN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PasteSeq for Windows Version 4.0
; SEQ ID NO 293
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-293
```

```
Query Match 26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 37.5%; Pred. No. 2.1e+02;
Matches 6; Conservative 3; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 2 APEPHGYLTAAVSPG 17
Db 3 APEPEVIMPSALSEG 18
```

```
RESULT 25
US-11-043-542-42
; Sequence 42, Application US/11043542
; Publication No. US20050289664A1
```

```
; GENERAL INFORMATION:
; APPLICANT: MOSHIRI, Farhad
; APPLICANT: HAO, Ming
; APPLICANT: KARUNANANDAA, Balasubramini
; APPLICANT: VALENTIN, Henry B.
; APPLICANT: VENKATESH, Tyagagondlu V.
; APPLICANT: WONG, Yun-Hua Huang
; TITLE OF INVENTION: Genes Encoding 4-Hydroxyphenylpyruvate Dioxygenase (HPPD) Enzyme
; FILE REFERENCE: REN-02-123
; CURRENT APPLICATION NUMBER: US/11/043,542
; PRIOR FILING DATE: 2005-01-26
; PRIOR APPLICATION NUMBER: US 60/539,309
; PRIOR FILING DATE: 2004-01-26
; NUMBER OF SEQ ID NOS: 44
; SOFTWARE: PatentIn version 3.3
; SEQ ID NO 42
; LENGTH: 20
; TYPE: PRT
; ORGANISM: Bacillus thuringiensis
US-11-043-542-42
```

```
Query Match 26.0%; Score 25; DB 7; Length 20;
Best Local Similarity 38.5%; Pred. No. 2.1e+02;
Matches 5; Conservative 1; Mismatches 7; Indels 0; Gaps 0;
```

```
QY 4 EPHGYLTAAVSP 16
Db 7 DBEGYLQIFTKP 19
```

```
RESULT 26
US-11-152-747-35
; Sequence 35, Application US/11152747
; Publication No. US20050251861A1
; GENERAL INFORMATION:
; APPLICANT: E. I. du Pont de Nemours, Inc.
; APPLICANT: Cheng, Qiong
; APPLICANT: Tao, Luan
; TITLE OF INVENTION: CAROTENOID KETOYLASE GENE
; FILE REFERENCE: CL-1849 US NA
; CURRENT APPLICATION NUMBER: US/11/152,747
; CURRENT FILING DATE: 2005-06-14
; PRIOR APPLICATION NUMBER:
; PRIOR FILING DATE:
; NUMBER OF SEQ ID NOS: 47
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 35
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Deinococcus radiodurans
US-11-152-747-35
```

```
Query Match 25.0%; Score 24; DB 7; Length 9;
Best Local Similarity 62.5%; Pred. No. 5.5e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY 6 HGYLTA 13
Db 1 HNALVTAA 8
```

```
RESULT 27
US-11-054-515-3192
; Sequence 3192, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind BlyS
; FILE REFERENCE: PF523P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; CURRENT FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
```

```
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 3192
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-054-515-3192
```

```
Query Match      25.0%; Score 24; DB 7; Length 11;
Best Local Similarity 55.6%; Pred. No. 1.6e+02;
Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
```

Qy 1 DAEPHGYL 9

Db 1 DVPPPDGYL 9

```
RESULT 28
US-11-158-723-7
/ Sequence 7; Application US/11158723
/ Publication No. US20060002938A1
/ GENERAL INFORMATION:
/ APPLICANT: Gomer, Richard
/ APPLICANT: Pilling, Darrell
/ TITLE OF INVENTION: METHOD OF DETECTING THE INHIBITION OF
/ TITLE OF INVENTION: FIBROCYTE FORMATION AND METHODS AND COMPOSITIONS FOR
/ TITLE OF INVENTION: ENHANCING FIBROCYTE FORMATION
/ FILE REFERENCE: 002376.1029
/ CURRENT APPLICATION NUMBER: US/11/158,723
/ PRIOR FILING DATE: 2005-06-22
/ PRIOR APPLICATION NUMBER: 60/436,046
/ PRIOR FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: 60/436,027
/ PRIOR FILING DATE: 2002-12-23
/ PRIOR APPLICATION NUMBER: 60/515,776
/ PRIOR FILING DATE: 2003-10-30
/ PRIOR APPLICATION NUMBER: 60/519,467
/ PRIOR FILING DATE: 2003-11-12
/ PRIOR APPLICATION NUMBER: 60/525,175
/ PRIOR FILING DATE: 2003-11-26
/ PRIOR APPLICATION NUMBER: PCT/US03/41183
/ PRIOR FILING DATE: 2003-12-22
/ NUMBER OF SEQ ID NOS: 8
/ SOFTWARE: FaastSeq for Windows Version 4.0
/ SEQ ID NO 7
/ LENGTH: 11
/ TYPE: PRT
/ ORGANISM: Human
US-11-158-723-7
```

```
Query Match      25.0%; Score 24; DB 7; Length 11;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
```

```
Qy 5 PHGYLTA 12
| | | | |
Db 1 PGGYFEA 8
```

```
RESULT 29
US-10-507-662-53
/ Sequence 63; Application US/10507662
/ Publication No. US20050255102A1
/ GENERAL INFORMATION:
/ APPLICANT: BIOGEN, INC.
/ APPLICANT: THE REGENTS OF THE UNIVERSITY OF CALIFORNIA
/ TITLE OF INVENTION: ANTI-ALPHA-V BETA-6 ANTIBODIES
/ FILE REFERENCE: A136PCT
/ CURRENT APPLICATION NUMBER: US/10/507,662
/ PRIOR FILING DATE: 2004-09-13
/ PRIOR APPLICATION NUMBER: 60/364,991
/ PRIOR FILING DATE: 2002-03-13
/ PRIOR APPLICATION NUMBER: 60/426,286
/ PRIOR FILING DATE: 2002-11-13
/ NUMBER OF SEQ ID NOS: 64
/ SOFTWARE: PatencIn Ver. 2.1
/ SEQ ID NO 53
/ LENGTH: 12
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-507-662-53
```

```
Query Match      25.0%; Score 24; DB 6; Length 12;
Best Local Similarity 37.5%; Pred. No. 1.8e+02;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;
```

Qy 3 FEPHGYL 10

Db 3 YGPHSYAM 10

```
RESULT 30
US-11-054-515-2602
/ Sequence 2602; Application US/11054515
/ Publication No. US2005025532A1
/ GENERAL INFORMATION:
/ APPLICANT: Ruben et al.
/ TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
/ FILE REFERENCE: PFS23p3
/ CURRENT APPLICATION NUMBER: US/11/054,515
/ PRIOR FILING DATE: 2005-02-10
/ PRIOR APPLICATION NUMBER: 60/543,296
/ PRIOR FILING DATE: 2004-02-11
/ PRIOR APPLICATION NUMBER: 60/580,347
/ PRIOR FILING DATE: 2004-06-18
/ PRIOR APPLICATION NUMBER: 10/293,418
/ PRIOR FILING DATE: 2002-11-14
/ PRIOR APPLICATION NUMBER: 60/331,469
/ PRIOR FILING DATE: 2001-11-16
/ PRIOR APPLICATION NUMBER: 60/340,817
/ PRIOR FILING DATE: 2001-12-19
/ PRIOR APPLICATION NUMBER: 09/880,748
/ PRIOR FILING DATE: 2001-06-15
/ PRIOR APPLICATION NUMBER: 60/293,499
/ PRIOR FILING DATE: 2001-05-25
/ PRIOR APPLICATION NUMBER: 60/277,379
/ PRIOR FILING DATE: 2001-03-21
/ PRIOR APPLICATION NUMBER: 60/276,248
/ PRIOR FILING DATE: 2001-03-16
/ PRIOR APPLICATION NUMBER: 60/240,816
/ PRIOR FILING DATE: 2000-10-17
/ Remaining Prior Application data removed - See file wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 3247
/ SEQ ID NO 2602
/ LENGTH: 14
/ TYPE: PRT
/ ORGANISM: Homo sapiens
```


US-11-054-515-2602

Query Match 25.0%; Score 24; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYLL 10
|:|:|
DB 8 PHDHL 13

RESULT 31

US-11-054-515-2909
Sequence 2909, Application US/11054515
Publication No. US2005025532A1

GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunosepecifically Bind Blys
FILE REFERENCE: P5523P3
CURRENT APPLICATION NUMBER: US/11/054,515

CURRENT FILING DATE: 2005-02-10
PRIOR APPLICATION NUMBER: 60/543,296
PRIOR FILING DATE: 2004-02-11

PRIOR APPLICATION NUMBER: 60/580,347
PRIOR FILING DATE: 2004-06-18
PRIOR APPLICATION NUMBER: 10/293,418

PRIOR FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748

PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248

PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17

Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 2909

LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapiens

US-11-054-515-2909
Query Match 25.0%; Score 24; DB 7; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.3e+02;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 8 YLLTAA 13
|:|:|
DB 4 YMTAA 9

RESULT 32

US-10-467-657-9074
Sequence 9074, Application US/10467657
Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: FONTANA Maria Rita
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657
CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8

PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 9074
LENGTH: 16
TYPE: PRT

ORGANISM: Neisseria gonorrhoeae
US-10-467-657-9074

Query Match 25.0%; Score 24; DB 6; Length 16;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGVLTAASP 16
|:|:|:|
DB 2 HNFLEPSADTP 12

RESULT 33

US-10-467-657-9075
Sequence 9075, Application US/10467657
Publication No. US20050260581A1

GENERAL INFORMATION:
APPLICANT: CHIRON SPA
APPLICANT: PIZZA Mariagrazia
APPLICANT: MASIGNANI Vega
APPLICANT: MONACI Elisabetta
TITLE OF INVENTION: GONOCOCCAL PROTEINS AND NUCLEIC ACIDS
FILE REFERENCE:
CURRENT APPLICATION NUMBER: US/10/467,657

CURRENT FILING DATE: 2003-08-11
PRIOR APPLICATION NUMBER: GB-0103424.8
PRIOR FILING DATE: 2001-02-12

NUMBER OF SEQ ID NOS: 9218
SOFTWARE: SeqWin99, version 1.04
SEQ ID NO 9075

LENGTH: 16
TYPE: PRT
ORGANISM: Neisseria gonorrhoeae

US-10-467-657-9075
Query Match 25.0%; Score 24; DB 6; Length 16;
Best Local Similarity 36.4%; Pred. No. 2.4e+02;
Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGVLTAASP 16
|:|:|:|
DB 2 HNFLEPSADTP 12

RESULT 34

US-11-022-562-176
Sequence 176, Application US/11022562
Publication No. US20050249742A1

GENERAL INFORMATION:
APPLICANT: Ruprecht, Ruth M.
APPLICANT: Shisong, Jiang
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE
FILE REFERENCE: DFN-043CN
CURRENT APPLICATION NUMBER: US/11/022,562

CURRENT FILING DATE: 2004-12-22
PRIOR APPLICATION NUMBER: PCT/US03/20322
PRIOR FILING DATE: 2003-06-27

PRIOR APPLICATION NUMBER: 60/392718
PRIOR FILING DATE: 2002-06-27
NUMBER OF SEQ ID NOS: 340

SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 176
LENGTH: 20
TYPE: PRT
ORGANISM: Simian Immunodeficiency Virus

US-11-022-562-176

Query Match 25.0%; Score 24; DB 7; Length 20;

Best Local Similarity 45.5%; Pred. No. 3.1e+02;

Matches 5; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 7 GYLTTAAVSPG 17

DB 4 GFLATAGSAMG 14

RESULT 35

US-11-128-900-118

Sequence 118, Application US/11128900

Publication No. US20050287136A1

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILEEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1 DIV3

CURRENT APPLICATION NUMBER: US/11/128,900

PRIOR FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 10/776649

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: US 10/612497

PRIOR APPLICATION NUMBER: 2003-07-01

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 60/113647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 118

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-11-128-900-118

Query Match 25.0%; Score 24; DB 7; Length 20;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18

DB 10 TLTSLSPGE 17

RESULT 36

US-11-128-900-119

Sequence 119, Application US/11128900

Publication No. US20050287136A1

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILEEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1 DIV3

CURRENT APPLICATION NUMBER: US/11/128,900

PRIOR FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 10/776649

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: US 10/612497

PRIOR APPLICATION NUMBER: 2003-07-01

PRIOR APPLICATION NUMBER: US 09/472087

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 60/113647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 119

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-11-128-900-119

Query Match 25.0%; Score 24; DB 7; Length 20;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18

DB 10 TLTSLSPGE 17

RESULT 37

US-11-128-900-121

Sequence 121, Application US/11128900

Publication No. US20050287136A1

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILEEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1 DIV3

CURRENT APPLICATION NUMBER: US/11/128,900

PRIOR FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 10/776649

PRIOR FILING DATE: 2004-02-10

PRIOR APPLICATION NUMBER: US 10/612497

PRIOR APPLICATION NUMBER: 2003-07-01

PRIOR FILING DATE: 1999-12-23

PRIOR APPLICATION NUMBER: US 60/113647

PRIOR FILING DATE: 1998-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 121

LENGTH: 20

TYPE: PRT

ORGANISM: Homo sapiens

US-11-128-900-121

Query Match 25.0%; Score 24; DB 7; Length 20;

Best Local Similarity 50.0%; Pred. No. 3.1e+02;

Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18

DB 12 TLTSLSPGE 19

RESULT 38

US-11-128-900-122

Sequence 122, Application US/11128900

Publication No. US20050287136A1

GENERAL INFORMATION:

APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEU, MARK J.

APPLICANT: MUELLER, EILEEN E.

APPLICANT: HANKE, JEFFREY H.

APPLICANT: GILMAN, STEVEN C.

APPLICANT: DAVIS, C. GEOFFREY

APPLICANT: CORVALAN, JOSE R.

```
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 122
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-122
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 TAAVSPGK 18
        |::|||:
Db      10 TSLSPGSR 17
```

```
RESULT 39
US-11-128-900-123
/ Sequence 123, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKS, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 123
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-123
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 TAAVSPGK 18
        |::|||:
Db      10 TSLSPGSR 17
```

```
RESULT 40
US-11-128-900-124
/ Sequence 124, Application US/11128900
```

```
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKS, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 124
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-124
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

```
QY      11 TAAVSPGK 18
        |::|||:
Db      10 TSLSPGSR 17
```

```
RESULT 41
US-11-128-900-125
/ Sequence 125, Application US/11128900
/ Publication No. US20050287136A1
/ GENERAL INFORMATION:
/ APPLICANT: HANSON, DOUGLAS C.
/ APPLICANT: NEVEU, MARK J.
/ APPLICANT: MUELLER, EILEEN E.
/ APPLICANT: HANKS, JEFFREY H.
/ APPLICANT: GILMAN, STEVEN C.
/ APPLICANT: DAVIS, C. GEOFFREY
/ APPLICANT: CORVALAN, JOSE R.
/ TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4
/ FILE REFERENCE: ABX-PF1 DIV3
/ CURRENT APPLICATION NUMBER: US/11/128,900
/ CURRENT FILING DATE: 2005-05-12
/ PRIOR APPLICATION NUMBER: US 10/776649
/ PRIOR FILING DATE: 2004-02-10
/ PRIOR APPLICATION NUMBER: US 10/612497
/ PRIOR APPLICATION NUMBER: 2003-07-01
/ PRIOR APPLICATION NUMBER: US 09/472087
/ PRIOR FILING DATE: 1999-12-23
/ PRIOR APPLICATION NUMBER: US 60/113647
/ PRIOR FILING DATE: 1998-12-23
/ NUMBER OF SEQ ID NOS: 147
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 125
/ LENGTH: 20
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-11-128-900-125
```

```
Query Match          25.0%; Score 24; DB 7; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+02;
Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
```

QY 11 TAASPRGX 18
|:|||||:
Db 10 TUSLSPGE 17

RESULT 42
US-10-919-492-1
; Sequence 1, Application US/10919492
; Publication No. US20050282249A1
; GENERAL INFORMATION:
; APPLICANT: STOUENARD, PETER
; APPLICANT: HANSEN, OLE CAI
; TITLE OF INVENTION: RECOMBINANT HEXOSE OXIDASE, A METHOD OF PRODUCING
; TITLE OF INVENTION: SAME AND USE OF SUCH ENZYME
; FILE REFERENCE: 14923.0014
; CURRENT APPLICATION NUMBER: US/10/919,492
; CURRENT FILING DATE: 2004-08-17
; PRIOR APPLICATION NUMBER: 09/824,053
; PRIOR FILING DATE: 2001-04-03
; PRIOR APPLICATION NUMBER: 08/669,304
; PRIOR FILING DATE: 1996-07-12
; PRIOR APPLICATION NUMBER: PCT/DK96/00238
; PRIOR FILING DATE: 1996-06-04
; PRIOR APPLICATION NUMBER: 08/476,910
; PRIOR FILING DATE: 1995-06-07
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: Patentin Ver. 3.2
; SEQ ID NO 1
; LENGTH: 8
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
US-10-919-492-1

Query Match 24.0%; Score 23; DB 6; Length 8;
Best Local Similarity 60.0%; Pred. No. 5.5e+04;
Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 3 PEPHG 7
:||||:
Db 1 YEPYG 5

RESULT 43
US-10-859-643-31
; Sequence 31, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-31

Query Match 24.0%; Score 23; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
|:|||||:
Db 3 DCFCPH 8

RESULT 44
US-10-859-643-115
; Sequence 115, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 115
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-115

Query Match 24.0%; Score 23; DB 6; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
|:|||||:
Db 3 DCFCPH 8

RESULT 45
US-10-859-643-698
; Sequence 698, Application US/10859643
; Publication No. US20060002993A1
; GENERAL INFORMATION:
; APPLICANT: Chaillita-Bid, Pia M.
; APPLICANT: Raitano, Arthur B.
; APPLICANT: Paris, Mary
; APPLICANT: Hubert, Rene S.
; APPLICANT: Morrison, Karen Jane Meyrick
; APPLICANT: Jakobovits, Aya
; TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
; TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
; FILE REFERENCE: 511582006203
; CURRENT APPLICATION NUMBER: US/10/859,643
; CURRENT FILING DATE: 2004-06-02
; PRIOR APPLICATION NUMBER: US 10/005,480
; PRIOR FILING DATE: 2001-11-07
; NUMBER OF SEQ ID NOS: 765
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 698
; LENGTH: 9
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-859-643-698

Query Match 24.0%; Score 23; DB 6; Length 9;

Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 46

US-11-097-864-31
Sequence 31, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-31

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 47

US-11-097-864-115
Sequence 115, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 115
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-115

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 48

US-11-097-864-698
Sequence 698, Application US/11097864
Publication No. US20050265924A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006205
CURRENT APPLICATION NUMBER: US/11/097,864
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 698
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-864-698

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 49

US-11-097-912-31
Sequence 31, Application US/11097912
Publication No. US20050265921A1
GENERAL INFORMATION:
APPLICANT: Challita-Bid, Pia M.
APPLICANT: Raitano, Arthur B.
APPLICANT: Paris, Mary
APPLICANT: Hubert, Rene S.
APPLICANT: Morrison, Karen Jane Meyrick
APPLICANT: Jakobovits, Aya
TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B
TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
FILE REFERENCE: 511582006204
CURRENT APPLICATION NUMBER: US/11/097,912
PRIOR FILING DATE: 2005-04-01
PRIOR APPLICATION NUMBER: US 10/062,109
PRIOR FILING DATE: 2002-01-31
PRIOR APPLICATION NUMBER: US 10/005,480
PRIOR FILING DATE: 2001-11-07
NUMBER OF SEQ ID NOS: 765
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 31
LENGTH: 9
TYPE: PRT
ORGANISM: Homo Sapien
US-11-097-912-31

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 50
US-11-097-912-115

Sequence 115, Application US/11097912
Publication No. US20050265921A1

GENERAL INFORMATION:

APPLICANT: Chailita-Eld, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B

TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 511582006204

CURRENT APPLICATION NUMBER: US/11/097,912

PRIOR FILING DATE: 2005-04-01

PRIOR APPLICATION NUMBER: US 10/062,109

PRIOR FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: US 10/005,480

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 765

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 115

LENGTH: 9

TYPE: PRT

ORGANISM: Homo Sapien

US-11-097-912-115

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 51
US-11-097-912-698

Sequence 698, Application US/11097912
Publication No. US20050265921A1

GENERAL INFORMATION:

APPLICANT: Chailita-Eld, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B

TITLE OF INVENTION: USEFUL IN TREATMENT AND DETECTION OF CANCER

FILE REFERENCE: 511582006204

CURRENT APPLICATION NUMBER: US/11/097,912

PRIOR FILING DATE: 2005-04-01

PRIOR APPLICATION NUMBER: US 10/062,109

PRIOR FILING DATE: 2002-01-31

PRIOR APPLICATION NUMBER: US 10/005,480

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 765

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 698

LENGTH: 9

TYPE: PRT

ORGANISM: Homo Sapien

US-11-097-912-698

Query Match 24.0%; Score 23; DB 7; Length 9;
Best Local Similarity 66.7%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 52
US-10-859-643-100

Sequence 100, Application US/10859643
Publication No. US2006000293A1

GENERAL INFORMATION:

APPLICANT: Chailita-Eld, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

FILE REFERENCE: 511582006203

CURRENT APPLICATION NUMBER: US/10/859,643

PRIOR FILING DATE: 2004-06-02

PRIOR APPLICATION NUMBER: US 10/005,480

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 765

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 100

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapien

US-10-859-643-100

Query Match 24.0%; Score 23; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 53
US-10-859-643-433

Sequence 433, Application US/10859643
Publication No. US2006000293A1

GENERAL INFORMATION:

APPLICANT: Chailita-Eld, Pia M.

APPLICANT: Raitano, Arthur B.

APPLICANT: Paris, Mary

APPLICANT: Hubert, Rene S.

APPLICANT: Morrison, Karen Jane Meyrick

APPLICANT: Jakobovits, Aya

TITLE OF INVENTION: Nucleic Acid and Corresponding Protein

TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of

FILE REFERENCE: 511582006203

CURRENT APPLICATION NUMBER: US/10/859,643

PRIOR FILING DATE: 2004-06-02

PRIOR APPLICATION NUMBER: US 10/005,480

PRIOR FILING DATE: 2001-11-07

NUMBER OF SEQ ID NOS: 765

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 433

LENGTH: 10

TYPE: PRT

ORGANISM: Homo Sapien

US-10-859-643-433

Query Match 24.0%; Score 23; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 4 DCRCPH 9

RESULT 54

US-10-859-643-619
/ Sequence 619, Application US/10859643
/ Publication No. US20060029924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: Nucleic Acid and Corresponding Protein
/ TITLE OF INVENTION: Entitled 161P2F10B Useful in Treatment and Detection of
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/10/859,643
/ CURRENT FILING DATE: 2004-06-02
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 619
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-10-859-643-619

Query Match 24.0%; Score 23; DB 6; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 4 DCRCPH 9

RESULT 55

US-11-097-864-100
/ Sequence 100, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 100
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-100

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 3 DCRCPH 8

RESULT 56

US-11-097-864-433
/ Sequence 433, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 433
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-433

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAFEPH 6
| | | |
Db 4 DCRCPH 9

RESULT 57

US-11-097-864-619
/ Sequence 619, Application US/11097864
/ Publication No. US20050265924A1
/ GENERAL INFORMATION:
/ APPLICANT: Chailita-Bid, Pia M.
/ APPLICANT: Raitano, Arthur B.
/ APPLICANT: Paris, Mary
/ APPLICANT: Hubert, Rene S.
/ APPLICANT: Morrison, Karen Jane Meyrick
/ APPLICANT: Jakobovits, Aya
/ TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN NAMED 161P2F10B
/ TITLE OF INVENTION: USEFUL IN THE TREATMENT AND DETECTION OF CANCER
/ FILE REFERENCE: 511582006205
/ CURRENT APPLICATION NUMBER: US/11/097,864
/ CURRENT FILING DATE: 2005-04-01
/ PRIOR APPLICATION NUMBER: US 10/062,109
/ PRIOR FILING DATE: 2002-01-31
/ PRIOR APPLICATION NUMBER: US 10/005,480
/ PRIOR FILING DATE: 2001-11-07
/ NUMBER OF SEQ ID NOS: 765
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 619
/ LENGTH: 10
/ TYPE: PRT
/ ORGANISM: Homo Sapien
US-11-097-864-619

US-11-097-864-619

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 4 DCFCPH 9

RESULT 58

US-11-097-912-100

; Sequence 100, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:

; APPLICANT: Chailita-Bid, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Paris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B

; FILE REFERENCE: 511582006204

; CURRENT APPLICATION NUMBER: US/11/097,912

; PRIOR FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 10/062,109

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: US 10/005,480

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 100

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapien

US-11-097-912-100

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 3 DCFCPH 8

RESULT 59

US-11-097-912-433

; Sequence 433, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:

; APPLICANT: Chailita-Bid, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Paris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B

; FILE REFERENCE: 511582006204

; CURRENT APPLICATION NUMBER: US/11/097,912

; PRIOR FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 10/062,109

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: US 10/005,480

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 433

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapien
US-11-097-912-433

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 4 DCFCPH 9

RESULT 60

US-11-097-912-619

; Sequence 619, Application US/11097912
; Publication No. US20050265921A1
; GENERAL INFORMATION:

; APPLICANT: Chailita-Bid, Pia M.

; APPLICANT: Raitano, Arthur B.

; APPLICANT: Paris, Mary

; APPLICANT: Hubert, Rene S.

; APPLICANT: Morrison, Karen Jane Meyrick

; APPLICANT: Jakobovits, Aya

; TITLE OF INVENTION: NUCLEIC ACID AND CORRESPONDING PROTEIN ENTITLED 161P2F10B

; FILE REFERENCE: 511582006204

; CURRENT APPLICATION NUMBER: US/11/097,912

; PRIOR FILING DATE: 2005-04-01

; PRIOR APPLICATION NUMBER: US 10/062,109

; PRIOR FILING DATE: 2002-01-31

; PRIOR APPLICATION NUMBER: US 10/005,480

; PRIOR FILING DATE: 2001-11-07

; NUMBER OF SEQ ID NOS: 765

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 619

; LENGTH: 10

; TYPE: PRT

; ORGANISM: Homo Sapien

US-11-097-912-619

Query Match 24.0%; Score 23; DB 7; Length 10;
Best Local Similarity 66.7%; Pred. No. 2.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | |
Db 4 DCFCPH 9

RESULT 61

US-10-511-559-637

; Sequence 637, Application US/10511559
; Publication No. US20050265304A1
; GENERAL INFORMATION:

; APPLICANT: JONES, Tim

; APPLICANT: BAKER, Matthew

; APPLICANT: CARR, Francis, J.

; TITLE OF INVENTION: MODIFIED FACTOR VIII

; FILE REFERENCE: MER-133

; CURRENT APPLICATION NUMBER: US/10/511,559

; PRIOR FILING DATE: 2004-10-15

; PRIOR APPLICATION NUMBER: PCT/EP03/04063

; PRIOR FILING DATE: 2003-04-17

; PRIOR APPLICATION NUMBER: EP 02008712.8

; PRIOR FILING DATE: 2002-04-18

; PRIOR APPLICATION NUMBER: EP 03006554.4

; PRIOR FILING DATE: 2003-03-24

; NUMBER OF SEQ ID NOS: 1147

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 637

; LENGTH: 13

; TYPE: PRT

; ORGANISM: Artificial Sequence


```

; FEATURE:
; OTHER INFORMATION: Potential Epitope of human Factor VIII
US-10-511-559-637

Query Match          24.0%; Score 23; DB 6; Length 13;
Best Local Similarity 44.4%; Pred. No. 2.8e+02;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTJAVSP 16
DB 3 YACTTRISP 11

RESULT 62
US-10-966-371-14
; Sequence 14, Application US/10966371
; Publication No. US20050250692A1
; GENERAL INFORMATION:
; APPLICANT: Huang, Jung San
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR INHIBITING CELL PROLIFERATION
; FILE REFERENCE: SLU 03-006 US
; CURRENT APPLICATION NUMBER: US/10/966,371
; PRIOR FILING DATE: 2004-10-15
; PRIOR APPLICATION NUMBER: US 60/512,516
; PRIOR FILING DATE: 2003-10-17
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 14
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-966-371-14

Query Match          24.0%; Score 23; DB 6; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYL 10
DB 4 PHGITL 9

RESULT 63
US-11-054-515-2916
; Sequence 2916, Application US/11054515
; Publication No. US20050255532A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys
; FILE REFERENCE: PFS23P3
; CURRENT APPLICATION NUMBER: US/11/054,515
; PRIOR FILING DATE: 2005-02-10
; PRIOR APPLICATION NUMBER: 60/543,296
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/580,347
; PRIOR FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 10/293,418
; PRIOR FILING DATE: 2002-11-14
; PRIOR APPLICATION NUMBER: 60/331,469
; PRIOR FILING DATE: 2001-11-16
; PRIOR APPLICATION NUMBER: 60/340,817
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: 09/880,748
; PRIOR FILING DATE: 2001-06-15
; PRIOR APPLICATION NUMBER: 60/293,499
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 60/277,379
; PRIOR FILING DATE: 2001-03-21
; PRIOR APPLICATION NUMBER: 60/276,248
; PRIOR FILING DATE: 2001-03-16
; PRIOR APPLICATION NUMBER: 60/240,816
; PRIOR FILING DATE: 2000-10-17
; Remaining Prior Application data removed - See File Wrapper or PALM.

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; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 2916
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-054-515-2916

Query Match          24.0%; Score 23; DB 7; Length 14;
Best Local Similarity 57.1%; Pred. No. 3.1e+02;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEPHGYL 9
DB 6 YBSGGYL 12

RESULT 64
US-11-073-347-116
; Sequence 116, Application US/11073347
; Publication No. US20050260234A1
; GENERAL INFORMATION:
; APPLICANT: SIMARD, John J. L.
; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
; FILE REFERENCE: MANK.015C1
; CURRENT APPLICATION NUMBER: US/11/073,347
; PRIOR FILING DATE: 2005-03-04
; PRIOR APPLICATION NUMBER: 10/094,699
; PRIOR FILING DATE: 2002-03-07
; PRIOR APPLICATION NUMBER: 60/274,063
; PRIOR FILING DATE: 2001-03-07
; NUMBER OF SEQ ID NOS: 159
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 116
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Homo sapien
US-11-073-347-116

Query Match          24.0%; Score 23; DB 7; Length 14;
Best Local Similarity 66.7%; Pred. No. 3.1e+02;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APEPHG 7
DB 1 APEPQG 6

RESULT 65
US-11-022-562-35
; Sequence 35, Application US/11022562
; Publication No. US20050249742A1
; GENERAL INFORMATION:
; APPLICANT: Ruprecht, Ruth M.
; TITLE OF INVENTION: SHISONG, JIANG
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING
; FILE REFERENCE: DFN-043CN
; CURRENT APPLICATION NUMBER: US/11/022,562
; PRIOR FILING DATE: 2004-12-22
; PRIOR APPLICATION NUMBER: PCT/US03/20322
; PRIOR FILING DATE: 2003-06-27
; PRIOR APPLICATION NUMBER: 60/392718
; PRIOR FILING DATE: 2002-06-27
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 35
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Human Immunodeficiency Virus
US-11-022-562-35

```

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0;

```
QY      7 GYLTTAAVSP 16
      |::|::|
Db      4 GQMVHQALSP 13
```

RESULT 66
US-11-073-347-110

```

Sequence 110, Application US/11073347
Publication No. US20050260234v1
GENERAL INFORMATION:
APPLICANT: SIMARD, John J. L.
APPLICANT: DIAMOND, David C.
TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
TITILE OF INVENTION: CANCER
FILE REFERENCE: MAN/K. 015C1
CURRENT APPLICATION NUMBER: US/11/073,347
CURRENT FILING DATE: 2005-03-04
PRIOR APPLICATION NUMBER: 10/094,659
PRIOR FILING DATE: 2002-03-07
PRIOR APPLICATION NUMBER: 60/274,063
PRIOR FILING DATE: 2001-03-07
NUMBER OF SEQ ID NOS: 159
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 110
LENGTH: 15
TYPE: PRT
ORGANISM: Homo sapien
US-11-073-347-110

```

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	66.7%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	0;	Mismatches 2;
			Indels	0;
			Gaps	0;

OY	2	A F E P H G	7
Db	1	A F S P Q G	6

RESULT 67
US-11-045-024-13033

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; Sequence 13033, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:

```

: APPLICANT: Sette, Alessandro
 : APPLICANT: Sidney, John
 : APPLICANT: Southwood, Scott
 : APPLICANT: Livingston, Brian
 : APPLICANT: Chesnut, Robert
 : APPLICANT: Baker, Denise Marie
 : APPLICANT: Cells, Serban
 : APPLICANT: Kubo, Ralph
 : APPLICANT: Grey, Howard M.
 : APPLICANT: Eplimmune Inc.

```

; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions

```

FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28

;; PRIOR APPLICATION NUMBER: US 09/412,863
;; PRIOR FILING DATE: 1999-10-05
;; PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR APPLICATION NUMBER: 08/027,146

; PRIOR FILING DATE: 1993-03-05
 ; PRIOR APPLICATION NUMBER: US 08/073,205
 ; PRIOR FILING DATE: 1993-06-04
 ; PRIORITY INFORMATION NUMBER: 93-06/03-205

; PRIOR APPLICATION NUMBER: US 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: US 08/159,184
 ; PRIOR FILING DATE: 1993-11-03

! PRIOR FILING DATE: 1993-11-29
! PRIOR APPLICATION NUMBER: US 08/159,339

```

1 PRIOR FILING DATE: 1993-11-29
2 PRIOR APPLICATION NUMBER: US 08/205,713
3 PRIOR FILING DATE: 1994-03-04
4 PRIOR APPLICATION NUMBER: US 08/347,610
5 PRIOR FILING DATE: 1994-13-01
6 NUMBER OF SEQ ID NOS: 14538
7 SOFTWARE: PasteSeq for Windows Version 4.0.
8 SEQ ID NO 13033

```

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13033

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
			Indels	0;
			Gaps	0;

```
QY      7 GYLTAAVSP 16
      | :: |::|
Db      2 GQMVHQAI SP 11
```

RESULT 68
US-11-045-024-13034

; Sequence 13034, Application US/1104502
; Publication No. US20050271676A1
; PUBLICATION INFORMATION

```

; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney John

```

APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian

APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie

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; APPLICANT: Celis, Esteban
; APPLICANT: Kubo, Ralph

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APPLICANT: Grey, Howard M.
APPLICANT: Epiimmune Inc.

```

; TITLE OF INVENTION: Inducing cellular responses to human immunodeficiency
; TITLE OF INVENTION: Virus-1
; TITLE OF INVENTION: Using Peptide and Nucleic Acid Compositions
; PRIORITY REFERENCE: 2060 0040007

```

```

/ FIDELITY: 2080.004000,
; CURRENT APPLICATION NUMBER: US/11/045,024
: CURRENT FILING DATE: 2005-01-28

```

PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05

; PRIOR APPLICATION NUMBER: US 08/027,146
 ; PRIOR FILING DATE: 1993-03-05
 ;

;
; PRIOR APPLICATION NUMBER: US 08/073,205
;
; PRIOR FILING DATE: 1993-06-04
;

; PRIOR APPLICATION NUMBER: US 08/103,396
 ; PRIOR FILING DATE: 1993-08-06
 ; PRIOR APPLICATION NUMBER: US 08/150,184

PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339

/ PRIOR APPLICATION NUMBER: US 08/153,553
 ; PRIOR FILING DATE: 1993-11-29
 : PRIOR APPLICATION NUMBER: US 08/205,713

PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610

```

; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
;

```

```

; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 13034

```

```

; LENGTH: 15
; TYPE: PRT
; ORCA15CM. ITMAN TMTNDEETCTNCGV VTRYS

```

! ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13034

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 3.3e+02;		

Matches	4	Conservative	3	Mismatches	3	Indels	0	Gaps	0
Oy	7	GILLTAAVSP	16						

Db 1 GQMVHQAI SP 10

```
RESULT 69
US-11-045-024-13046
/ Sequence 13046, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Seteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 13046
/ LENGTH: 15
/ TYPE: PR
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13046

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAVSP 16
| : : | : |
Db 6 GQVWQAISP 15

RESULT 70
US-11-045-024-14210
/ Sequence 14210, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Seteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14210
/ LENGTH: 15
/ TYPE: PR
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14210

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

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/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14210
/ LENGTH: 15
/ TYPE: PR
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14210

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAVSP 16
| : : | : |
Db 2 GQVWQAISP 11

RESULT 71
US-11-045-024-14400
/ Sequence 14400, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cella, Seteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ CURRENT FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 14400
/ LENGTH: 15
/ TYPE: PR
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14400

Query Match          24.0%; Score 23; DB 7; Length 15;
Best Local Similarity 40.0%; Pred. No. 3.3e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
```

```

; SEQ ID NO 14400
;
; LENGTH: 15
;
; TYPE: PRT
;
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14400

```

Query Match	24.0%;	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%;	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0;

```

Qy      7 GYLTLTAAVSP 16
         | :: |::|
Db      2 GQMVHQALSP 11

```

RESULT 72
US-11-045-024-14417
; Sequence 14417, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:

1 APPLICANT: sette, Alessandro
 2 APPLICANT: Sidney, John
 3 APPLICANT: Southwood, Scott
 4 APPLICANT: Livingston, Brian
 5 APPLICANT: Chesnut, Robert
 6 APPLICANT: Baker, Denise Marie
 7 APPLICANT: Cells, Esteban
 8 APPLICANT: Kubo, Ralph
 9 APPLICANT: Grey, Howard M.
 10 APPLICANT: Epimmune Inc.
 11 TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
 12 TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
 13 FILE REFERENCE: 2060.004007
 14 CURRENT APPLICATION NUMBER: US/11/045,024

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1 CURRENT APPLICATION NUMBER: US/11/045,024
2 CURRENT FILING DATE: 2005-01-28
3 PRIOR APPLICATION NUMBER: US 09/412,863
4 PRIOR FILING DATE: 1999-10-05
5 PRIOR APPLICATION NUMBER: US 08/027,146
6 PRIOR FILING DATE: 1993-03-05
7 PRIOR APPLICATION NUMBER: US 08/073,205
8 PRIOR FILING DATE: 1993-06-04
9 PRIOR APPLICATION NUMBER: US 08/103,396
10 PRIOR FILING DATE: 1993-08-06
11 PRIOR APPLICATION NUMBER: US 08/159,184
12 PRIOR FILING DATE: 1993-11-29
13 PRIOR APPLICATION NUMBER: US 08/159,339
14 PRIOR FILING DATE: 1993-11-29
15 PRIOR APPLICATION NUMBER: US 08/205,713
16 PRIOR FILING DATE: 1994-03-04
17 PRIOR APPLICATION NUMBER: US 08/347,610
18 PRIOR FILING DATE: 1994-12-01
19 NUMBER OF SEQ ID NOS: 14528
20 SOFTWARE: FastSeq for Windows Version 4.0
21 SEQ ID NO 14417
22 LENGTH: 15
23 TYPE: PRT
24 ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
25 US-11-045-024-14417

```

Query Match	24.0%	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
				Indels 0;
				Gaps 0

QY 7 GYLTAAVSP 16
| :: ||
Db 2 GQMVHQATSP 11

RESULT 73
US-11-045-024-14477
; Sequence 14477, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:

? APPLICANT: Sette, Alessandro
 ? APPLICANT: Sidney, John
 ? APPLICANT: Southwood, Scott
 ? APPLICANT: Livingston, Brian
 ? APPLICANT: Chesnut, Robert
 ? APPLICANT: Baker, Denise Marie
 ? APPLICANT: Cells, Escoban
 ? APPLICANT: Kudo, Ralph
 ? APPLICANT: Grey, Howard M.

```

1  TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
2
3  TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
4
5  FILE REFERENCE: 2060.0040007
6
7  CURRENT APPLICATION NUMBER: US/11/045,024

```

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1 CURRENT FILING DATE: 2005-01-28
2 PRIOR APPLICATION NUMBER: US 09/412,863
3 PRIOR FILING DATE: 1999-10-05
4 PRIOR APPLICATION NUMBER: US 08/027,146
5 PRIOR FILING DATE: 1993-03-05
6 PRIOR APPLICATION NUMBER: US 08/073,205
7 PRIOR FILING DATE: 1993-06-04
8 PRIOR APPLICATION NUMBER: US 08/103,396
9 PRIOR FILING DATE: 1993-08-06
10 PRIOR APPLICATION NUMBER: US 08/159,184
11 PRIOR FILING DATE: 1993-11-29
12 PRIOR APPLICATION NUMBER: US 08/159,339
13 PRIOR FILING DATE: 1993-11-29
14 PRIOR APPLICATION NUMBER: US 08/205,713
15 PRIOR FILING DATE: 1994-03-04
16 PRIOR APPLICATION NUMBER: US 08/347,610
17 PRIOR FILING DATE: 1994-12-01
18 NUMBER OF SEQ ID NOS: 14528
19 SOFTWARE: FastSeq for Windows Version 4.0
20 SEQ ID NO 14477

```

ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-14477

Query Match	24.0%	Score 23;	DB 7;	Length 15;
Best Local Similarity	40.0%	Pred. No. 3.3e+02;		
Matches	4;	Conservative	3;	Mismatches 3;
			Indels	0;
			Gaps	0

QY 7 GYLTTAAVSP 16
| :: | : | |
Db 2 GQMVHQAIISP 11

RESULT 74
US-11-033-039-581
; Sequence 581, Application US/11033035
; Publication No. US20060002947A1

```

; GENERAL INFORMATION:
; APPLICANT: HUMPHREYS, ROBERT
; APPLICANT: XU, MINZHEN
; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPIOTOPE HYBRID PEPTIDE VACCINES
; FILE REFERENCE: RH-2011US01
; CURRENT APPLICATION NUMBER: US/11/033,039

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; SEQ ID NO 581
; LENGTH: 15
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-033-039-581

```

Query Match 24.0%; Score 23; DB 7; Length 15;
 Best Local Similarity 80.0%; Pred. No. 3.3e+02;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18
 : |||
 DB 8 LSPGK 12

RESULT 75

US-11-041-893-176
 ; Sequence 176, Application US/11041893
 ; Publication No. US2006002941A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Mahaitas, Gregory G.
 ; TITLE OF INVENTION: COMPOSITIONS COMPRISING IMMUNE RESPONSE
 ; FILE REFERENCE: 100123.401
 ; CURRENT APPLICATION NUMBER: US/11/041,893
 ; PRIOR FILING DATE: 2005-01-24
 ; PRIOR APPLICATION NUMBER: US 60/616,855
 ; PRIOR FILING DATE: 2004-10-06
 ; PRIOR APPLICATION NUMBER: US 60/538,713
 ; PRIOR FILING DATE: 2004-01-23
 ; NUMBER OF SEQ ID NOS: 295
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 176
 ; LENGTH: 15
 ; TYPE: PRT
 ; ORGANISM: Trypanosoma cruzi
 US-11-041-893-176

Query Match 24.0%; Score 23; DB 7; Length 15;
 Best Local Similarity 44.4%; Pred. No. 3.3e+02;
 Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HGYLTAAY 14
 : : |||
 DB 2 HNFTLVASV 10

RESULT 76

US-11-033-039-839
 ; Sequence 839, Application US/11033039
 ; Publication No. US2006002947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HUMPHREYS, ROBERT
 ; APPLICANT: XU, MINZHEN
 ; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
 ; FILE REFERENCE: REH-2017US01
 ; CURRENT APPLICATION NUMBER: US/11/033,039
 ; PRIOR FILING DATE: 2005-01-11
 ; PRIOR APPLICATION NUMBER: 10/245,871
 ; PRIOR FILING DATE: 2002-09-17
 ; PRIOR APPLICATION NUMBER: 10/197,000
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: 09/396,813
 ; PRIOR FILING DATE: 1999-09-14
 ; NUMBER OF SEQ ID NOS: 1452
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 839
 ; LENGTH: 16
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-11-033-039-839

Query Match 24.0%; Score 23; DB 7; Length 16;
 Best Local Similarity 60.0%; Pred. No. 3.6e+02;
 Matches 6; Conservative 1; Mismatches 1; Indels 2; Gaps 1;

QY 6 HG--YLLTAA 13
 || |||
 DB 5 HGSXYLATAS 14

RESULT 77

US-11-073-347-118
 ; Sequence 118, Application US/11073347
 ; Publication No. US20050260234A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SIMARD, John J. L.
 ; APPLICANT: DIAMOND, David C.
 ; TITLE OF INVENTION: ANTI-NEOVASCULATURE PREPARATIONS FOR
 ; FILE REFERENCE: MANK.015C1
 ; CURRENT APPLICATION NUMBER: US/11/073,347
 ; PRIOR FILING DATE: 2005-03-04
 ; PRIOR APPLICATION NUMBER: 10/094,699
 ; PRIOR FILING DATE: 2002-03-07
 ; PRIOR APPLICATION NUMBER: 60/274,063
 ; PRIOR FILING DATE: 2001-03-07
 ; NUMBER OF SEQ ID NOS: 159
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 118
 ; LENGTH: 17
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-11-073-347-118

Query Match 24.0%; Score 23; DB 7; Length 17;
 Best Local Similarity 66.7%; Pred. No. 3.8e+02;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APEPHG 7
 |||
 DB 1 AEPGQ 6

RESULT 78

US-11-033-039-993
 ; Sequence 993, Application US/11033039
 ; Publication No. US2006002947A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HUMPHREYS, ROBERT
 ; APPLICANT: XU, MINZHEN
 ; TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES
 ; FILE REFERENCE: REH-2017US01
 ; CURRENT APPLICATION NUMBER: US/11/033,039
 ; PRIOR FILING DATE: 2005-01-11
 ; PRIOR APPLICATION NUMBER: 10/245,871
 ; PRIOR FILING DATE: 2002-09-17
 ; PRIOR APPLICATION NUMBER: 10/197,000
 ; PRIOR FILING DATE: 2002-07-17
 ; PRIOR APPLICATION NUMBER: 09/396,813
 ; PRIOR FILING DATE: 1999-09-14
 ; NUMBER OF SEQ ID NOS: 1452
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 993
 ; LENGTH: 18
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
 ; OTHER INFORMATION: hybrid peptide
 ; FEATURE:
 ; NAME/KEY: MOD_RES
 ; LOCATION: (5)-(5)
 ; OTHER INFORMATION: Ava
 US-11-033-039-993

Query Match 24.0%; Score 23; DB 7; Length 18;
 Best Local Similarity 40.0%; Pred. No. 4.1e+02;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAYSP 16
 : : |||

Db 8 GQMVHQAISP 17

RESULT 79

US-11-033-039-1048

/ Sequence 1048, Application US/11033039

/ Publication No. US2006002947A1

/ GENERAL INFORMATION:

/ APPLICANT: HUMPHREYS, ROBERT

/ TITLE OF INVENTION: LI-KEY/ANTIGENIC EPITOPE HYBRID PEPTIDE VACCINES

/ FILE REFERENCE: REH-2017US01

/ CURRENT FILING DATE: 2005-01-11

/ PRIOR FILING DATE: 2005-01-11

/ PRIOR FILING DATE: 2002-09-17

/ PRIOR APPLICATION NUMBER: 10/245,871

/ PRIOR FILING DATE: 2002-09-17

/ PRIOR APPLICATION NUMBER: 10/197,000

/ PRIOR FILING DATE: 2002-07-17

/ PRIOR APPLICATION NUMBER: 09/396,813

/ PRIOR FILING DATE: 1999-09-14

/ NUMBER OF SEQ ID NOS: 1452

/ SOFTWARE: PatentIn version 3.3

/ SEQ ID NO 1048

/ LENGTH: 18

/ TYPE: PRT

/ ORGANISM: Artificial Sequence

/ FEATURE:

/ OTHER INFORMATION: Description of Artificial Sequence: Synthetic

/ FEATURE:

/ NAME/KEY: MOD_RES

/ LOCATION: (5)..(5)

/ OTHER INFORMATION: Ava

US-11-033-039-1048

Query Match 24.0%; Score 23; DB 7; Length 18;

Best Local Similarity 44.4%; Pred. No. 4.1e+02;

Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 7 GYLTPRAVS 15

Db 10 GFLTGSPS 18

RESULT 80

US-11-054-515-3036

/ Sequence 3036, Application US/11054515

/ Publication No. US2005025532A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruben et al.

/ TITLE OF INVENTION: Antibodies that Immunospecifically Bind Blys

/ FILE REFERENCE: PF533P3

/ CURRENT APPLICATION NUMBER: US/11/054,515

/ CURRENT FILING DATE: 2005-02-10

/ PRIOR APPLICATION NUMBER: 60/543,296

/ PRIOR FILING DATE: 2004-02-11

/ PRIOR APPLICATION NUMBER: 60/580,347

/ PRIOR FILING DATE: 2004-06-18

/ PRIOR APPLICATION NUMBER: 10/293,418

/ PRIOR FILING DATE: 2002-11-14

/ PRIOR APPLICATION NUMBER: 60/331,469

/ PRIOR FILING DATE: 2001-11-16

/ PRIOR APPLICATION NUMBER: 60/340,817

/ PRIOR FILING DATE: 2001-12-19

/ PRIOR APPLICATION NUMBER: 09/880,748

/ PRIOR FILING DATE: 2001-06-15

/ PRIOR APPLICATION NUMBER: 60/293,499

/ PRIOR FILING DATE: 2001-05-25

/ PRIOR APPLICATION NUMBER: 60/277,379

/ PRIOR FILING DATE: 2001-03-21

/ PRIOR APPLICATION NUMBER: 60/276,248

/ PRIOR FILING DATE: 2001-03-16

/ PRIOR APPLICATION NUMBER: 60/240,816

/ PRIOR FILING DATE: 2000-10-17

/ Remaining Prior Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 3247

/ SEQ ID NO 3036

/ LENGTH: 19

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-11-054-515-3036

Query Match 24.0%; Score 23; DB 7; Length 19;

Best Local Similarity 66.7%; Pred. No. 4.4e+02;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 PEPHG 8

Db 11 FYPSGI 16

RESULT 81

US-11-022-562-286

/ Sequence 286, Application US/11022562

/ Publication No. US20050249742A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruprecht, Ruth M.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE

/ FILE REFERENCE: DFN-043CN

/ CURRENT APPLICATION NUMBER: US/11/022,562

/ CURRENT FILING DATE: 2004-12-22

/ PRIOR APPLICATION NUMBER: PCT/US03/20322

/ PRIOR FILING DATE: 2003-06-27

/ PRIOR APPLICATION NUMBER: 60/392718

/ PRIOR FILING DATE: 2002-06-27

/ NUMBER OF SEQ ID NOS: 340

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 286

/ LENGTH: 20

/ TYPE: PRT

/ ORGANISM: Human Immunodeficiency Virus

US-11-022-562-286

Query Match 24.0%; Score 23; DB 7; Length 20;

Best Local Similarity 40.0%; Pred. No. 4.6e+02;

Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTPRAVSP 16

Db 10 GQMVHQAISP 19

RESULT 82

US-11-022-562-287

/ Sequence 287, Application US/11022562

/ Publication No. US20050249742A1

/ GENERAL INFORMATION:

/ APPLICANT: Ruprecht, Ruth M.

/ TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR MODULATING

/ TITLE OF INVENTION: A CYTOTOXIC T LYMPHOCYTE IMMUNE RESPONSE

/ FILE REFERENCE: DFN-043CN

/ CURRENT APPLICATION NUMBER: US/11/022,562

/ CURRENT FILING DATE: 2004-12-22

/ PRIOR APPLICATION NUMBER: PCT/US03/20322

/ PRIOR FILING DATE: 2003-06-27

/ PRIOR APPLICATION NUMBER: 60/392718

/ PRIOR FILING DATE: 2002-06-27

/ NUMBER OF SEQ ID NOS: 340

/ SOFTWARE: FastSeq for Windows Version 4.0

/ SEQ ID NO 287

/ LENGTH: 20

/ TYPE: PRT

/ ORGANISM: Human Immunodeficiency Virus

US-11-022-562-287

Query Match 24.0%; Score 23; DB 7; Length 20;
Best Local Similarity 40.0%; Pred. No. 4.6e+02;
Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 7 YLTLTAVSP 16
DB 10 GCMVHQALSP 19

RESULT 83

US-11-045-024-3558
; Sequence 3558, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3558
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3558

Query Match 23.4%; Score 22.5; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 8 YL-LTAAVSP 16
DB 1 YLALTLALIKP 10

RESULT 84

US-11-045-024-10541
; Sequence 10541, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian

; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Bsteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.

; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10541
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-10541

Query Match 23.4%; Score 22.5; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;

QY 8 YL-LTAAVSP 16
DB 1 YLALTLALIKP 10

RESULT 85
US-11-045-024-12349
; Sequence 12349, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Celis, Bsteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; PRIOR FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184

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; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 12349
; LENGTH: 11
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12349
```

```

Query Match      23.4%; Score 22.5; DB 7; Length 11;
Best Local Similarity 60.0%; Pred. No. 2.9e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
```

```
QY      8 YL-LTRAVSP 16
      |||||:|
Db      1 YLALTRALIKP 10
```

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RESULT 86
US-11-045-024-13314
; Sequence 13314, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO: 13314
; LENGTH: 15
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-13314
```

```

Query Match      23.4%; Score 22.5; DB 7; Length 15;
Best Local Similarity 60.0%; Pred. No. 4.1e+02;
Matches 6; Conservative 1; Mismatches 2; Indels 1; Gaps 1;
```

```
QY      8 YL-LTRAVSP 16
```

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Db      6 YLALTRALIKP 15
      |||||:|
```

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RESULT 87
US-10-503-575-197
; Sequence 197, Application US/10503575
; Publication No. US20050244823A1
; GENERAL INFORMATION:
; APPLICANT: Drifhout, Jan Wouter
; APPLICANT: van Veele, Petrus Antonius
; APPLICANT: Koning, Frits
; TITLE OF INVENTION: NOVEL EPITOPES FOR CELIAC DISEASE AND AUTOIMMUNE DISEASES, METHOD
; TITLE OF INVENTION: DETECTING THOSE AND NOVEL NON-ANTIGENIC FOOD COMPOUNDS
; FILE REFERENCE: 2799/72843-PCT-US
; CURRENT APPLICATION NUMBER: US/10/503,575
; CURRENT FILING DATE: 2004-08-04
; PRIOR APPLICATION NUMBER: PCT/NL03/00077
; PRIOR FILING DATE: 2003-02-04
; PRIOR APPLICATION NUMBER: EP 02075456.0
; PRIOR FILING DATE: 2002-02-04
; NUMBER OF SEQ ID NOS: 340
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 197
; LENGTH: 19
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-503-575-197
```

```

Query Match      23.4%; Score 22.5; DB 6; Length 19;
Best Local Similarity 58.3%; Pred. No. 5.3e+02;
Matches 7; Conservative 1; Mismatches 3; Indels 1; Gaps 1;
```

```
QY      7 GYLTA-AVSPG 17
      |||||:|
Db      2 GWLGAERQEPG 13
```

```

RESULT 88
US-11-045-024-1025
; Sequence 1025, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Esteban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: EpiImmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
```



```
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 1025
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1025

Query Match      22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVSPG 17
        ||:|
Db      2 AVNPG 6

RESULT 89
US-11-045-024-3518
/ Sequence 3518, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 3518
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3518

Query Match      22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
/ Sequence 4007, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 4007
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4007

Query Match      22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY      13 AVSPG 17
        ||:|
Db      3 AVNPG 7

RESULT 91
US-11-045-024-6362
/ Sequence 6362, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Celis, Basteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Bpimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
```

```
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6362
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-6362
```

```
Query Match          22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
Qy      13 AVSPG 17
Db      2 AVNPG 6
```

```
RESULT 92
US-11-045-024-10522
```

```
/ Sequence 10522, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10522
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

```
/ Sequence 10522, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 10522
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

```
US-11-045-024-10522
```

```
Query Match          22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      10 LTAASP 16
Db      1 LTAALIKP 7
```

```
RESULT 93
```

```
US-11-045-024-12335
/ Sequence 12335, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
/ APPLICANT: Chesnut, Robert
/ APPLICANT: Baker, Denise Marie
/ APPLICANT: Cells, Esteban
/ APPLICANT: Kubo, Ralph
/ APPLICANT: Grey, Howard M.
/ APPLICANT: Eptimmune Inc.
/ TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
/ FILE REFERENCE: 2060.0040007
/ CURRENT APPLICATION NUMBER: US/11/045,024
/ PRIOR FILING DATE: 2005-01-28
/ PRIOR APPLICATION NUMBER: US 09/412,863
/ PRIOR FILING DATE: 1999-10-05
/ PRIOR APPLICATION NUMBER: US 08/027,146
/ PRIOR FILING DATE: 1993-03-05
/ PRIOR APPLICATION NUMBER: US 08/073,205
/ PRIOR FILING DATE: 1993-06-04
/ PRIOR APPLICATION NUMBER: US 08/103,396
/ PRIOR FILING DATE: 1993-08-06
/ PRIOR APPLICATION NUMBER: US 08/159,184
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/159,339
/ PRIOR FILING DATE: 1993-11-29
/ PRIOR APPLICATION NUMBER: US 08/205,713
/ PRIOR FILING DATE: 1994-03-04
/ PRIOR APPLICATION NUMBER: US 08/347,610
/ PRIOR FILING DATE: 1994-12-01
/ NUMBER OF SEQ ID NOS: 14528
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 12335
/ LENGTH: 8
/ TYPE: PRT
/ ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
```

```
US-11-045-024-12335
```

```
Query Match          22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
Qy      10 LTAASP 16
Db      1 LTAALIKP 7
```

```
RESULT 94
```

```
US-11-045-024-12616
/ Sequence 12616, Application US/11045024
/ Publication No. US20050271676A1
/ GENERAL INFORMATION:
/ APPLICANT: Sette, Alessandro
/ APPLICANT: Sidney, John
/ APPLICANT: Southwood, Scott
/ APPLICANT: Livingston, Brian
```

APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Bateban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
APPLICANT: EpiImmune Inc.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/159,339
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713
PRIOR FILING DATE: 1994-03-04
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1994-12-01
NUMBER OF SEQ ID NOS: 14528
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 12616
LENGTH: 8
TYPE: PRT
ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-12616

Query Match 22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17
DB 3 AVMPG 7

RESULT 95
US-11-116-144-73
Sequence 73, Application US/11116144
Publication No. US20050277181A1
GENERAL INFORMATION:
APPLICANT: BERTHET, FRANCOIS XAVIER
APPLICANT: CASADEVAL, FRANCESC VAYREDA
APPLICANT: SANZ MARIA, MARIA CRUZ
APPLICANT: GARCIA, TERESA LLOP
APPLICANT: OLE, ANGELS MOR
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETECTING PATHOGEN
FILE REFERENCE: INL-084
CURRENT APPLICATION NUMBER: US/11/116,144
CURRENT FILING DATE: 2005-04-27
PRIOR APPLICATION NUMBER: PCT/ES04/000581
PRIOR FILING DATE: 2004-12-23
PRIOR APPLICATION NUMBER: EP 03380307.3
PRIOR FILING DATE: 2003-12-23
NUMBER OF SEQ ID NOS: 301
SOFTWARE: PatentIn Ver. 3.3
SEQ ID NO 73
LENGTH: 8
TYPE: PRT
ORGANISM: Bos taurus Immunodeficiency virus
US-11-116-144-73

Query Match 22.9%; Score 22; DB 7; Length 8;
Best Local Similarity 75.0%; Pred. No. 5.5e+04;

Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 4 EPHG 7
DB 2 KPHG 5

RESULT 96
US-10-999-866-60
Sequence 60, Application US/10999866
Publication No. US20050266004A1
GENERAL INFORMATION:
APPLICANT: GILES-KOMAR, Jill; SCALLON, Bernard J.; CAI, Ann
TITLE OF INVENTION: ANTI-HUMAN LYMPHOTOXIN ALPHA ANTIBODIES, COMPOSITIONS, METHODS
FILE REFERENCE: CEN5042NP
CURRENT APPLICATION NUMBER: US/10/999,866
CURRENT FILING DATE: 2004-11-30
PRIOR APPLICATION NUMBER: 60/527,794
PRIOR FILING DATE: 2003-12-08
NUMBER OF SEQ ID NOS: 61
SOFTWARE: PatentIn version 3.3
SEQ ID NO 60
LENGTH: 9
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE: MISC FEATURE
NAME/KEY: (1).(9)
LOCATION: (1).(9)
OTHER INFORMATION: HC CDR 3
US-10-999-866-60

Query Match 22.9%; Score 22; DB 6; Length 9;
Best Local Similarity 50.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFEPHY 8
DB 2 DVNMPGY 9

RESULT 97
US-11-045-024-1138
Sequence 1138, Application US/11045024
Publication No. US20050271676A1
GENERAL INFORMATION:
APPLICANT: Sette, Alessandro
APPLICANT: Sidney, John
APPLICANT: Southwood, Scott
APPLICANT: Livingston, Brian
APPLICANT: Chesnut, Robert
APPLICANT: Baker, Denise Marie
APPLICANT: Celis, Bateban
APPLICANT: Kubo, Ralph
APPLICANT: Grey, Howard M.
TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
FILE REFERENCE: 2060.0040007
CURRENT APPLICATION NUMBER: US/11/045,024
CURRENT FILING DATE: 2005-01-28
PRIOR APPLICATION NUMBER: US 09/412,863
PRIOR FILING DATE: 1999-10-05
PRIOR APPLICATION NUMBER: US 08/027,146
PRIOR FILING DATE: 1993-03-05
PRIOR APPLICATION NUMBER: US 08/073,205
PRIOR FILING DATE: 1993-06-04
PRIOR APPLICATION NUMBER: US 08/103,396
PRIOR FILING DATE: 1993-08-06
PRIOR APPLICATION NUMBER: US 08/159,184
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/347,610
PRIOR FILING DATE: 1993-11-29
PRIOR APPLICATION NUMBER: US 08/205,713

```
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1138
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-1138
```

```
Query Match      22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 AVSPG 17
      |||:|
DB      1 AVNPG 5
```

```
RESULT 98
US-11-045-024-3530
; Sequence 3530, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Eateban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3530
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-3530
```

```
Query Match      22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 57.1%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
```

```
QY      10 LTRAVSP 16
      |||:|
DB      2 LTRALINP 8
```

```
RESULT 99
US-11-045-024-4061
; Sequence 4061, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Eateban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
```

```
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
; PRIOR APPLICATION NUMBER: US 09/412,863
; PRIOR FILING DATE: 1999-10-05
; PRIOR APPLICATION NUMBER: US 08/027,146
; PRIOR FILING DATE: 1993-03-05
; PRIOR APPLICATION NUMBER: US 08/073,205
; PRIOR FILING DATE: 1993-06-04
; PRIOR APPLICATION NUMBER: US 08/103,396
; PRIOR FILING DATE: 1993-08-06
; PRIOR APPLICATION NUMBER: US 08/159,184
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/159,339
; PRIOR FILING DATE: 1993-11-29
; PRIOR APPLICATION NUMBER: US 08/205,713
; PRIOR FILING DATE: 1994-03-04
; PRIOR APPLICATION NUMBER: US 08/347,610
; PRIOR FILING DATE: 1994-12-01
; NUMBER OF SEQ ID NOS: 14528
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4061
; LENGTH: 9
; TYPE: PRT
; ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
US-11-045-024-4061
```

```
Query Match      22.9%; Score 22; DB 7; Length 9;
Best Local Similarity 80.0%; Pred. No. 5.5e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
```

```
QY      13 AVSPG 17
      |||:|
DB      3 AVNPG 7
```

```
RESULT 100
US-11-045-024-5639
; Sequence 5639, Application US/11045024
; Publication No. US20050271676A1
; GENERAL INFORMATION:
; APPLICANT: Sette, Alessandro
; APPLICANT: Sidney, John
; APPLICANT: Southwood, Scott
; APPLICANT: Livingston, Brian
; APPLICANT: Chesnut, Robert
; APPLICANT: Baker, Denise Marie
; APPLICANT: Cells, Eateban
; APPLICANT: Kubo, Ralph
; APPLICANT: Grey, Howard M.
; APPLICANT: Eptimmune Inc.
; TITLE OF INVENTION: Inducing Cellular Responses to Human Immunodeficiency
; TITLE OF INVENTION: Virus-1 Using Peptide and Nucleic Acid Compositions
; FILE REFERENCE: 2060.0040007
; CURRENT APPLICATION NUMBER: US/11/045,024
; CURRENT FILING DATE: 2005-01-28
```

/ PRIOR APPLICATION NUMBER: US 09/412,863
 / PRIOR FILING DATE: 1999-10-05
 / PRIOR APPLICATION NUMBER: US 08/027,146
 / PRIOR FILING DATE: 1993-03-05
 / PRIOR APPLICATION NUMBER: US 08/073,205
 / PRIOR FILING DATE: 1993-06-04
 / PRIOR APPLICATION NUMBER: US 08/103,396
 / PRIOR FILING DATE: 1993-08-06
 / PRIOR APPLICATION NUMBER: US 08/159,184
 / PRIOR FILING DATE: 1993-11-29
 / PRIOR APPLICATION NUMBER: US 08/159,339
 / PRIOR FILING DATE: 1993-11-29
 / PRIOR APPLICATION NUMBER: US 08/205,713
 / PRIOR FILING DATE: 1994-03-04
 / PRIOR APPLICATION NUMBER: US 08/347,610
 / PRIOR FILING DATE: 1994-12-01
 / NUMBER OF SEQ ID NOS: 14528
 / SOFTWARE: FastSeq for Windows Version 4.0
 / SEQ ID NO 5639
 / LENGTH: 9
 / TYPE: PRT
 / ORGANISM: HUMAN IMMUNODEFICIENCY VIRUS
 US-11-045-024-5639

Query Match 22.9%, Score 22, DB 7, Length 9,
 Best Local Similarity 80.0%, Pred. No. 5.5e+04,
 Matches 4, Conservative 1, Mismatches 0, Indels 0, Gaps 0,

QY 13 AVSPG 17
 ||:|
 Db 4 AVNPG 8

Search completed: January 20, 2006, 19:46:32
 Job time : 8.26923 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: January 20, 2006, 18:55:50 ; Search time 10.2115 Seconds
(without alignments)
169.602 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96
Sequence: 1 DAEPHGYLITAVSPK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 263416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 3886

Minimum DB seq length: 0

Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database :

1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	29	30.2	15	2 B56046	urinary tract ston
2	28	29.2	20	2 B39419	collagen alpha 5(I
3	28	29.2	20	2 A61264	MHC class I histoc
4	27	28.1	9	2 S63491	diseasimulatory sulf
5	27	28.1	20	2 S68028	iodochronine 5'-mo
6	27	28.1	20	2 A36016	granulocyte inhibi
7	25	26.0	10	2 PT0213	T-cell receptor al
8	25	26.0	13	2 S63492	diseasimulatory sulf
9	25	26.0	14	2 B38222	exonuclease ABC c
10	25	26.0	16	2 H35141	T-cell receptor de
11	25	26.0	16	4 A33171	hypothetical prote
12	25	26.0	20	2 S23981	outer layer protei
13	25	26.0	13	2 B47415	mannose-1-phosphat
14	24	25.0	14	2 PH1305	Ig heavy chain DJ
15	24	25.0	14	4 S00843	hypothetical prote
16	24	25.0	15	2 S10741	phosphoglucosylase
17	24	25.0	16	2 S66613	protein p128 - Frl
18	23.5	24.5	16	2 A59155	multicystatin - Frl
19	23	24.0	11	1 GMR0L	leucosulfakinin -
20	23	24.0	16	2 PH1604	Ig H chain V-D-J r
21	23	24.0	16	2 B36300	T-cell receptor de
22	23	24.0	18	2 T78841	chromoprotein rec
23	23	24.0	20	2 H28949	ribosomal protein
24	22	22.9	13	2 PH1772	T-cell receptor al
25	22	22.9	17	2 S59512	probable integrin
26	22	22.9	20	2 A61276	superoxide dismuta
27	22	22.9	20	2 S46479	retinoid-X-recepto
28	21	21.9	8	2 PH1618	Ig H chain V-D-J r
29	21	21.9	9	4 S15594	orf 1 para 5'-regi

30	21	21.9	10	2 A59173	nuclease Bhl (RC 3
31	21	21.9	12	2 F84132	hypothetical prote
32	21	21.9	13	2 PC1008	40K extracellular
33	21	21.9	14	2 S00150	ovostatin - duck (
34	21	21.9	16	2 A11488	taurocyamine kinase
35	21	21.9	18	2 B32473	histidine-rich pro
36	21	21.9	18	2 S36121	lectin - spurge (E
37	21	21.9	18	2 S27141	hypothetical prote
38	21	21.9	19	2 G49048	T-cell receptor be
39	21	21.9	19	2 PT0332	Ig heavy chain CRD
40	20.5	21.4	20	2 A20999	fructose-bisphosph
41	20	20.8	6	2 PT0715	T-cell receptor be
42	20	20.8	10	2 PT0243	Ig heavy chain CRD
43	20	20.8	10	2 PH0944	T-cell receptor be
44	20	20.8	10	2 A46030	gonadolibetin I -
45	20	20.8	10	2 S77990	cytochrome-c oxida
46	20	20.8	11	2 A60656	perilulafaklin - A
47	20	20.8	12	2 S70344	amine oxidase (cop
48	20	20.8	13	2 A46463	preabsorbing anti
49	20	20.8	14	1 LFB8WT	trp operon leader
50	20	20.8	14	2 A56632	neousulfakinin-II -
51	20	20.8	14	2 S27140	hypothetical prote
52	20	20.8	15	2 PH1342	Ig heavy chain DJ
53	20	20.8	15	2 PH1310	Ig heavy chain DJ
54	20	20.8	16	2 A44413	proteaseome endope
55	20	20.8	16	2 PH1637	Ig H chain V-D-J r
56	20	20.8	16	2 PH0773	T-cell receptor be
57	20	20.8	17	2 A44799	pyrogenic exotoxin
58	20	20.8	18	2 S45373	translational elonga
59	20	20.8	18	2 I59649	human leukocyte an
60	20	20.8	18	2 S48862	murine cyclin H -
61	20	20.8	18	2 I51427	hemoglobin alpha c
62	20	20.8	19	2 A34467	36K microfibril-as
63	20	20.8	20	2 A60801	acrosome stabilizi
64	19.5	20.3	20	2 A48367	glutaryl-CoA dehyd
65	19	19.8	5	2 PT0714	T-cell receptor be
66	19	19.8	9	2 PD0027	pev-tachykinin - p
67	19	19.8	12	2 S67528	napin - rape (frag
68	19	19.8	12	2 PH1190	T-cell receptor al
69	19	19.8	13	2 PT0263	Ig heavy chain CRD
70	19	19.8	14	1 LFB8WC	trp operon leader
71	19	19.8	14	2 PH1347	Ig heavy chain DJ
72	19	19.8	15	2 S24159	leukocyte elastase
73	19	19.8	15	2 S26535	T-cell receptor al
74	19	19.8	15	2 S29485	GTP-binding protei
75	19	19.8	15	2 A36315	recycling receptor
76	19	19.8	15	2 PA0006	lectin A3 - Paopho
77	19	19.8	16	2 A60551	leukocyte elastase
78	19	19.8	16	2 PT0282	Ig heavy chain CDR
79	19	19.8	16	2 S16376	L-serine dehydrata
80	19	19.8	17	2 S57991	hydroxyproline-ric
81	19	19.8	17	2 S09085	proteaseome chain 4
82	19	19.8	17	2 B31435	adherence lectin 1
83	19	19.8	18	2 PH1323	Ig heavy chain DJ
84	19	19.8	18	2 S28408	placelac-derived g
85	19	19.8	18	2 S20322	gluten - wheat
86	19	19.8	19	2 PH1339	Ig heavy chain DJ
87	19	19.8	19	2 A34233	trehalase inhibito
88	19	19.8	19	2 A56800	chymotrypsin I (EC
89	19	19.8	20	2 B34817	collagenolytic pro
90	19	19.8	20	2 C34817	collagenolytic pro
91	19	19.8	20	2 S07232	ribulose-bisphosph
92	19	19.8	20	2 A60372	pollen allergen Po
93	19	19.8	20	2 PH1326	Ig heavy chain DJ
94	19	19.8	20	2 S50175	kalikrein (PK-120
95	19	19.8	20	2 S45637	oxidoreductase - P
96	19	19.8	20	2 S29636	jacalin beta-1 cha
97	19	19.8	20	2 S71593	serine proteinase
98	19	19.8	20	2 A58903	metalloproteinase
99	18.5	19.3	16	2 S38292	30K allergen - rye
100	18	18.8	7	2 A33098	24K exoantigen -

ALIGNMENTS

RESULT 1

B56046

urinary tract stone matrix protein 2, 21K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 12-Apr-1995 #sequence_revision 12-Apr-1995 #text_change 12-Apr-1995

C/Accession: B56046

R/Binette, J.P.; Binette, M.B.; Gawinowicz, M.A.; Kendrick, N.

submitted to the Protein Sequence Database, February 1995.

A/Description: Isolation, characterization and sequence of stone proteins.

A/Reference number: A56046

A/Accession: B56046

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-15 <BIN>

A/Cross-references: UNIPARC:UPI000017C408

Query Match

Best Local Similarity 45.5%; Pred. No. 2e+02;

Matches 5; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTTAAVSFGK 18

DB 1 YLVLTQGVAPQ 11

RESULT 2

E39419

collagen alpha 5(IV) chain - bovine (fragment)

C/Species: Bos primigenius taurus (cattle)

C/Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 09-Jul-2004

C/Accession: E39419

R/Gunwar, S.; Ballester, F.; Kalluri, R.; Timoneda, J.; Chonko, A.M.; Edwards, S.J.; Noe

J. Biol. Chem. 266, 15318-15324, 1991

A/Title: Glomerular basement membrane. Identification of dimeric subunits of the noncoll

A/Reference number: A39419; MUID:91332055; PMID:1869555

A/Accession: E39419

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <GUN>

A/Cross-references: UNIPROT:Q7M2X3; UNIPARC:UPI00001773C8

C/Suprafamily: collagen alpha 1(IV) chain

C/Keywords: coiled coil; extracellular matrix; glycoprotein; trimer; triple helix

Query Match

Best Local Similarity 66.7%; Pred. No. 4e+02;

Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYYLT 11

DB 10 HGFYLT 15

RESULT 3

A61264

MHC class I histocompatibility antigen B-P15 alpha chain - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 31-Dec-2004

C/Accession: A61264

R/Moller, L.B.; Kaufman, J.; Verland, S.; Salomonson, J.; Avila, D.; Lambrie, J.D.; Skjod

Immunogenetics 34, 110-120, 1991

A/Title: Variations in the cytoplasmic region account for the heterogeneity of the chick

A/Reference number: A61264; MUID:91331615; PMID:1869304

A/Accession: A61264

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <MOL>

A/Cross-references: UNIPROT:Q95593; UNIPROT:Q31412; UNIPROT:Q9G1P6; UNIPARC:UPI0000176F9

Query Match

Best Local Similarity 29.2%; Score 28; DB 2; Length 20;

Best Local Similarity 50.0%; Pred. No. 4e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTTAAVSFG 17

DB 7 YISTAMTDPG 16

RESULT 4

S63491

disialylatory sulfite reductase beta chain, membrane-bound - Desulfovibrio desulfuricans

C/Species: Desulfovibrio desulfuricans

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C/Accession: S63491

R/Staubert, J.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A/Title: Molecular properties of the disialylatory sulfite reductase from Desulfovibrio

A/Reference number: S63489; MUID:96085152; PMID:8521853

A/Accession: S63491

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-9 <STR>

A/Cross-references: UNIPARC:UPI000017AB65

Query Match

Best Local Similarity 71.4%; Pred. No. 2.8e+05;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 AFEPHGY 8

DB 1 AFEPHGY 7

RESULT 5

S68028

iodochromine 5'-monodeiodinase - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C/Accession: S68028

R/Zhou, L.X.; Dehal, S.S.; Knäuper, D.; Morrell, S.; McKenzie, B.A.; Eccleston Jr., E.D.,

Arch. Biochem. Biophys. 322, 390-394, 1995

A/Title: Cytochrome P450 catalyzed covalent binding of methoxychlor to rat hepatic, micr

A/Reference number: S68028; MUID:96032659; PMID:7574712

A/Accession: S68028

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <ZHO>

A/Cross-references: UNIPARC:UPI00001761A4

C/Suprafamily: protein disulfide-isomerase; thioredoxin homology

Query Match

Best Local Similarity 50.0%; Pred. No. 5.8e+02;

Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFPHGYLT 10

DB 11 EALAAHYLT 20

RESULT 6

A36016

granulocyte inhibitory protein - human

C/Species: Homo sapiens (man)

C/Date: 11-Jan-1991 #sequence_revision 11-Jan-1991 #text_change 09-Jul-2004

C/Accession: A36016

R/Hoerl, W.H.; Haag-Weber, M.; Georgopoulos, A.; Block, L.H.

Proc. Natl. Acad. Sci. U.S.A. 87, 6353-6357, 1990

A/Title: Physicochemical characterization of a polypeptide present in uremic serum that

A/Reference number: A36016; MUID:90349614; PMID:2385596

A/Accession: A36016

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <HOB>
 A/Cross-references: UNIPROT:Q7M4S4; UNIPARC:UPI000002CDGD
 C/Superfamily: immunoglobulin V region; immunoglobulin homology

Query Match 28.1%; Score 27; DB 2; Length 20;
 Best Local Similarity 62.5%; Pred. No. 5.8e+02;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAAVSPGK 18
 DB 10 TLVSFSGR 17

RESULT 7

PT0213
 T-cell receptor alpha chain V-J region (7-10-D-3) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 30-May-1997

C/Accession: PT0213

R/Nakano, N.; Kikutani, H.; Nishimoto, H.; Kishimoto, T.

J. Exp. Med. 173, 1091-1097, 1991

A/Title: T cell receptor V gene usage of Islet beta cell-reactive T cells is not restricted

A/Reference number: PT0209; MUID:91217621; PMID:1902501

A/Accession: PT0213

A/Molecule type: mRNA

A/Residues: 1-10 <NAK>

A/Cross-references: UNIPARC:UPI000017C790

C/Keywords: T-cell receptor

Query Match 26.0%; Score 25; DB 2; Length 10;
 Best Local Similarity 100.0%; Pred. No. 6.1e+02;
 Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17
 DB 2 AVSPG 6

RESULT 8

S63492

dissimilatory sulfite reductase beta chain, soluble - Desulfovibrio desulfuricans (fragm

C/Species: Desulfovibrio desulfuricans

C/Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 17-Mar-1999

C/Accession: S63492

R/Stecher, U.; Arendsen, A.F.; Hagen, W.R.; Kroneck, P.M.H.

Eur. J. Biochem. 233, 873-879, 1995

A/Title: Molecular properties of the dissimilatory sulfite reductase from Desulfovibrio

A/Reference number: S63489; MUID:96085152; PMID:8521853

A/Accession: S63492

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-13 <STR>

A/Cross-references: UNIPARC:UPI000017AB66

Query Match 26.0%; Score 25; DB 2; Length 13;
 Best Local Similarity 71.4%; Pred. No. 8e+02;
 Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APEPHGY 8
 DB 1 APTPTGY 7

RESULT 9

B36222

excinuclease ABC chain C (uvrC) [imported] - Pseudomonas fluorescens (fragment)

C/Species: Pseudomonas fluorescens

C/Date: 04-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 20-Jun-2000

C/Accession: B36222

R/Laville, J.; Voisard, C.; Keel, C.; Maurhofer, M.; Defago, G.; Haas, D.

Proc. Natl. Acad. Sci. U.S.A. 89, 1562-1566, 1992

A/Title: Global control in Pseudomonas fluorescens mediating antibiotic synthesis and su

A/Reference number: A38222; MUID:92179223; PMID:1311842

A/Contents: CHAO
 A/Accession: B38222
 A/Status: preliminary
 A/Molecule type: DNA
 A/Residues: 1-14 <LAV>
 A/Cross-references: UNIPARC:UPI000017A97D
 A/Note: sequence extracted from NCBI backbone (NCBIN:85369, NCBIPI:94242)

Query Match 26.0%; Score 25; DB 2; Length 14;
 Best Local Similarity 36.4%; Pred. No. 8.6e+02;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 DAFPHGYLT 11
 DB 3 BQFDSAPLST 13

RESULT 10

H35141

T-cell receptor delta chain V region (105-23) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 31-Aug-1990 #sequence_revision 31-Aug-1990 #text_change 30-May-1997

C/Accession: H35141

R/Sim, G.K.; Augustin, A.

Cell 61, 397-405, 1990

A/Title: Dominantly inherited expression of BID, an invariant undiversified T cell rece

A/Reference number: A35141; MUID:90242386; PMID:2110506

A/Accession: H35141

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-16 <SIM>

A/Cross-references: UNIPARC:UPI000017C859

C/Keywords: T-cell receptor

Query Match 26.0%; Score 25; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 9.9e+02;
 Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 7 GYLTAAVSPGK 18
 DB 4 GYLTCGIRAPDK 15

RESULT 11

A33171

hypothetical protein lpxA 3'-region - Escherichia coli (fragment)

C/Species: Escherichia coli

C/Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 22-Oct-1999

C/Accession: A33171

R/Coleman, U.; Raetz, C.R.H.

J. Bacteriol. 170, 1268-1274, 1988

A/Title: First committed step of lipid A biosynthesis in Escherichia coli: sequence of

A/Reference number: A33171; MUID:88139188; PMID:3377952

A/Accession: A33171

A/Molecule type: DNA

A/Residues: 1-16 <COL>

A/Cross-references: UNIPARC:UPI000017CEB5; GB:M19334; GB:M18265; GB:M18266; NID:G450760

C/Comment: This is the hypothetical translation of a sequence that was not reported as

Query Match 26.0%; Score 25; DB 4; Length 16;
 Best Local Similarity 62.5%; Pred. No. 9.9e+02;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLTTAAVS 15
 DB 9 YLITGRYS 16

RESULT 12

S23981

outer layer protein - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 22-Nov-1993 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004

C/Accession: S23981
R.Kido, S.; Morimoto, A.; Kim, F.; Doi, Y.
Biochem. J. 286, 17-22, 1992
A/Title: Isolation of a novel protein from the outer layer of the vitelline membrane.
A/Reference number: S23981; PMID:92392273; PMID:1520265
A/Accession: S23981
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-20 <KID>
A/Cross-references: UNIPROT:Q9PS49; UNIPARC:UPI00001389A5

Query Match 26.0%; Score 25; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HGYLTAAPV 14
||| : |
DB 12 HGXYIRSKV 20

RESULT 13
B47415
mannose-1-phosphate guanylyltransferase (EC 2.7.7.13) 43K alpha chain - pig (fragment)
N/Alternate names: GDP-mannose pyrophosphorylase 43K alpha chain
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 25-Feb-1994 #sequence_revision 12-Aug-1996 #text_change 12-Aug-1996
C/Accession: B47415
R.Szumilo, T.; Drake, R.R.; York, J.L.; Elbein, A.D.
J. Biol. Chem. 268, 17943-17950, 1993
A/Title: GDP-mannose pyrophosphorylase. Purification to homogeneity, properties, and use
A/Reference number: A47415; PMID:93352609; PMID:7688733
A/Accession: B47415
A/Molecule type: protein
A/Residues: 1-13 <SZU>
A/Cross-references: UNIPARC:UPI000017C470
C/Experimental source: liver
C/Complex: The enzyme appears to be a heterodimer of alpha and beta chains.
C/Function:
A/Description: generates GDP-mannose and pyrophosphate from mannose-1-phosphate and GTP
A/Note: also catalyzes synthesis of GDP-glucose from glucose-1-phosphate (EC 2.7.7.34 ac
C/Keywords: blocked amino end; nucleotidyltransferase

Query Match 25.0%; Score 24; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 1.2e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYLL 10
||| : |
DB 8 PHPFL 13

RESULT 14
PH1305
Ig heavy chain DJ region (clone C85-1B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1305
R.Wasserman, R.; Gailit, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; PMID:93094761; PMID:1460419
A/Accession: PH1305
A/Molecule type: DNA
A/Residues: 1-14 <WAS>
A/Cross-references: UNIPARC:UPI000017C252
C/Keywords: heterotetramer; immunoglobulin

Query Match 25.0%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 GYLTAAPV 16
||| : |

DB 5 GYTTGAREP 14

RESULT 15
S00843
hypothetical protein kgsa 5'-region - Escherichia coli
C/Species: Escherichia coli
C/Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C/Accession: S00843
R.Ivan Gemen, B.; Koete, H.J.; Plooy, C.A.M.; Bodlaender, J.; van Knippenberg, P.H.
Biochimie 69, 841-848, 1987
A/Title: Characterization of the kgsa gene of Escherichia coli determining kasugamycin s
A/Reference number: S00843; PMID:88107880; PMID:3122846
A/Accession: S00843
A/Molecule type: DNA
A/Residues: 1-14 <VAN>
A/Cross-references: UNIPROT:Q47335; UNIPARC:UPI00000B9024; EMBL:X06536; NID:G41884; PIDN
C/Comment: This is the hypothetical translation of a sequence that was not reported as a

Query Match 25.0%; Score 24; DB 4; Length 14;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LTTAAVSPK 18
||| : |
DB 5 LRRRLISPK 14

RESULT 16
S10741
phosphoglucosyltransferase (EC 5.4.2.2) - rabbit (fragment)
C/Species: Oryctolagus cuniculus (domestic rabbit)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 03-Jul-2004
C/Accession: S10741
R.Marchase, R.B.; Richardson, K.L.; Srisomarp, C.; Drake, R.R.; Haley, B.E.
Arch. Biochem. Biophys. 280, 122-129, 1990
A/Title: Resolution of phosphoglucosyltransferase and the 62-kDa acceptor for the glucosylphosph
A/Reference number: S10741; PMID:90282481; PMID:2162150
A/Accession: S10741
A/Molecule type: protein
A/Residues: 1-15 <MAR>
A/Cross-references: UNIPROT:Q7M2K5; UNIPARC:UPI000017C5D3
C/Keywords: intramolecular transferase; isomerase; phosphoprotein

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.4e+03;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 7 GYLTAAPV 16
||| : |
DB 4 GILTRSHMP 13

RESULT 17
S66613
protein p12E - Friend murine leukemia virus (fragments)
C/Species: Friend murine leukemia virus
C/Date: 15-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S66613
R.Hensel, J.; Hntz, M.; Karas, M.; Linder, D.; Stahl, B.; Geyer, R.
Eur. J. Biochem. 232, 373-380, 1995
A/Title: Localization of the palmitoylation site in the transmembrane protein p12E of F
A/Reference number: S66613; PMID:96035869; PMID:7556184
A/Accession: S66613
A/Molecule type: protein
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-9;10-16 <HEN>
A/Cross-references: UNIPARC:UPI000017A87F; UNIPARC:UPI000017A880

Query Match 25.0%; Score 24; DB 2; Length 16;
Best Local Similarity 71.4%; Pred. No. 1.5e+03;
Matches 5; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

OY 10 LTAAVSP 16
|||
Db 5 LTLALSP 11

RESULT 18

A59155
multicytatin - tomato (fragment)
C/Species: Lycopersicon esculentum (tomato)
C/Date: 07-Dec-1999 #sequence_revision 07-Dec-1999 #text_change 09-Jul-2004
C/Accession: A59155
R/Jacinto, T.; Fernandez, K.V.S.; Machado, O.L.T.; Siqueira-Junior, C.L.
Plant Sci. 138, 35-42, 1998
A/Title: Leaves of transgenic tomato plants overexpressing prosystemin accumulate high 1
A/Reference number: A59155
A/Accession: A59155
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-16 <MAC>
A/Cross-references: UNIPROT:Q7M1V9; UNIPARC:UPI000017B08D
A/Note: 37 kDa CNBR fragment
C/Keywords: cysteine proteinase inhibitor

Query Match 24.0%; Score 23.5; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.8e+03;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;
OY 8 YLLT-AAVSPCK 18
|||
Db 1 YITFAATDAGK 12

RESULT 19

GMROL
leucosulfakinin - Madeira cockroach
N/Alternate names: LSK
C/Species: Leucophaea maderae (Madeira cockroach)
C/Date: 17-Mar-1987 #sequence_revision 17-Mar-1987 #text_change 09-Jul-2004
C/Accession: A01622
R/Nachman, R.J.; Holman, G.M.; Haddon, W.F.; Ling, N.
Science 234, 71-73, 1986
A/Title: Leucosulfakinin, a sulfated insect neuropeptide with homology to gastrin and ch
A/Reference number: A01622; MUID:6315858; PMID:3749893
A/Accession: A01622
A/Molecule type: protein
A/Residues: 1-11 <MAC>
A/Cross-references: UNIPROT:P04428; UNIPARC:UPI000012B960
C/Superfamily: gastrin
C/Keywords: amidated carboxyl end; hormone; sulfoprotein
P/6/Binding site: sulfate (Tyr) (covalent) #status experimental
P/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.4e+03;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;
OY 1 DAFEPHGYL 9
|||
Db 1 EQFEDYGHM 9

RESULT 20

PH1604
Ig H chain V-D-J region (wild-type clone 327) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C/Accession: PH1604
R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A/Title: Molecular characterization of transgene-induced immunodeficiency in B-less mice
A/Reference number: PH1580; MUID:93301609; PMID:8315387
A/Accession: PH1604
A/Molecule type: DNA

A/Residues: 1-16 <LEV>
A/Cross-references: UNIPARC:UPI000017C6C0
A/Experimental source: bone marrow pre-B lymphocyte
C/Keywords: immunoglobulin

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 2.1e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
OY 5 PHGYLL 10
|||
Db 4 PHRWLL 9

RESULT 21

B36300
T-cell receptor delta chain V-J region - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 28-Mar-1991 #sequence_revision 28-Mar-1991 #text_change 30-May-1997
C/Accession: B36300
R/Mattis, L.A.; Fry, A.M.; Cron, R.Q.; Cotterman, M.M.; Dick, R.F.; Bluestone, J.A.
Science 245, 746-749, 1989
A/Title: Structure and specificity of a class II MHC alloreactive gammadelta T cell rec
A/Reference number: A36300; MUID:89368895; PMID:2528206
A/Accession: B36300
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: RNA
A/Residues: 1-16 <MAT>
A/Cross-references: UNIPARC:UPI000017C861
C/Keywords: T-cell receptor

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 33.3%; Pred. No. 2.1e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;
OY 7 GYLLTAAVSRCK 18
|||
Db 3 GYIPIGIRGK 14

RESULT 22

I78841
thrombopoietin receptor - mouse (fragment)
C/Species: Mus sp. (mouse)
C/Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 05-Nov-1999
C/Accession: I78841
R/Alexander, W.S.; Dunn, A.R.
Oncogene 10, 795-803, 1995
A/Title: Structure and transcription of the genomic locus encoding murine c-Mpl, a rece
A/Reference number: I58350; MUID:9516571; PMID:762460
A/Accession: I78841
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 118 <RSS>
A/Cross-references: UNIPARC:UPI0000004PB; GB:S76842; NID:9912990; PIDN:AAB33462.1; PID
C/Genetics:
A/Gene: c-Mpl1

Query Match 24.0%; Score 23; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 2.4e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
OY 4 EPHG 7
|||
Db 1 QPHG 4

RESULT 23

H28949
ribosomal protein H2C12 [validated] - Haloarcula marismortui (fragment)
C/Species: Haloarcula marismortui
C/Date: 30-Jun-1989 #sequence_revision 30-Jun-1989 #text_change 09-Jul-2004
C/Accession: H28949

R;Walsh, M.J.; McDougall, J.; Wittmann-Liebold, B.
Biochemistry 27, 6867-6876, 1988
A;Title: Extended N-terminal sequencing of proteins of archaeobacterial ribosomes blotted
A;Reference number: A28926; PMID:89062418; PMID:3196689
A;Accession: H28949
A;Molecule type: protein
A;Residues: 1-20 <MAL>
A;Cross-references: UNIPROT:P12740; UNIPARC:UPI0000134270
A;Note: the protein is designated as ribosomal protein Lc12
C;Keywords: protein biosynthesis

Query Match 24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 33.3%; Pred. No. 2.7e+03;
Matches 4; Conservative 2; Mismatches 6; Indels 0; Gaps 0;

QY 6 HGYLELPAVSPG 17
| | | | |
DB 5 YSYRDATKXPG 16

RESULT 24

PH1772
T cell receptor alpha chain V region (clone 2V alpha 23-3) - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C;Accession: PH1772
R;Porcelli, S.; Yockey, C.E.; Brenner, M.B.; Balx, S.P.
J. Exp. Med. 178, 1-16, 1993
A;Title: Analysis of T cell antigen receptor (TCR) expression by human peripheral blood
A;Reference number: PH1754; PMID:93301585; PMID:8391057
A;Accession: PH1772
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-13 <POR>
A;Cross-references: UNIPARC:UPI000017C37C

Query Match 22.9%; Score 22; DB 2; Length 13;
Best Local Similarity 62.5%; Pred. No. 2.5e+03;
Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 AEPHNGYL 9
| | | | |
DB 3 AVEPAGQL 10

RESULT 25

S59512
probable integrin alpha3 beta1 - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-Mar-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C;Accession: S59512
R;McCormick, J.T.; Johnstone, R.M.
Biochem. J. 311, 743-751, 1995
A;Title: Identification of the integrin alpha(3)beta(1) as a component of a partially pu
A;Reference number: S59512; PMID:96067588; PMID:7487928
A;Accession: S59512
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-17 <MCC>
A;Cross-references: UNIPROT:Q7M0D8; UNIPARC:UPI00000353C9

Query Match 22.9%; Score 22; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 3.3e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17
| | | | |
DB 13 AVNPG 17

RESULT 26

A61276

superoxide dismutase (EC 1.15.1.1) (Fe/Mn) homolog - chicken (fragment)
N;Alternate names: osteoclast membrane glycoprotein
C;Species: Gallus gallus (chicken)
C;Date: 12-May-1994 #sequence_revision 12-May-1994 #text_change 05-Mar-1999
C;Accession: A61276
R;Oursler, M.J.; Li, L.; Osoby, P.
J. Cell. Biochem. 46, 219-233, 1991
A;Title: Purification and characterization of an osteoclast membrane glycoprotein with h
A;Reference number: A61276; PMID:92129474; PMID:1723067
A;Accession: A61276
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-20 <OUR>
A;Cross-references: UNIPARC:UPI000017C038
C;Function: catalyzes the dismutation of 2 molecules of peroxide radical to dioxygen
C;Keywords: metalloprotein; oxidoreductase

Query Match 22.9%; Score 22; DB 2; Length 20;
Best Local Similarity 80.0%; Pred. No. 3.9e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAEP 5
| | | | |
DB 12 DALRP 16

RESULT 27

S46479
retinoid-X-receptor-gamma - chicken
C;Species: Gallus gallus (chicken)
C;Date: 15-Jul-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
C;Accession: S46479
R;Seleiro, E.A.P.; Darling, D.; Brickell, P.M.
Biochem. J. 301, 283-288, 1994
A;Title: The chicken retinoid-X-receptor-gamma gene gives rise to two distinct species c
A;Reference number: S46478; PMID:94311845; PMID:8037682
A;Accession: S46479
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-20 <SEL>
A;Cross-references: UNIPROT:Q91380; UNIPARC:UPI000017C033; GB:S72435; NID:G619294; PIDN

Query Match 22.9%; Score 22; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 3.9e+03;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8
| | | | |
DB 17 PHSY 20

RESULT 28

PH1618
Ig H chain V-D-J region (clone B-lees 33) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
C;Accession: PH1618
R;Levinson, D.A.; Campos-Torres, J.; Leder, P.
J. Exp. Med. 178, 317-329, 1993
A;Title: Molecular characterization of transgene-induced immunodeficiency in B-lees mice
A;Reference number: PH1580; PMID:93301609; PMID:8315387
A;Accession: PH1618
A;Molecule type: DNA
A;Residues: 1-8 <LEV>
A;Cross-references: UNIPARC:UPI000017C6A7
A;Experimental source: bone marrow pre-B lymphocyte
C;Keywords: immunoglobulin

Query Match 21.9%; Score 21; DB 2; Length 8;
Best Local Similarity 100.0%; Pred. No. 2.8e+05;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGX 8
|||
Db 4 HGX 6

RESULT 29

S15594
orf 1 para 5'-region - human
C/Species: Homo sapiens (man)
C/Date: 04-Jun-1999 #sequence_revision 04-Jun-1999 #text_change 28-Jun-1999
C/Accession: S15594
R/Brand: N.J.; Petkovich, M.; Chambon, P.
Nucleic Acids Res. 18, 6799-6806, 1990
A/Title: Characterization of a functional promoter for the human retinotic acid receptor-
A/Reference number: S15594; MUID:91088249; PMID:2175878
A/Accession: S15594
A/Molecule type: DNA
A/Residues: 1-9 <BRA>
A/Cross-references: UNIPARC:UPI000017CEBB; EMBL:X56057; NID:935875
C/Date: this ORF from Fig. 2 is not annotated in GenBank entry HSRARL1, release 111.0
C/Comment: This sequence is not thought to be translated.
A/Genetics:
A/Gene: GDB:RARA
A/Cross-references: GDB:120337; OMIM:180240
A/Map position: 17q12-17q12

Query Match 21.9%; Score 21; DB 4; Length 9;
Best Local Similarity 42.9%; Pred. No. 2.8e+05;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
QY 10 LTAAVSP 16
: |||:
Db 1 MAAAIAP 7

RESULT 30

A59173
nuclease Bn1 (EC 3.1.-.-) - Basidiobolus haplosporius (fragment)
C/Species: Basidiobolus haplosporius
C/Date: 18-Feb-2000 #sequence_revision 18-Feb-2000 #text_change 09-Jul-2004
C/Accession: A59173
R/Brand: N.; Shankar, V.
submitted to the protein Sequence Database, February 2000
A/Description: Single-strand-specific, guanylic acid preferential nuclease from Basidiob-
A/Reference number: A59173
A/Accession: A59173
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-10 <DBS>
A/Cross-references: UNIPROT:Q7M4X1; UNIPARC:UPI000017CAF9
A/Note: extracellular, single-strand-specific nuclease
C/Keyword: hydrolase

Query Match 21.9%; Score 21; DB 2; Length 10;
Best Local Similarity 80.0%; Pred. No. 2.8e+03;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
QY 7 GYLIT 11
: |||:
Db 5 GHLLT 9

RESULT 31

P84132
hypothetical protein BH3862 [Imported] - Bacillus halodurans (strain C-125)
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 09-Jul-2004
C/Accession: P84132
R/Takam, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.; Hira
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: P84132

A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-12 <STO>
A/Cross-references: UNIPROT:Q9K670; UNIPARC:UPI00000C4307; GB:AP001520; GB:BA000004; NI
C/Genetics:
A/Experimental source: strain C-125
A/Gene: BH3862

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 3.4e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 8 YLTAAV 14
: |||:
Db 3 YLTXTI 9

RESULT 32

PC1008
40K extracellular proteinase - Dichelobacter nodosus (fragment)
C/Species: Dichelobacter nodosus
C/Date: 31-Dec-1993 #sequence_revision 31-Dec-1993 #text_change 09-Jul-2004
C/Accession: PC1008
R/Gong, Y.H.; Moses, B.
Acta Microbiol. Sin. 31, 433-437, 1991
A/Title: Overexpression of an extracellular bacteroides nodosus protease in E.coli and
A/Reference number: PC1008
A/Accession: PC1008
A/Molecule type: protein
A/Residues: 1-13 <GON>
A/Cross-references: UNIPROT:Q7M1A2; UNIPARC:UPI000017AB53
A/Note: article in Chinese with English abstract
C/Comment: This protease is involved in the pathogenesis of footrot.

Query Match 21.9%; Score 21; DB 2; Length 13;
Best Local Similarity 41.7%; Pred. No. 3.7e+03;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;
QY 2 AEPHGYLTAAV 13
: |||:
Db 1 AFRIRNHLISIA 12

RESULT 33

S00150
ovostatin - duck (fragment)
N/Alternate names: ovomacroglobulin
C/Species: Anas platyrhynchos (domestic duck)
C/Date: 19-Mar-1997 #sequence_revision 01-Aug-1997 #text_change 09-Jul-2004
C/Accession: S00150
R/Nagase, H.; Harris Jr., B.D.; Brew, K.
J. Biol. Chem. 261, 1421-1426, 1986
A/Title: Evidence for a thiol ester in duck ovostatin (ovomacroglobulin).
A/Reference number: S00150; MUID:86111792; PMID:3511043
A/Accession: S00150
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-14 <NAG>
A/Cross-references: UNIPROT:Q7LZ22; UNIPARC:UPI000017BFD1
A/Note: part of this sequence, including the amino end of the mature chicken and duck p.

Query Match 21.9%; Score 21; DB 2; Length 14;
Best Local Similarity 45.5%; Pred. No. 4e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;
QY 4 EPHGYLTAAV 14
: |||:
Db 4 EPGYLTMPAV 14

RESULT 34

A11488
taurocyamine kinase (EC 2.7.3.4) - lugworm (fragment)

C/Species: *Arenicola marina* (lugworm, rock worm)
C/Date: 05-Jun-1987 #sequence_rev: 05-Jun-1987 #text_change: 09-Jul-2004
C/Accession: A11488
R/Brevet, A.; Zeltoun, Y.; Pradel, L.A.
Biochim. Biophys. Acta 393, 1-9, 1975
A/Title: Comparative structural studies of the active site of ATP:guanidine phosphotransferase
A/Reference number: A11488; MUID:75184095; PMID:166684
C/Accession: A11488
A/Molecule type: protein
A/Residues: 1-16

A/Cross-references: UNIPROT:P11917; UNIPARC:UPI0000125121
C/Keywords: phosphotransferase

Query Match 21.9%; Score 21; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 4.6e+03;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 7 GYLLTRAVSPG 17
DB 2 GYLGTCTNIG 12

RESULT 35
B32473
histidine-rich protein C, peptide P-5 - liver fluke (fragment)
C/Species: *Fasciola hepatica* (liver fluke)
C/Date: 25-Sep-1989 #sequence_rev: 03-May-1994 #text_change: 09-Jul-2004
C/Accession: B32473
R/Walte, J.H.; Rice-Ficht, A.C.
Biochemistry 28, 6104-6110, 1989
A/Title: A histidine-rich protein from the liver fluke *Fasciola hepatica*
A/Reference number: A32473; MUID:89375343; PMID:2775756
C/Accession: B32473
A/Molecule type: protein
A/Residues: 1-18 <MAL>
A/Cross-references: UNIPROT:Q7M3X9; UNIPARC:UPI0000177DAS
A/Note: 18-Gly and 18-His were also found
C/Superfamily: period clock protein; EGF homology
C/Keywords: egg yolk
P1,5/Modified site: 3', 4'-dihydroxyphenylalanine (Tyr) #status experimental

Query Match 21.9%; Score 21; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HG Y 8
DB 3 HG Y 5

RESULT 36
S36121
lectin - euphorbia characias)
C/Species: *Euphorbia characias*
C/Date: 09-Dec-1993 #sequence_rev: 27-Feb-1997 #text_change: 09-Jul-2004
C/Accession: S36121
R/Scitpe, F.; Ilicastro, F.; Morini, M.C.; Parente, A.; Savino, G.; Abbondanza, A.; Bolog
Biochim. Biophys. Acta 1158, 33-39, 1993
A/Title: Purification and partial characterization of a mitogenic lectin from the latex
A/Reference number: S36120; MUID:93357266; PMID:8353129
C/Accession: S36121
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-18 <SNI>
A/Cross-references: UNIPROT:P33886; UNIPARC:UPI00001256C0

Query Match 21.9%; Score 21; DB 2; Length 18;
Best Local Similarity 75.0%; Pred. No. 5.2e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8
DB 10 PNGY 13

RESULT 37
S27141
hypothetical protein 2 estrogen receptor 5'-region - human
C/Species: *Homo sapiens* (man)
C/Date: 05-Mar-1994 #sequence_rev: 12-May-1995 #text_change: 16-Aug-2004
C/Accession: S27141
R/Keaveney, M.; Klug, J.; Gannon, F.
DNA Seq. 2, 347-358, 1992
A/Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
A/Reference number: S27140; MUID:93075998; PMID:1476547
C/Accession: S27141
A/Status: translation not shown
A/Molecule type: DNA
A/Residues: 1-18 <KBA>
A/Cross-references: UNIPARC:UPI000011DP56; EMBL:X62462; NID:g31201; PIDN:CAA44320.1; PIC
C/Genetics: 13/2
A/Introns: 13/2

Query Match 21.9%; Score 21; DB 2; Length 18;
Best Local Similarity 37.5%; Pred. No. 5.2e+03;
Matches 3; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 1 DAFEPHGY 8
DB 7 DVLDPAGW 14

RESULT 38
G49048
T-cell receptor beta chain V region (CDR3 junction, clone Vbeta20.1) - human (fragment)
C/Species: *Homo sapiens* (man)
C/Date: 21-Jan-1994 #sequence_rev: 18-Nov-1994 #text_change: 30-May-1997
C/Accession: G49048
R/Stod, M.; Kjeldsen-Kragh, J.; Suleyman, S.; Vinje, O.; Natvig, J.B.; Forre, O.
Eur. J. Immunol. 22, 2413-2418, 1992
A/Title: Limited heterogeneity of T cell receptor variable region gene usage in juvenile
A/Reference number: A49048; MUID:9287250; PMID:1387614
C/Accession: G49048
A/Status: preliminary; not compared with conceptual translation
A/Molecule type: mRNA
A/Residues: 1-19 <SIO>
A/Cross-references: UNIPARC:UPI0000176DED
A/Experimental source: patient SS, IL-2R+ synovial T-cells
A/Note: sequence extracted from NCBI backbone (NCBI:P113269)
C/Superfamily: immunoglobulin V region; immunoglobulin homology
C/Keywords: T-cell receptor

Query Match 21.9%; Score 21; DB 2; Length 19;
Best Local Similarity 100.0%; Pred. No. 5.5e+03;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HG Y 8
DB 14 HG Y 16

RESULT 39
PT0332
Ig heavy chain CRD3 region (clone U2-139) - human (fragment)
C/Species: *Homo sapiens* (man)
C/Date: 30-Sep-1993 #sequence_rev: 30-Sep-1993 #text_change: 16-Aug-1996
C/Accession: PT0332
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337; PMID:1899102
C/Accession: PT0332
A/Molecule type: DNA
A/Residues: 1-19 <YAM>
A/Cross-references: UNIPARC:UPI000017C21A
A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 21.9%; Score 21; DB 2; Length 19;
Best Local Similarity 50.0%; Pred. No. 5.5e+03;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 DAPPHGY 8
| | | | |
| | | | |
Db 1 DAPPPYY 8

RESULT 40

A20999

Fructose-bisphosphate aldolase (BC 4.1.2.13) - chicken (fragment)

C/Species: Gallus gallus (chicken)

C/Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004

C/Accession: A20999

R/Leibherz, H.G.; Bates, O.J.; Bradshaw, R.A.

J. Biol. Chem. 259, 1132-1135, 1984

A/Title: Cellular fructose-P2 aldolase has a derivatized (blocked) NH2 terminus.

A/Reference number: A20999, MUID:84111506, PMID:6693379

A/Accession: A20999

A/Molecule type: protein

A/Residues: 1-20 <LBB>

A/Cross-references: UNIPROT:Q7LZB8; UNIPARC:UPI0000175PFS

C/Superfamily: fructose-bisphosphate aldolase

C/Keywords: aldehyde-lyase, carbon-carbon lyase, gluconeogenesis, glycolysis, pentose ph

Query Match 21.4%; Score 20.5; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 7e+03;
Matches 5; Conservative 2; Mismatches 2; Indels 3; Gaps 1;

Qy 5 PHGYLNAVSP 16
| | | | |
| | | | |
Db 1 PHGY--PALTP 9

RESULT 41

PT0715

T-cell receptor beta chain V-D-J region (165-3A) - mouse (fragment)

C/Species: Mus musculus (house mouse)

C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 30-May-1997

C/Accession: PT0715

R/Peeney, A.J.

J. Exp. Med. 174, 115-124, 1991

A/Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.

A/Reference number: PT0509, MUID:91277601, PMID:1711558

A/Accession: PT0715

A/Status: translation not shown

A/Molecule type: DNA

A/Residues: 1-6 <PBB>

A/Cross-references: UNIPARC:UPI000017C847

A/Experimental source: newborn thymus, strain BALB/c

C/Keywords: T-cell receptor

Query Match 20.8%; Score 20; DB 2; Length 6;
Best Local Similarity 66.7%; Pred. No. 2.8e+05;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 13 AVSPGK 18
| | | | |
| | | | |
Db 1 ASSPGQ 6

RESULT 42
PT0243
Ig heavy chain CND3 region (clone 2-103A) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C/Accession: PT0243

R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and

A/Reference number: PT0222, MUID:91108337, PMID:1899102

A/Accession: PT0243

A/Molecule type: DNA

A/Residues: 1-10 <YAM>

A/Cross-references: UNIPARC:UPI000017C1B3

A/Experimental source: B lymphocyte

C/Keywords: heterotetramer; immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 10;
Best Local Similarity 42.9%; Pred. No. 4.1e+03;
Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 3 FBPHGYL 9
| | | | |
| | | | |
Db 4 YDSSGYL 10

RESULT 43

PH0944

T-cell receptor beta chain V-D-J region (clone 15) - rat (fragment)

C/Species: Rattus norvegicus (Norway rat)

C/Date: 09-Oct-1992 #sequence_revision 09-Oct-1992 #text_change 30-May-1997

C/Accession: PH0944

R/Gold, D.P.; Offner, H.; Sun, D.; Wiley, S.; Vandenbark, A.A.; Wilson, D.B.

J. Exp. Med. 174, 1467-1476, 1991

A/Title: Analysis of T cell receptor beta chains in Lewis rats with experimental allergy

A/Reference number: PH0941, MUID:92078857, PMID:1836012

A/Accession: PH0944

A/Molecule type: mRNA

A/Residues: 1-10 <GOL>

A/Cross-references: UNIPARC:UPI000017C9B1

A/Experimental source: complete Freund's adjuvant-immunized lymph node

A/Note: the authors translated the codon GAC for residue 9 as Glu

C/Keywords: T-cell receptor

Query Match 20.8%; Score 20; DB 2; Length 10;
Best Local Similarity 57.1%; Pred. No. 4.1e+03;
Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 2 APBPHGY 8
| | | | |
| | | | |
Db 2 ASSPGCV 8

RESULT 44

A46030

Gonadoliberin I - spiny dogfish

N/Alternate names: gonadotropin-releasing hormone

C/Species: Squalus acanthias (spiny dogfish)

C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004

C/Accession: A46030

R/Lovejoy, D.A.; Fischer, W.H.; Ngamwongchon, S.; Craig, A.G.; Nahorniak, C.S.; Peter,

Proc. Natl. Acad. Sci. U.S.A. 89, 6373-6377, 1992

A/Title: Distinct sequence of gonadotropin-releasing hormone (GNRH) in dogfish brain pr

A/Reference number: A46030, MUID:92335300, PMID:1631133

A/Accession: A46030

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-10 <LOV>

A/Cross-references: UNIPROT:P27429; UNIPARC:UPI000012B910

C/Keywords: hormone; pyroglutamic acid

F/1/Modified site: pyroglutamic acid (Glu) #status experimental

Query Match 20.8%; Score 20; DB 2; Length 10;
Best Local Similarity 75.0%; Pred. No. 4.1e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGVL 9
| | | | |
| | | | |
Db 5 HGWL 8

RESULT 45

S77990
cytochrome-c oxidase (EC 1.9.3.1) chain VIIc - bigeye tuna (fragment)
C/Species: Thunnus obesus (bigeye tuna)
C/Date: 17-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 09-Jul-2004
C/Accession: S77990
R/Arnold, S.; Lee, J.; Kim, M.; Song, E.; Linder, D.; Lottspeich, F.; Kadenbach, B.
submitted to the Protein Sequence Database, June 1997
A/Reference number: S77980
A/Accession: S77990
A/Molecule type: protein
A/Residues: 1-10 <ARN>
A/Cross-references: UNIPROT:P80982; UNIPARC:UPI0000128169
A/Experimental source: heart; liver
C/Genetics:
A/Genome: nuclear
C/Function:
A/Pathway: oxidative phosphorylation; respiratory chain
C/Keywords: electron transfer; membrane-associated complex; mitochondrial inner membrane

Query Match 20.8%; Score 20; DB 2; Length 10;
Best Local Similarity 66.7%; Pred. No. 4.1e+03; Indels 0; Gaps 0;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 13 AVSPGK 18
| | | |
Db 4 AEGPGK 9

RESULT 46
A60656
perisulfakinin - American cockroach
C/Species: Periplaneta americana (American cockroach)
C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Jul-2004
C/Accession: A60656
R/Venestra, J.A.
Neuropeptides 14, 145-149, 1989
A/Title: Isolation and structure of two gastrin/CKK-like neuropeptides from the American
A/Reference number: A60656; MUID:90137190; PMID:2615921
A/Accession: A60656
A/Molecule type: protein
A/Residues: 1-11 <VEE>
A/Cross-references: UNIPROT:P36885; UNIPARC:UPI0000128962
C/Comment: This neuropeptide stimulates hindgut contractions.
C/Keyword: amidated carboxyl end; neuropeptide; sulfoprotein
F/6/Binding site: sulfate (Tyr) (covalent) #status experimental
F/11/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.8%; Score 20; DB 2; Length 11;
Best Local Similarity 22.2%; Pred. No. 4.5e+03; Indels 0; Gaps 0;
Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFPHGYL 9
| | | |
Db 1 EDPDDYGHM 9

RESULT 47
S70344
amine oxidase (copper-containing) (EC 1.4.3.6) I - Aspergillus niger (fragments)
C/Species: Aspergillus niger
C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Apr-1998
C/Accession: S70344
R/Frederick, I.; Pec, P.; Lubova, L.; Toyama, H.; Matsushita, K.; Hirota, S.; Kitagawa, T.
Biochim. Biophys. Acta 1295, 59-72, 1996
A/Title: Two amine oxidases from Aspergillus niger AKU 3302 contain topa quinone as the
A/Reference number: S70344; MUID:96283794; PMID:8679675
A/Accession: S70344
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-7;8-12 <FRB>
A/Cross-references: UNIPARC:UPI000017B3B5; UNIPARC:UPI000017B3B6
C/Keywords: oxidoreductase

Query Match 20.8%; Score 20; DB 2; Length 12;
Best Local Similarity 75.0%; Pred. No. 5e+03; Indels 0; Gaps 0;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHG 7
| | | |
Db 4 EPHG 7

RESULT 48
A46463
preabsorbing antigen (PA-Ag) - Streptococcus sp. (fragment)
C/Species: Streptococcus sp.
C/Date: 18-Jun-1993 #sequence_revision 25-Apr-1997 #text_change 20-Sep-1999
C/Accession: A46463
R/Toshizawa, N.; Oshima, S.; Sagel, I.; Shmidtzu, J.; Treiser, G.
J. Immunol. 149, 3110-3116, 1992
A/Title: Role of a streptococcal antigen in the pathogenesis of acute poststreptococcal
A/Reference number: A46463; MUID:92251171; PMID:1578137
A/Accession: A46463
A/Molecule type: protein
A/Residues: 1-13 <YOS>
A/Cross-references: UNIPARC:UPI00000866E6; P1DN:AAB22148.1; P1D:G249161
A/Note: sequence extracted from NCBI backbone (NCBIP:100561)

Query Match 20.8%; Score 20; DB 2; Length 13;
Best Local Similarity 66.7%; Pred. No. 5.4e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 12 AAVSPG 17
| | | |
Db 5 AASAPG 10

RESULT 49
LFBWMT
trp operon leader peptide - Salmonella typhimurium
C/Species: Salmonella typhimurium
C/Date: 02-Apr-1982 #sequence_revision 02-Apr-1982 #text_change 03-Jul-2004
C/Accession: A03590
R/Lee, F.; Bertrand, K.; Bennett, G.; Yanofsky, C.
J. Mol. Biol. 121, 193-217, 1978
A/Title: Comparison of the nucleotide sequences of the initial transcribed regions of the
A/Reference number: A02850; MUID:78196931; PMID:351195
A/Accession: A03590
A/Molecule type: DNA
A/Residues: 1-14 <LEB>
A/Cross-references: UNIPROT:P03054; UNIPARC:UPI000012892E
C/Genetics:
A/Gene: trpL; trpE
C/Function:
A/Description: involved in control of tryptophan operon transcription by attenuation
C/Superfamily: trp leader peptide

Query Match 20.8%; Score 20; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 5.8e+03; Indels 0; Gaps 0;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 EEPHGYLTA 12
| | | |
Db 5 FALHGMWRTS 14

RESULT 50
A56632
neousulfakinin-II - flesh fly (Sarcophaga bullata)
N/Alternate names: Neb-SK-II
N/Contains: neousulfakinin-I (Neb-SK-I)
C/Species: Sarcophaga bullata
C/Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Jul-2004
C/Accession: A56632
R/Fonagy, A.; Schoofs, L.; Proost, P.; Van Damme, J.; De Loof, A.
Comp. Biochem. Physiol. C 103, 135-142, 1992

A/Title: Isolation and primary structure of two sulfakinin-like peptides from the flesh
 A/Reference number: A56632; MUID:93083101; PMID:1360367
 A/Accession: A56632
 A/Molecule type: Protein
 A/Residues: 1-14 <FON>
 A/Cross-references: UNIPROT:P41493; UNIPARC:UPI000013054D
 A/Experimental source: head
 A/Note: sequence extracted from NCBI backbone (NCBIP:120391)
 C/Keywords: amidated carboxyl end; neuropeptide; sulfoprotein
 F/1-14/Product: neosulfakinin-I #status experimental <NSK2>
 F/6-14/Product: neosulfakinin-I #status experimental <NSK1>
 F/9/Binding site: sulfate (Tyr) (covalent) #status predicted
 F/14/Modified site: amidated carboxyl end (Phe) #status experimental

Query Match 20.8%; Score 20; DB 2; Length 14;
 Best Local Similarity 22.2%; Pred. No. 5.8e+03;
 Matches 2; Conservative 5; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFPHGYL 9
 | | | | |
 Db 4 EQFDYGHM 12

RESULT 51
 S27140
 hypothetical protein 1 estrogen receptor 5'-region - human
 C/Species: Homo sapiens (man)
 C/Date: 05-Mar-1994 #sequence_revision 12-May-1995 #text_change 16-Aug-2004
 C/Accession: S27140
 R/Keaveney, M.; Klug, J.; Gannon, F.
 DNA Seq. 2, 347-358, 1992
 A/Title: Sequence analysis of the 5' flanking region of the human estrogen receptor gene
 A/Reference number: S27140; MUID:93075998; PMID:1476547
 A/Accession: S27140
 A/Status: translation not shown
 A/Molecule type: DNA
 A/Residues: 1-14 <KBA>
 A/Cross-references: UNIPARC:UPI000011DF55; EMBL:X62462; NID:931201; PIND:CAA4319.1; PIR

Query Match 20.8%; Score 20; DB 2; Length 14;
 Best Local Similarity 27.3%; Pred. No. 5.8e+03;
 Matches 3; Conservative 4; Mismatches 4; Indels 0; Gaps 0;

QY 6 HGULTAAVSP 16
 | | | | |
 Db 4 HSFPLSHSLP 14

RESULT 52
 PH1342
 Ig heavy chain DJ region (clone C507-95) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: PH1342
 R/Messerman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1342
 A/Molecule type: DNA
 A/Residues: 1-15 <MAS>
 A/Cross-references: UNIPARC:UPI000017C240
 C/Keywords: heterotetramer; immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 15;
 Best Local Similarity 75.0%; Pred. No. 6.3e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8
 | | | | |
 Db 4 PRGY 7

RESULT 53
 PH1310
 Ig heavy chain DJ region (clone C770-107) - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C/Accession: PH1310
 R/Messerman, R.; Gallil, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
 A/Reference number: PH1302; MUID:93094761; PMID:1460419
 A/Accession: PH1310
 A/Molecule type: DNA
 A/Residues: 1-15 <MAS>
 A/Cross-references: UNIPARC:UPI000017C24P
 C/Keywords: heterotetramer; immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 15;
 Best Local Similarity 50.0%; Pred. No. 6.3e+03;
 Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 7 GULTAAVSP 16
 | | | | |
 Db 6 GALTGARBP 15

RESULT 54
 A44413
 proteasome endopeptidase complex (EC 3.4.25.1) 24K chain - bovine (fragment)
 N/Alternate names: multicatalytic proteinase complex 24K chain; proteasome
 N/Contents: multicatalytic proteinase complex 24K chain; proteasome
 C/Species: Bos primigenius taurus (cattle)
 C/Date: 30-Apr-1993 #sequence_revision 23-Mar-1995 #text_change 09-Jul-2004
 C/Accession: A44413; B44413
 R/Yu, B.; Pereira, M.E.; Wilk, S.
 J. Biol. Chem. 268, 2029-2036, 1993
 A/Title: Changes in the structure and catalytic activities of the bovine pituitary mult
 A/Reference number: A44413; MUID:9311959; PMID:8420977
 A/Accession: A44413
 A/Molecule type: Protein
 A/Residues: 1-16 <YU>
 A/Cross-references: UNIPROT:Q9TRJ7; UNIPARC:UPI00000867F3
 A/Experimental source: pituitary
 A/Note: sequence extracted from NCBI backbone (NCBIP:123115)
 C/Superfamily: multicatalytic endopeptidase complex chain C9
 C/Keywords: hydrolase

Query Match 20.8%; Score 20; DB 2; Length 16;
 Best Local Similarity 42.9%; Pred. No. 6.7e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 6 HGULTAA 12
 | | | | |
 Db 10 HGVIYAA 16

RESULT 55
 PH1637
 Ig H chain V-D-J region (clone B-Jess 226) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 C/Date: 02-Jun-1994 #sequence_revision 02-Jun-1994 #text_change 17-Mar-1999
 C/Accession: PH1637
 R/Levinson, D.A.; Campos-Torres, J.; Leder, P.
 J. Exp. Med. 178, 317-329, 1993
 A/Title: Molecular characterization of transgene-induced immunodeficiency in B-Jess mic
 A/Reference number: PH1580; MUID:93101609; PMID:8315387
 A/Accession: PH1637
 A/Molecule type: DNA
 A/Residues: 1-16 <LBY>
 A/Cross-references: UNIPARC:UPI000017C6A0
 A/Experimental source: bone marrow pre-B lymphocyte
 C/Keywords: immunoglobulin

Query Match 20.8%; Score 20; DB 2; Length 16;

Best Local Similarity 50.0%; Pred. No. 6,7e+03;
Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 6 HGVLTT 11
| : |
| : |
Db 4 HGAMVT 9

RESULT 56

PH0773
T-cell receptor beta chain (C7) - mouse (fragment)
C/Species: Mus musculus (house mouse)
C/Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 05-Nov-1999
C/Accession: PH0773
R/Gasanova, J.L.; Romero, P.; Widmann, C.; Koutileky, P.; Maryanski, J.L.
J. Exp. Med. 174, 1371-1383, 1991
A/Title: T cell receptor genes in a series of class I major histocompatibility complex-I
allelic exclusion and antigen-specific repertoire.
A/Reference number: PH0746; PMID:92078846; PMID:1836010
A/Accession: PH0773
A/Molecule type: mRNA
A/Residues: 1-16 <CNS>
A/Cross-references: UNIPARC:UPI0000115FC0; EMBL:X60868; NID:950247; PIDD:CAA43257.1; PII
A/Experimental sources: T lymphocyte
C/Keywords: T-cell receptor

Query Match 20.8%; Score 20; DB 2; Length 16;
Best Local Similarity 66.7%; Pred. No. 6,7e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 13 AVSPGK 18
| : |
| : |
Db 2 ASSPGQ 7

RESULT 57

A44799
pyrogenic exotoxin C - Streptococcus pyogenes (fragment)
C/Species: Streptococcus pyogenes
C/Date: 24-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 31-Dec-2004
C/Accession: A44799
R/Kapur, V.; Nelson, K.; Schlievert, P.M.; Selander, R.K.; Musser, J.M.
Infect. Immun. 60, 3513-3517, 1992
A/Title: Molecular population genetic evidence of horizontal spread of two alleles of the
A/Reference number: A44799; PMID:92363541; PMID:1500157
A/Accession: A44799
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-17 <KAP>
A/Cross-references: UNIPROT:P13380; UNIPROT:Q8NKK2; UNIPARC:UPI000017AC80
A/Experimental sources: strain T18P, MGAS 1585
A/Note: sequence inconsistent with the nucleotide translation
C/Suprafamily: enterotoxin B
C/Keywords: exotoxin

Query Match 20.8%; Score 20; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 7,1e+03;
Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTPAVSP 16
| : |
| : |
Db 2 ILISTISP 9

RESULT 58

S45373
translation elongation factor EF-1a - common tobacco
C/Species: Nicotiana tabacum (common tobacco)
C/Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Jul-2004
C/Accession: S45373
R/Marty, I.; Brugidou, C.; Chartier, Y.; Meyer, Y.
Plant J. 4, 265-278, 1993

A/Title: Growth-related gene expression in Nicotiana tabacum mesophyll protoplasts.
A/Reference number: S45373; PMID:94035181; PMID:8220482

A/Accession: S45373
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-18 <MAR>
A/Cross-references: UNIPROT:Q40499; UNIPARC:UPI00000A6737; EMBL:Z14080; NID:9443955; PII

Query Match 20.8%; Score 20; DB 2; Length 18;
Best Local Similarity 33.3%; Pred. No. 7,5e+03;
Matches 5; Conservative 2; Mismatches 8; Indels 0; Gaps 0;

QY 4 BPHGYLTPAVSPGK 18
| : |
| : |
Db 3 DPHGKVTQAQKK 17

RESULT 59

I59649
human leukocyte antigen alpha chain - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C/Accession: I59649
R/Fogdell, A.; Olerup, O.
Tissue Antigens 44, 19-24, 1994
A/Title: The DOA1*0104 allele is carried by DRB1*1001- and DRB1*1401-positive haplotypes
A/Reference number: I59649; PMID:95064785; PMID:7974465
A/Accession: I59649
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-18 <RES>
A/Cross-references: UNIPROT:Q30216; UNIPARC:UPI000008A43F; GB:S75685; NID:9913771; PIDD
C/Genetics: GDB:HLA-DQA1
A/Gene: GDB:HLA-DQA1
A/Cross-references: GDB:120638; OMIM:146880
A/Map position: 6p21.3-6p21.3

Query Match 20.8%; Score 20; DB 2; Length 18;
Best Local Similarity 57.1%; Pred. No. 7,5e+03;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LTPAVSP 16
| : |
| : |
Db 5 LTTMNSP 11

RESULT 60

S48862
murine cyclin H - mouse
C/Species: Mus musculus (house mouse)
C/Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C/Accession: S48862
R/Hall, F.L.; Wu, L.
submitted to the EMBL Data Library, October 1994
A/Reference number: S48862
A/Accession: S48862
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-18 <HNL>
A/Cross-references: UNIPROT:Q61458; UNIPARC:UPI000016CCB5; EMBL:X82441; NID:9563899; PII

Query Match 20.8%; Score 20; DB 2; Length 18;
Best Local Similarity 36.4%; Pred. No. 7,5e+03;
Matches 4; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

QY 3 FEPHGYLTPAA 13
| : |
| : |
Db 8 YHPRITMLTCA 18

RESULT 61

I51427
hemoglobin alpha chain - African clawed frog (fragment)

C;Species: *Xenopus laevis* (African clawed frog)
 C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 09-Jul-2004
 C;Accession: I51427
 R;Patient: R.K.; Elington, J.A.; Kay, R.M.; Williams, J.G.
 Cell 21, 565-573, 1980
 A;Title: Internal organization of the major adult alpha- and beta-globin genes of *X.laevis*
 A;Reference number: I51427; PMID:81001900; PMID:6250724
 A;Accession: I51427
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-18 <PRT>
 A;Cross-references: UNIPROT:P67468; UNIPARC:UPI00001770CF; GB:J00975; NID:g214198; PID:g
 C;Keywords: blood; oxygen carrier

Query Match 20.8%; Score 20; DB 2; Length 18;
 Best Local Similarity 50.0%; Pred. No. 7.5e+03;
 Matches 6; Conservative 0; Mismatches 4; Indels 2; Gaps 1;

QY 6 HGVLTAAYSPG 17
 DB 7 HAYDL-RVDPG 16

RESULT 62
 A34467
 35K microfibril-associated protein - pig (fragment)
 C;Species: *Sus scrofa domestica* (domestic pig)
 C;Date: 08-Jun-1990 #sequence_revision 08-Jun-1990 #text_change 09-Jul-2004
 C;Accession: A34467
 R;Kobayashi, R.; Teshima, Y.; Maunda, H.; Shozawa, T.; Numata, Y.; Miyauchi, K.; Hayakawa, J.
 Biol. Chem. 264, 17437-17444, 1989
 A;Title: Isolation and characterization of a new 36-kDa microfibril-associated glycoprotein
 A;Reference number: A34467; PMID:90008913; PMID:2793866
 C;Accession: A34467
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-19 <KOB>
 A;Cross-references: UNIPROT:Q7M366; UNIPARC:UPI000017C450

Query Match 20.8%; Score 20; DB 2; Length 19;
 Best Local Similarity 60.0%; Pred. No. 8e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFBP 5
 DB 10 DKFOP 14

RESULT 63
 A60801
 acrosome stabilizing factor large chain - rabbit (fragment)
 C;Species: *Oryctolagus cuniculus* (domestic rabbit)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 C;Accession: A60801
 R;Wilson, W.L.; Oliphant, G.
 Biol. Reprod. 37, 159-169, 1987
 A;Title: Isolation and biochemical characterization of the subunits of the rabbit sperm
 A;Reference number: A60801; PMID:88000873; PMID:3651543
 A;Accession: A60801
 A;Molecule type: protein
 A;Residues: 1-20 <WIL>
 A;Cross-references: UNIPARC:UPI000017C5B3
 C;Comment: spermatozoa must undergo capacitation and the acrosome reaction to become cap
 C;Keywords: glycoprotein; semen

Query Match 20.8%; Score 20; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 8.4e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 BPHGYLL 10
 DB 12 BPHGYLL 18

RESULT 64
 A48367
 glutaryl-CoA dehydrogenase (BC 1.3.99.7) - *Pseudomonas* sp. (fragment)
 C;Species: *Pseudomonas* sp.
 C;Date: 01-Dec-1993 #sequence_revision 29-Sep-1999 #text_change 29-Sep-1999

C;Accession: A48367
 R;Harrel, U.; Eckel, E.; Koch, J.; Fuchs, G.; Linder, D.; Buckel, W.
 Arch. Microbiol. 159, 174-181, 1993
 A;Title: Purification of glutaryl-CoA dehydrogenase from *Pseudomonas* sp., an enzyme inv.
 A;Reference number: A48367; PMID:93175988; PMID:8439237
 A;Accession: A48367
 A;Molecule type: protein
 A;Residues: 1-20 <HAR>
 A;Cross-references: UNIPARC:UPI00000BDFCE; PIDN:AAB25430.1; PID:g265706
 A;Experimental source: strain KB 740
 A;Note: sequence extracted from NCBI backbone (NCBIP:125304)

Query Match 20.3%; Score 19.5; DB 2; Length 20;
 Best Local Similarity 55.6%; Pred. No. 1e+04;
 Matches 5; Conservative 2; Mismatches 1; Indels 1; Gaps 1;

QY 1 DAFBPHGYL 9
 DB 8 DADPY-YL 15

RESULT 65
 PT0714
 T-cell receptor beta chain V-D-J region (165-31) - mouse (fragment)
 C;Species: *Mus musculus* (house mouse)
 C;Date: 17-Jul-1992 #sequence_revision 17-Jul-1992 #text_change 09-Jul-2004
 C;Accession: PT0714
 R;Feeney, A.J.
 J. Exp. Med. 174, 115-124, 1991
 A;Title: Junctional sequences of fetal T cell receptor beta chains have few N regions.
 A;Reference number: PT0509; PMID:91277601; PMID:1711558
 A;Accession: PT0714
 A;Status: translation not shown
 A;Molecule type: DNA
 A;Residues: 1-5 <FRB>
 A;Cross-references: UNIPROT:Q8BGR5; UNIPARC:UPI000017C849
 A;Experimental source: newborn thymus, strain BALB/c
 C;Keywords: T-cell receptor

Query Match 19.8%; Score 19; DB 2; Length 5;
 Best Local Similarity 80.0%; Pred. No. 2.8e+05;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 13 AVSPG 17
 DB 1 ASSPG 5

RESULT 66
 PD0027
 pcy-tachykinin - penaeid shrimp (*Penaeus vannamei*) (fragment)
 C;Species: *Penaeus vannamei*
 C;Date: 21-Aug-1998 #sequence_revision 21-Aug-1998 #text_change 09-Jul-2004
 C;Accession: PD0027
 R;Nieto, J.; Veelaert, D.; Derna, R.; Waelkens, E.; Ceratians, A.; Coast, G.; Devereese, B.
 Biochem. Biophys. Res. Commun. 248, 406-411, 1998
 A;Title: Identification of one tachykinin- and two kinin-related peptides in the brain c
 A;Reference number: PD0027; PMID:98342103; PMID:9675150
 A;Accession: PD0027
 A;Molecule type: protein
 A;Residues: 1-9 <NIB>
 A;Cross-references: UNIPROT:Q7M3L3; UNIPARC:UPI000017CB0C
 C;Comment: This peptide belongs to myotropic neuropeptides.

Query Match 19.8%; Score 19; DB 2; Length 9;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYL 9
| | : |
| | : |
DB 2 PSGRF 6

RESULT 67
S67528
napin - rape (fragments)
C/Species: Brassica napus (rape)
C/Date: 14-Feb-1997 #sequence_revision 13-Mar-1997 #text_change 13-Mar-1997
C/Accession: S67528
R/Muren, E.; Ek, B.; Rask, L.
Eur. J. Biochem. 227, 316-321, 1995
A/Title: Processing of the 2S storage protein pronapin in Brassica napus and in transfor
A/Reference number: S67528; MUID:95154306; PMID:7851402
A/Accession: S67528
A/Status: preliminary
A/Molecule type: protein
A/Residues: 1-67-12 <MUR>
A/Cross-references: UNIPARC:UPI000017B02B; UNIPARC:UPI000017B02C

Query Match 19.8%; Score 19; DB 2; Length 12;
Best Local Similarity 60.0%; Pred. No. 7.3e+03;
Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEPHG 7
| | | |
| | | |
DB 5 FRPG 9

RESULT 68
PH190
T-cell receptor alpha chain V region (Cw3/10.1) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 16-Jul-1999
C/Accession: PH190
R/Casanova, J.L.; Cerotini, J.C.; Matthes, M.; Necker, A.; Gounnier, H.; Barra, C.; Wic
J. Exp. Med. 176, 439-447, 1992
A/Title: H-2-restricted cytolytic T lymphocytes specific for HLA display T cell receptor
A/Reference number: S26512; MUID:92364546; PMID:1380061
A/Accession: PH190
A/Status: preliminary
A/Molecule type: mRNA
A/Residues: 1-12 <CAS>
A/Cross-references: UNIPARC:UPI000017C395

Query Match 19.8%; Score 19; DB 2; Length 12;
Best Local Similarity 42.9%; Pred. No. 7.3e+03;
Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 APEPHG 8
| | | |
| | | |
DB 2 AVSEHGF 8

RESULT 69
PT0263
Ig heavy chain CRD3 region (clone 2-121B) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
C/Accession: PT0263
R/Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
J. Exp. Med. 173, 395-407, 1991
A/Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J
A/Reference number: PT0222; MUID:91108337; PMID:1899102
A/Accession: PT0263
A/Molecule type: DNA
A/Residues: 1-13 <YAM>
A/Cross-references: UNIPARC:UPI000017C1F0
A/Experimental source: B lymphocyte
C/Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 13;
Best Local Similarity 75.0%; Pred. No. 7.9e+03;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGYL 9
| | | |
| | | |
DB 7 YGYL 10

RESULT 70
LPEBWC
trp operon leader peptide - Citrobacter freundii
C/Species: Citrobacter freundii
C/Date: 14-Nov-1983 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
C/Accession: A03592
R/Blumenberg, M.; Yanofsky, C.
J. Bacteriol. 152, 57-62, 1982
A/Title: Evolutionary divergence of the Citrobacter freundii tryptophan operon regulator
A/Reference number: A91792; MUID:83007061; PMID:6749821
A/Accession: A03592
A/Molecule type: DNA
A/Residues: 1-14 <BLU>
A/Cross-references: UNIPROT:P03056; UNIPARC:UPI000012B89A
A/Genetics:
A/Gene: trpL
C/Function:
A/Description: involved in control of tryptophan operon transcription by attenuation
C/Superfamily: trp leader peptide

Query Match 19.8%; Score 19; DB 1; Length 14;
Best Local Similarity 40.0%; Pred. No. 8.5e+03;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 3 FEPHGYLTA 12
| | | | | : |
| | | | | : |
DB 5 FVLHGMMWRTS 14

RESULT 71
PH1347
Ig heavy chain DJ region (clone C100-103A) - human (fragment)
C/Species: Homo sapiens (man)
C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
C/Accession: PH1347
R/Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
J. Exp. Med. 176, 1577-1581, 1992
A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph
A/Reference number: PH1302; MUID:93094761; PMID:1460419
A/Accession: PH1347
A/Molecule type: DNA
A/Residues: 1-14 <WAS>
A/Cross-references: UNIPARC:UPI000017C21C
C/Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 14;
Best Local Similarity 44.4%; Pred. No. 8.5e+03;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLITRAVAVSP 16
| | | | | | |
| | | | | | |
DB 6 FLITGAREP 14

RESULT 72
S24159
leukocyte elastase (EC 3.4.21.37) - sheep (fragment)
N/Alternate names: neutrophil elastase
C/Species: Ovis orientalis aries, Ovis ammon aries (domestic sheep)
C/Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004
C/Accession: S24159
R/Junger, W.G.; Hallstrom, S.; Liu, F.C.; Redl, H.; Schlag, G.
Biol. Chem. Hoppe-Seyler 373, 691-698, 1992

A/Title: The enzymatic and release characteristics of sheep neutrophil elastase: a compd
 A/Reference number: 824159; PMID:93039751; PMID:1418684
 A/Accession: 824159
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <JUN>
 A/Cross-references: UNIPROT:Q9TRL3; UNIPARC:UPI0000086FBA
 A/Superfamily: trypsin; trypsin homology
 C/Keywords: hydrolase; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 APEPHGY 8
 DB 6 AARPAHW 12

RESULT 73

S25535
 T-cell receptor alpha chain V region (clone Cw3/10.1) - mouse (fragment)
 C/Species: Mus musculus (house mouse)
 A/Variety: clone Cw3/10.1
 C/Date: 11-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 17-Mar-1999
 C/Accession: S25535
 R/Casanova, J.L.; Cerottini, J.C.; Mattes, M.; Necker, A.; Gournier, H.; Barra, C.; Wild
 J. Exp. Med. 176, 439-447, 1992
 A/Title: H-2-restricted cytolytic T lymphocyte specific for HLA display T cell receptor
 A/Reference number: S25512; PMID:92364546; PMID:1380061
 A/Accession: S25535
 A/Molecule type: mRNA
 A/Residues: 1-15 <CNS>
 A/Cross-references: UNIPARC:UPI00001769C2; EMBL:X67986
 A/Experimental source: cytolytic T lymphocyte, clone Cw3/10.1
 C/Superfamily: immunoglobulin V region; immunoglobulin homology
 C/Keywords: T-cell receptor

Query Match 19.8%; Score 19; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 APEPHGY 8
 DB 2 AVSHGPF 8

RESULT 74

S29485
 GTP-binding protein o-ral - Pacific electric ray (fragment)
 C/Species: Torpedo californica (Pacific electric ray)
 C/Date: 22-Nov-1993 #sequence_revision 27-Feb-1997 #text_change 13-Mar-1997
 C/Accession: S29485
 R/Volkhardt, W.; Peyssner, J.; Elferink, L.A.; Schiller, R.H.
 FEBS Lett. 317, 53-56, 1993
 A/Title: Association of three small GTP-binding proteins with cholinergic synaptic vesicle
 A/Reference number: S29485; PMID:93154521; PMID:8428634
 A/Accession: S29485
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <VOL>
 A/Cross-references: UNIPARC:UPI000017BPJ3

Query Match 19.8%; Score 19; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 EPHHG 7
 DB 9 YBPTG 13

RESULT 75

A36315
 recycling receptor p180 - human (fragment)
 C/Species: Homo sapiens (man)
 C/Date: 25-Jan-1991 #sequence_revision 25-Jan-1991 #text_change 30-Sep-1993
 C/Accession: A36315
 R/Isacke, C.M.; van der Geer, P.; Hunter, T.; Trowbridge, I.S.
 Mol. Cell. Biol. 10, 2606-2618, 1990
 A/Title: p180, a novel recycling transmembrane glycoprotein with restricted cell type e.
 A/Reference number: A36315; PMID:90258846; PMID:2188094
 A/Accession: A36315
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-15 <ISA>
 A/Cross-references: UNIPARC:UPI000017C3J7

Query Match 19.8%; Score 19; DB 2; Length 15;
 Best Local Similarity 42.9%; Pred. No. 9.1e+03;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 4 EPHGYLL 10
 DB 9 EPHVFLI 15

RESULT 76

PA0006
 lectin A3 - Psophocarpus scandens (fragment)
 C/Species: Psophocarpus scandens
 C/Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
 C/Accession: PA0006
 R/Kort, A.A.
 Phytochemistry 27, 2847-2855, 1988
 A/Title: Isolation and characterization of the lectins from the seeds of Psophocarpus s.
 A/Reference number: PA0005
 A/Accession: PA0006
 A/Molecule type: protein
 A/Residues: 1-15 <KOR>
 A/Cross-references: UNIPROT:P22583; UNIPARC:UPI000012B3BR
 A/Experimental source: seed
 C/Comment: The seeds of Psophocarpus contain two distinct groups of lectins which can b
 C/Keywords: lectin

Query Match 19.8%; Score 19; DB 2; Length 15;
 Best Local Similarity 60.0%; Pred. No. 9.1e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAPBP 5
 DB 9 NVFEP 13

RESULT 77

A60551
 Leukocyte elastase (EC 3.4.21.37) - dog (fragment)
 C/Species: Canis lupus familiaris (dog)
 C/Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jul-2004
 C/Accession: A60551
 R/Axelsson, L.; Bergenfelt, M.; Björck, P.; Olsson, R.; Olsson, K.
 Scand. J. Clin. Lab. Invest. 50, 35-42, 1990
 A/Title: Release of immunoreactive canine leukocyte elastase normally and in endotoxin s
 A/Reference number: A60551; PMID:90193608; PMID:1690443
 A/Accession: A60551
 A/Molecule type: protein
 A/Residues: 1-16 <AXE>
 A/Cross-references: UNIPROT:Q8MDJ1; UNIPARC:UPI0000175CJF
 C/Superfamily: trypsin; trypsin homology
 C/Keywords: hydrolase; leukocyte; lysosome; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 16;
 Best Local Similarity 40.0%; Pred. No. 9.8e+03;
 Matches 2; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 4 EPHGY 8

Db 8 QPHAW 12

RESULT 78

PT0282

Ig heavy chain CDR3 region (clone 4-94A) - human (fragment)

C1Species: Homo sapiens (man)

C1Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996

C1Accession: PT0282

R.Yanada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.

J. Exp. Med. 173, 395-407, 1991

A1Title: Preferential utilization of specific immunoglobulin heavy chain diversity and J

A1Reference number: PT0222; MUID:91108337; PMID:1899102

C1Accession: PT0282

A1Molecule type: DNA

A1Residues: 1-16 <YAM>

A1Cross-references: UNIPARC:UPI000017C1DA

A1Experimental source: B lymphocyte

C1Keywords: heterotrimer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 16;
Best Local Similarity 60.0%; Pred. No. 9.8e+03;
Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 AEPHG 7
| | |
Db 9 FDPWG 13

RESULT 79

S16376

L-serine dehydratase beta chain - Peptostreptococcus asaccharolyticus

C1Species: Peptostreptococcus asaccharolyticus

C1Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C1Accession: S16376

R.Grabowski, R.; Buckel, W.

Eur. J. Biochem. 199, 89-94, 1991

A1Title: Purification and properties of an iron-sulfur-containing and pyridoxal-phosphat

A1Reference number: S16224; MUID:91293139; PMID:2065681

A1Accession: S16376

A1Status: preliminary

A1Molecule type: protein

A1Residues: 1-16 <EUR>

A1Cross-references: UNIPROT:P33074; UNIPARC:UPI000017ABR6

Query Match 19.8%; Score 19; DB 2; Length 16;
Best Local Similarity 35.7%; Pred. No. 9.8e+03;
Matches 5; Conservative 2; Mismatches 7; Indels 0; Gaps 0;

QY 2 AEPHYLLTAAS 15
| | | | |
Db 3 APEVMPGVWGPSS 16

RESULT 80

S57991

hydroxyproline-rich protein - Sebania rostrata (fragment)

C1Species: Sebania rostrata

C1Date: 13-Jan-1996 #sequence_revision 01-Mar-1996 #text_change 09-Jul-2004

C1Accession: S57991

R.Goormachtig, S.; Valerio-Lepintec, M.; Szczyglowski, K.; van Montagu, M.; Holsters, M.

submitted to the EMBL Data Library, March 1995

A1Description: Use of differential display to identify novel Sebania rostrata genes ent

A1Reference number: S57991

A1Accession: S57991

A1Status: preliminary

A1Molecule type: mRNA

A1Residues: 1-17 <GOO>

A1Cross-references: UNIPROT:Q41400; UNIPARC:UPI000004ACD95; EMBL:Z48673; NID:G899484; PID

Query Match 19.8%; Score 19; DB 2; Length 17;

Best Local Similarity 75.0%; Pred. No. 1e+04;
Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8
| | |
Db 3 PHY 6

RESULT 81

S09085

proteasome chain 4 - rat (fragment)

N1Alternate names: multicatalytic proteinase chain 4

C1Species: Rattus norvegicus (Norway rat)

C1Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 18-Jun-1993

C1Accession: S09085

R.Lilley, K.S.; Davison, M.D.; Rivett, A.J.

FEBS Lett. 262, 327-329, 1990

A1Title: N-terminal sequence similarities between components of the multicatalytic prote

A1Reference number: S09082; MUID:90242957; PMID:2335214

A1Accession: S09085

A1Molecule type: protein

A1Residues: 1-17 <LIL>

A1Cross-references: UNIPARC:UPI000017C99F

Query Match 19.8%; Score 19; DB 2; Length 17;
Best Local Similarity 28.6%; Pred. No. 1e+04;
Matches 2; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 2 AEPHGY 8
| | | | |
Db 1 SFSFYAF 7

RESULT 82

B31435

adherence lectin light chain - Entamoeba histolytica (fragment)

C1Species: Entamoeba histolytica

C1Date: 31-Jul-1989 #sequence_revision 31-Jul-1989 #text_change 09-Jul-2004

C1Accession: B31435

R.Petri Jr., W.A.; Chapman, M.D.; Snodgrass, T.; Mann, B.J.; Broman, J.; Ravdin, J.I.

J. Biol. Chem. 264, 3007-3012, 1989

A1Title: Subunit structure of the galactose and N-acetyl-D-galactosamine-inhibitable adh

A1Reference number: A31435; MUID:89123408; PMID:2536731

A1Accession: B31435

A1Status: preliminary

A1Molecule type: protein

A1Residues: 1-17 <PET>

A1Cross-references: UNIPROT:Q24846; UNIPARC:UPI000017B5D4

Query Match 19.8%; Score 19; DB 2; Length 17;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
| | | | |
Db 7 DQFSPN 12

RESULT 83

PH1323

Ig heavy chain DJ region (clone C174-113) - human (fragment)

C1Species: Homo sapiens (man)

C1Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C1Accession: PH1323

R.Wasserman, R.; Gallili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A1Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A1Reference number: PH1302; MUID:93094761; PMID:1460419

A1Accession: PH1323

A1Molecule type: DNA

A1Residues: 1-18 <WAS>

A1Cross-references: UNIPARC:UPI0000176937

C1Superfamily: immunoglobulin V region; immunoglobulin homology

C/Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 18;

Best Local Similarity 60.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEPHG 7

11 FDPWG 15

RESULT 84

S28408

platelet-derived growth factor receptor beta - pig (fragment)

C/Species: Sus scrofa domestica (domestic pig)

C/Date: 27-Jan-1995 #sequence_revision 27-Jan-1995 #text_change 07-May-1999

C/Accession: S28408

R/Reinstated: L.; Mori, S.; Arridsson, A.K.; Eriksson, A.; Wernstedt, C.; Hellman, U.;

EMBO J. 11, 3911-3919, 1992

A/Title: Identification of two C-terminal autophosphorylation sites in the PDGF beta-rec

A/Reference number: S28408; MUID:93010986; PMID:1356585

A/Accession: S28408

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-4;5-18 <ROB>

A/Cross-references: UNIPARC:UPI000017C472; UNIPARC:UPI000017C473

C/Keywords: growth factor receptor

Query Match 19.8%; Score 19; DB 2; Length 18;

Best Local Similarity 44.4%; Pred. No. 1.1e+04;

Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 10 LTAVSFGK 18

3 LDXAVQPN 11

RESULT 85

S20322

gluten - wheat

C/Species: Triticum aestivum (common wheat)

C/Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C/Accession: S20322

R/Pukdomo, S.; Yoshikawa, M.

FEBS Lett. 286, 107-111, 1992

A/Title: Opioid peptides derived from wheat gluten: their isolation and characterization

A/Reference number: S20322; MUID:92111773; PMID:1309704

A/Accession: S20322

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-18 <FUK>

A/Cross-references: UNIPROT:Q7M1G0; UNIPARC:UPI000017B139

Query Match 19.8%; Score 19; DB 2; Length 18;

Best Local Similarity 50.0%; Pred. No. 1.1e+04;

Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 3 FEPHG 8

2 YPTGY 7

RESULT 86

PH1339

Ig heavy chain DJ region (clone C272-119) - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C/Accession: PH1339

R/Waberman, R.; Gallili, N.; Ito, Y.; Ketchard, B.A.; Shane, S.; Rovera, G.

J. Exp. Med. 176, 1577-1581, 1992

A/Title: Predominance of fetal type DJH joining in young children with B precursor lymph

A/Reference number: PH1302; MUID:93094761; PMID:1460419

A/Accession: PH1339

A/Molecule type: DNA

A/Residues: 1-19 <RAS>

A/Cross-references: UNIPARC:UPI000017C23A

C/Keywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 19;

Best Local Similarity 60.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 3 FEPHG 7

12 FDPWG 16

RESULT 87

A34233

trehalase inhibitor - American cockroach (fragment)

C/Species: Periplaneta americana (American cockroach)

C/Date: 07-Sep-1990 #sequence_revision 07-Sep-1990 #text_change 09-Jul-2004

C/Accession: A34233

R/Hayakawa, Y.; Jahagirdar, A.P.; Yaguchi, M.; Downer, R.G.H.

J. Biol. Chem. 264, 16165-16169, 1989

A/Title: Purification and characterization of trehalase inhibitor from hemolymph of the

A/Reference number: A34233; MUID:89380218; PMID:2777784

A/Accession: A34233

A/Molecule type: protein

A/Residues: 1-19 <HAY>

A/Cross-references: UNIPROT:P19986; UNIPARC:UPI000012DA2D

Query Match 19.8%; Score 19; DB 2; Length 19;

Best Local Similarity 75.0%; Pred. No. 1.2e+04;

Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGY 8

5 PHVY 8

RESULT 88

A56900

chymotrypsin I (EC 3.4.21.-) - penaeid shrimp (Penaeus vanamei) (fragment)

C/Species: Penaeus vanamei

C/Date: 11-Aug-1995 #sequence_revision 11-Aug-1995 #text_change 09-Jul-2004

C/Accession: A56900

R/Van Wormhout, A.; Le Chevalier, P.; Selloes, D.

Comp. Biochem. Physiol. B 103, 675-680, 1992

A/Title: Purification, biochemical characterization and N-terminal sequence of a serine

apoda).

A/Reference number: A56900; MUID:93092601; PMID:1458841

A/Accession: A56900

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <VAN>

A/Cross-references: UNIPROT:O18487; UNIPARC:UPI0000175C07

A/Note: sequence extracted from NCBI backbone (NCBI:P120229)

A/Note: a second variant, designated chymotrypsin II, had an identical N-terminal sequ

C/Comment: This enzyme has chymotrypsin and collagenolytic activities.

C/Superfamily: trypsin; trypsin homology

C/Keywords: hydrolase; protein digestion; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 20;

Best Local Similarity 40.0%; Pred. No. 1.2e+04;

Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTAAV 14

9 PHSWPQQAAL 18

RESULT 89

B34817

collagenolytic proteinase (EC 3.4.21.-), 36K, chain A - red king crab (fragment)

C/Species: Paralithodes cambratica (red king crab)

CjDate: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
 CjAccession: B34817
 RjKlimova, O.A.; Borukhov, S.I.; Solovyeva, N.I.; Balaevskaya, T.O.; Strongin, A.Y.
 Biochem. Biophys. Res. Commun. 166, 1411-1420, 1990
 AjTitle: The isolation and properties of collagenolytic proteases from crab hepatopancre
 AjReference number: A34817; PMID:90165951; PMID:2154979
 AjAccession: B34817
 AjStatus: preliminary
 AjMolecule type: protein
 AjResidues: 1-20 <KLI>
 AjCross-references: UNIPROT:P20732; UNIPARC:UPI0000127E39
 CjSuperfamily: trypsin; trypsin homology
 CjKeywords: hydrolase; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18
 |||:
 Db 7 VTPGE 11

RESULT 90
 C34817
 collagenolytic proteinase (EC 3.4.21.-), 36K, chain B - red king crab (fragment)
 CjSpecies: Paratithodes camtschatica (red king crab)
 CjDate: 13-Jul-1990 #sequence_revision 13-Jul-1990 #text_change 09-Jul-2004
 CjAccession: C34817
 RjKlimova, O.A.; Borukhov, S.I.; Solovyeva, N.I.; Balaevskaya, T.O.; Strongin, A.Y.
 Biochem. Biophys. Res. Commun. 166, 1411-1420, 1990
 AjTitle: The isolation and properties of collagenolytic proteases from crab hepatopancre
 AjReference number: A34817; PMID:90165951; PMID:2154979
 AjAccession: C34817
 AjStatus: preliminary
 AjMolecule type: protein
 AjResidues: 1-20 <KLI>
 AjCross-references: UNIPROT:P20733; UNIPARC:UPI0000127E37
 CjSuperfamily: trypsin; trypsin homology
 CjKeywords: hydrolase; serine proteinase

Query Match 19.8%; Score 19; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 14 VSPGK 18
 |||:
 Db 7 VTPGE 11

RESULT 91
 S07232
 ribulose-bisphosphate carboxylase subunit-binding protein alpha chain - garden pea (frag
 NjAlternate names: rubisco subunit-binding protein alpha chain
 CjSpecies: Pisum sativum (garden pea)
 CjDate: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 09-Jul-2004
 CjAccession: S07232
 RjMugrove, J.E.; Johnson, R.A.; Ellis, R.J.
 Eur. J. Biochem. 163, 529-534, 1987
 AjTitle: Dissociation of the ribulosebiphosphate-carboxylase large-subunit binding prot
 AjReference number: S07232; PMID:87161853; PMID:3549295
 AjAccession: S07232
 AjMolecule type: protein
 AjResidues: 1-20 <MUS>
 AjCross-references: UNIPROT:P08936; UNIPARC:UPI000017834B
 CjComment: This protein binds the newly synthesized large subunit and the newly imported
 CjSuperfamily: chaperonin groEL
 CjKeywords: chlotriplast; heterododecamer; molecular chaperone

Query Match 19.8%; Score 19; DB 2; Length 20;
 Best Local Similarity 60.0%; Pred. No. 1.2e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 2 AEPBH 6
 |||:
 Db 6 AFDQH 10

RESULT 92
 A60372
 pollen allergen Poa-pi - Kentucky bluegrass (fragment)
 CjSpecies: Poa pratensis (Kentucky bluegrass)
 CjDate: 11-Feb-1993 #sequence_revision 11-Feb-1993 #text_change 31-Dec-2004
 CjAccession: A60372; A33086
 RjEkremodoullah, A.K.M.
 Int. Arch. Allergy Appl. Immunol. 93, 371-377, 1990
 AjTitle: Two-dimensional gel electrophoretic analyses of Kentucky bluegrass and rye gras
 ence of Poa p 1 allergen.
 AjReference number: A60372; PMID:91317571; PMID:2101126
 AjAccession: A60372
 AjMolecule type: protein
 AjResidues: 1-20 <EKR>
 AjCross-references: UNIPARC:UPI00001794BC
 CjSuperfamily: Major pollen allergen/expansion
 CjKeywords: hydroxyproline; pollen
 Fj5/8/Modified site: hydroxyproline (Pro) #status experimental

Query Match 19.8%; Score 19; DB 2; Length 20;
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 12 AAVSPG 17
 |||:
 Db 2 AKVPPG 7

RESULT 93
 PH1326
 Ig heavy chain DJ region (clone C515-116) - human (fragment)
 CjSpecies: Homo sapiens (man)
 CjDate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999
 CjAccession: PH1326
 RjWasserman, R.; Galili, N.; Ito, Y.; Reichard, B.A.; Shane, S.; Rovera, G.
 J. Exp. Med. 176, 1577-1581, 1992
 AjTitle: Predominance of fetal type DJH joining in young children with B precursor lymph
 AjReference number: PH1302; PMID:93094761; PMID:1460419
 AjAccession: PH1326
 AjMolecule type: DNA
 AjResidues: 1-20 <MAS>
 AjCross-references: UNIPARC:UPI000017C242
 CjKeywords: heterotetramer; immunoglobulin

Query Match 19.8%; Score 19; DB 2; Length 20;
 Best Local Similarity 57.1%; Pred. No. 1.2e+04;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPHG 7
 |||:
 Db 11 DAFDIWG 17

RESULT 94
 S50175
 kallikrein (PK-120) - human
 CjSpecies: Homo sapiens (man)
 CjDate: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 21-Jul-1995
 CjAccession: S50175
 RjPu, X.P.; Iwamoto, A.; Nishimura, H.; Nagasawa, S.
 Biochim. Biophys. Acta 1208, 338-343, 1994
 AjTitle: Purification and characterization of a novel substrate for plasma kallikrein (F
 AjReference number: S50175; PMID:95035036; PMID:7947966
 AjAccession: S50175
 AjStatus: preliminary
 AjMolecule type: protein
 AjResidues: 1-20 <PUX>

A/Cross-references: UNIPARC:UPI000017C287

Query Match 19.8%; Score 19; DB 2; Length 20;
Best Local Similarity 44.4%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTTAAVSP 16
| | | | |
| | | | |
DB 8 YSLDLAILP 16

RESULT 95

S45637

oxidoreductase - Proteus vulgaris (fragment)

C/Species: Proteus vulgaris

C/Date: 10-Dec-1994 #sequence_revision 13-Mar-1997 #text_change 09-Jul-2004

C/Accession: S45637

R/Trautwein, T.; Krause, F.; Lottepelech, F.; Simon, H.

Eur. J. Biochem. 222, 1025-1032, 1994

A/Title: The (2R)-hydroxycarboxylate-viologen-oxidoreductase from Proteus vulgaris is a

A/Reference number: S45637; PMID:9428804; PMID:8026480

A/Accession: S45637

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <TRA>

A/Cross-references: UNIPROT:Q9R4Y1; UNIPARC:UPI00000B9A19

Query Match 19.8%; Score 19; DB 2; Length 20;
Best Local Similarity 57.1%; Pred. No. 1.2e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 9 LTTAAVS 15
| | | | |
| | | | |
DB 14 LTTGALS 20

RESULT 96

S29636

Jacalin beta-1 chain - Artocarpus champedon (fragment)

C/Species: Artocarpus champedon

C/Date: 19-Mar-1997 #sequence_revision 17-Jul-1998 #text_change 09-Jul-2004

C/Accession: S29636

R/Ngoc, L.D.; Brillard, M.; Hoebeke, J.

Biochim. Biophys. Acta 1156, 219-222, 1993

A/Title: The alpha- and beta-subunits of the jacalins are cleavage products from a 17-kD

A/Reference number: S29635; PMID:93152601; PMID:8427879

A/Accession: S29636

A/Molecule type: protein

A/Residues: 1-20 <NGO>

A/Cross-references: UNIPROT:Q9S8T0; UNIPARC:UPI00000A4123

A/Experimental source: seed

C/Complex: heterotetramer; two alpha and two beta chains

C/Function: seed storage protein

A/Note: Jacalin for D-galactosyl-beta-1-3-N-acetylgalactosamine, a tumor-associated T-cell

A/Keyword: heterotetramer; lectin; seed; storage protein

Query Match 19.8%; Score 19; DB 2; Length 20;
Best Local Similarity 38.5%; Pred. No. 1.2e+04;
Matches 5; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 4 EPHGYLTTAAVSP 16
| | | | |
| | | | |
DB 2 EQSGISQTVIVGP 14

RESULT 97

S71593

serine proteinase inhibitor, 33K - human (fragment)

C/Species: Homo sapiens (man)

C/Date: 19-Mar-1998 #sequence_revision 17-Apr-1998 #text_change 09-Jul-2004

C/Accession: S71593

R/Rao, C.N.; Liu, Y.Y.; Peavey, C.L.; Woodley, D.T.

Arch. Biochem. Biophys. 317, 311-314, 1995

A/Title: Novel extracellular matrix-associated serine proteinase inhibitors from human

A/Reference number: S71592; PMID:9517668; PMID:7872799

A/Accession: S71593

A/Molecule type: protein

A/Residues: 1-20 <RAO>

A/Cross-references: UNIPROT:Q9UC66; UNIPARC:UPI00000727A3

C/Function: involved in turnover of connective tissues

A/Description: serine proteinase inhibitor

Query Match 19.8%; Score 19; DB 2; Length 20;
Best Local Similarity 75.0%; Pred. No. 1.2e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 4 EPHG 7
| | | | |
| | | | |
DB 5 EPHG 8

RESULT 98

A58903

metalloproteinase AP34 (EC 3.4.24.-) - Aeromonas caviae (fragment)

C/Species: Aeromonas caviae

C/Date: 31-Dec-2001 #sequence_revision 31-Dec-2001 #text_change 09-Jul-2004

C/Accession: A58903

R/Toma, C.

submitted to the Protein Sequence Database, November 1998

A/Description: Metalloproteinase AP34.

A/Reference number: A58903

A/Accession: A58903

A/Status: preliminary

A/Molecule type: protein

A/Residues: 1-20 <TOM>

A/Cross-references: UNIPROT:Q7M027; UNIPARC:UPI000017CB88

C/Keywords: hydrolase; metalloproteinase

Query Match 19.8%; Score 19; DB 2; Length 20;
Best Local Similarity 45.5%; Pred. No. 1.2e+04;
Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

QY 1 DAEPPHGYLTT 11
| | | | |
| | | | |
DB 2 DMTGPGNVKT 12

RESULT 99

S38292

30K allergen - rye (fragment)

C/Species: Secale cereale (rye)

C/Date: 19-May-1994 #sequence_revision 27-Feb-1997 #text_change 09-Jul-2004

C/Accession: S38292

R/Petersen, A.; Schramm, G.; Becker, W.M.; Schlaak, M.

Biol. Chem. Hoppe-Seyler 374, 855-861, 1993

A/Title: Comparison of four grass pollen species concerning their allergens of grass gr

A/Reference number: S38288; PMID:94092339; PMID:7505588

A/Accession: S38292

A/Molecule type: protein

A/Residues: 1-16 <PET>

A/Cross-references: UNIPROT:Q7M263; UNIPARC:UPI000017B111

Query Match 19.3%; Score 18.5; DB 2; Length 16;
Best Local Similarity 45.5%; Pred. No. 1.2e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 3; Gaps 1;

QY 7 GYLTTAAVSPG 17
| | | | |
| | | | |
DB 4 GY--APAPG 11

RESULT 100

A33098

244K exoantigen - malaria parasite (Plasmodium falciparum) (fragments)

C:Species: Plasmodium falciparum
 C:Date: 24-Aug-1990 #sequence_revision 24-Aug-1990 #text_change 03-Jun-2000
 C/Accession: A33098
 R/Nichols, J.H.; Hager, L.P.
 submitted to the Protein Sequence Database, May 1990
 A/Reference number: A33098
 A/Accession: A33098
 A/Status: preliminary
 A/Molecule type: protein
 A/Residues: 1-7 <NIC>
 A/Cross-references: UNIPARC:UPI000017B5E9

Query Match 18.8%; Score 18; DB 2; Length 7;
 Best Local Similarity 60.0%; Pred. No. 2.8e+05;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy	13 AVSPG 17	:
Db	1 ALGPG 5	

Search completed: January 20, 2006, 19:12:13
 Job time : 11.2115 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: January 20, 2006, 18:54:54 ; Search time 59.8846 Seconds

(without alignment)
212.066 Million cell updates/sec

Title: US-09-662-293-6

Perfect score: 96
Sequence: 1 DAFEPHGYLLTAASPRK 18

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 14590

Minimum DB seq length: 0
Maximum DB seq length: 20

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 100 summaries

Database : Uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysts of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	30	31.2	20	1	SODP_PASPI
2	29	30.2	17	2	Q7T150_CHICK
3	28	29.2	15	2	Q86865_VIRU
4	28	29.2	20	2	Q7M2X3_BOVIN
5	27	28.1	16	2	Q21922_GCAUD
6	27	28.1	19	2	Q9UC80_HUMAN
7	27	28.1	20	2	Q7M4S4_HUMAN
8	26.5	27.6	19	2	Q47554_ECOLI
9	26	27.1	12	2	Q53183_RHOSO
10	26	27.1	15	2	Q86867_VIRU
11	26	27.1	15	2	Q86869_VIRU
12	25	26.0	15	1	UC16_MALIZ
13	25	26.0	15	2	Q71UK9_HALCO
14	25	26.0	16	2	Q9UTM3_RAT
15	25	26.0	17	2	Q9HRO1_PARR
16	25	26.0	17	2	Q9HRO2_AJBD8
17	25	26.0	17	2	Q9HRO3_AJBD8
18	25	26.0	19	2	Q423U7_PLABR
19	25	26.0	20	1	VMO3_CHICK
20	25	26.0	20	2	Q8MW61_HUMAN
21	25	26.0	20	2	Q9TWL3_BOMBO
22	25	26.0	20	2	Q9SVV2_MOUSE
23	24	25.0	10	2	Q6LCT8_RAT
24	24	25.0	12	2	Q05328_SPHFN
25	24	25.0	14	2	Q47335_ECOLI
26	24	25.0	15	2	Q7M2K5_RABYT
27	24	25.0	16	2	Q77489_TUPGL
28	24	25.0	16	2	Q56385_GCYAN
29	24	25.0	18	2	Q86WJ4_HUMAN
30	24	25.0	19	2	Q8TDB3_HUMAN
31	24	25.0	20	2	Q9PRY1_TORCA

32	23.5	24.5	16	2	Q7M1V9_LYCES	Q7M1V9_LYCES
33	23.5	24.5	19	2	Q9UCG2_HUMAN	Q9UCG2_HUMAN
34	23	24.0	11	1	LSK1_LEUMA	P04428_leucophaea
35	23	24.0	12	2	Q4YEX5_PLABR	Q4YEX5_plasmodium
36	23	24.0	13	1	ADPB_TENMO	P83109_tenebrio mo
37	23	24.0	13	2	Q9UDC6_HUMAN	Q9UDC6_homo sapien
38	23	24.0	16	2	Q4YX27_PLABR	Q4YX27_plasmodium
39	23	24.0	17	2	Q6R3U8_HUMAN	Q6R3U8_homo sapien
40	23	24.0	17	2	Q29395_CANPA	Q29395_canis famli
41	23	24.0	18	2	Q424N4_PLABR	Q424N4_plasmodium
42	23	24.0	18	2	Q6LD80_PMDRI	Q6LD80_mus sp. chr
43	23	24.0	18	2	Q7ZNT3_9H1Y1	Q7ZNT3_human immun
44	23	24.0	19	2	Q9SGI3_ABTAL	Q9SGI3_abies alba
45	23	24.0	20	1	PL1_LUFLU	P83363_lupinus lut
46	23	24.0	20	1	PL6_LUFLU	P83368_lupinus lut
47	23	24.0	20	2	Q9BRP3_HUMAN	Q9BRP3_homo sapien
48	23	24.0	20	2	Q9R4U5_STRSL	Q9R4U5_streptococ
49	22	22.9	9	2	Q81IS2_MOUSE	Q81IS2_mus musculu
50	22	22.9	10	2	Q9MJ05_PODCU	Q9MJ05_podospora c
51	22	22.9	10	2	Q9QY21_PMDRI	Q9QY21_rattus sp.
52	22	22.9	11	2	Q86D31_TRYCR	Q86D31_trypanosoma
53	22	22.9	14	2	Q9MWQ3_PODCU	Q9MWQ3_podospora c
54	22	22.9	14	2	Q5Q817_TRIMA	Q5Q817_trichechus
55	22	22.9	14	2	Q5Q8J5_CYCDI	Q5Q8J5_cyclopes d
56	22	22.9	14	2	Q5Q8J7_SPAEH	Q5Q8J7_spatialax leuc
57	22	22.9	15	1	GSTR1_PSDRO	P82989_pseudomonas
58	22	22.9	15	2	Q05694_MOUSE	Q05694_mus musculu
59	22	22.9	15	2	Q69353_HNV2	Q69353_human herpe
60	22	22.9	16	2	Q9TRR1_RABYT	Q9TRR1_oryctolagus
61	22	22.9	16	2	Q9QZY3_MOUSE	Q9QZY3_mus musculu
62	22	22.9	17	2	Q61C11_HUMAN	Q61C11_homo sapien
63	22	22.9	17	2	Q7MOD8_MOUSE	Q7MOD8_mus musculu
64	22	22.9	18	2	Q7SMF5_HUMAN	Q7SMF5_homo sapien
65	22	22.9	19	2	Q5C123_SCHJA	Q5C123_schistosoma
66	22	22.9	19	2	Q4YGN5_PLABR	Q4YGN5_plasmodium
67	22	22.9	19	2	Q4WZ87_9EUTH	Q4WZ87_hanis temm
68	22	22.9	19	2	Q7TBG5_ADE08	Q7TBG5_human adeno
69	22	22.9	20	1	PL3_LUFLU	P83365_lupinus lut
70	22	22.9	20	2	Q8NFW3_HUMAN	Q8NFW3_homo sapien
71	22	22.9	20	2	Q6JCN3_ECOLI	Q6JCN3_escherichia
72	21.5	22.4	16	2	Q9PRR9_GAVES	Q9PRR9_aaes (ducks
73	21.5	22.4	18	2	Q5GKS4_COXBU	Q5GKS4_coxiella bu
74	21.5	22.4	20	2	Q8A465_BRARE	Q8A465_baccharidano
75	21	21.9	9	2	Q84U84_SORBN	Q84U84_glycine max
76	21	21.9	10	2	Q7M4X1_9ZYGO	Q7M4X1_basidiobolu
77	21	21.9	10	2	Q9R7J8_HELIPY	Q9R7J8_homo sapien
78	21	21.9	10	2	Q9R7J8_HELIPY	Q9R7J8_helicobacte
79	21	21.9	11	2	Q86D32_TRYCR	Q86D32_trypanosoma
80	21	21.9	11	2	Q9TRW5_BOVIN	Q9TRW5_bos taurus
81	21	21.9	12	2	Q9K670_BACHD	Q9K670_bacillus ha
82	21	21.9	12	2	Q88575_9PICO	Q88575_thellex's e
83	21	21.9	12	2	Q88576_9PICO	Q88576_thellex's e
84	21	21.9	12	2	Q88577_9PICO	Q88577_thellex's e
85	21	21.9	12	2	Q88578_9PICO	Q88578_thellex's e
86	21	21.9	12	2	Q88579_9PICO	Q88579_thellex's e
87	21	21.9	12	2	Q88580_9PICO	Q88580_thellex's e
88	21	21.9	12	2	Q88581_9PICO	Q88581_thellex's e
89	21	21.9	13	2	Q88582_9PICO	Q88582_thellex's e
90	21	21.9	13	2	Q18890_ATBBE	Q18890_ateles belz
91	21	21.9	13	2	Q7M1A2_BACNO	Q7M1A2_bacteroides
92	21	21.9	14	2	Q6ZYT7_9CARY	Q6ZYT7_silene ural
93	21	21.9	14	2	Q7L622_ANNPL	Q7L622_aaes platyr
94	21	21.9	15	2	Q6ZYT6_9CARY	Q6ZYT6_silene ural
95	21	21.9	15	2	Q9S016_ORZSA	Q9S016_oryza sativ
96	21	21.9	16	1	Q9QV62_9MDRI	Q9QV62_mus sp. dif
97	21	21.9	16	1	KTRC_AREMA	P1317_arenicola m
98	21	21.9	16	2	Q44513_ANNVA	Q44513_anabaena va
99	21	21.9	17	2	Q14316_HUMAN	Q14316_homo sapien
100	21	21.9	17	2	Q7RQV2_PLAYO	Q7RQV2_plasmodium

ALIGNMENTS

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RESULT 1
SODF PASPI
ID SODF PASPI STANDARD; PRT; 20 AA.
AC P81527;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Superoxide dismutase [Fe] (BC 1.15.1.1) (Fragment).
GN NamesoB;
OS Pasteurella piscicida (Photobacterium damsela subsp. piscicida).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Vibrionales;
OC Vibrionaceae; Photobacterium.
OX NCBI_TaxID=38294;
RN [1]
RP PROTEIN SEQUENCE.
RC STRAIN=MT1415;
RC MEDLINE=99173752; PubMed=10075430;
RA Barnes A.C., Balebona M.C., Horne M.T., Ellis A.E.;
RT "Superoxide dismutase and catalase in Photobacterium damsela subsp.
RT piscicida and their roles in resistance to reactive oxygen species.";
RT Microbiology 145:483-494(1999).
CC -1- FUNCTION: Destroys radicals which are normally produced within the
CC cells and which are toxic to biological systems.
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2)O(2).
CC -1- COFACTOR: Binds 1 iron ion per subunit (By similarity).
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Periplasmic.
CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.
CC -----
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CC removed.
CC -----
CC HSP; P09157; IISC.
CC InterPro: IPR001189; SODismutase.
CC DR PANTHER: PTHR11404; SODismutase; 1.
CC Pfam: PF00081; Sod_Fe_N; 1.
CC Direct protein sequencing; Iron; Metal-binding; Oxidoreductase;
CC Periplasmic.
CC FT NON TER 20
CC SEQUENCE 20 AA; 2153 MW; A8D31FDA8553B6D CRC64;

Query Match 31.2%; Score 30; DB 1; Length 20;
Best Local Similarity 83.3%; Pred. No. 1.5e+03;
Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFEPH 6
DB 12 DALEPH 17

RESULT 2
07T190 CHICK PRELIMINARY; PRT; 17 AA.
ID 07T190;
AC 07T190;
DT 01-OCT-2003 (TREMBLrel. 25, Created)
DT 01-OCT-2003 (TREMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Tissue inhibitor of metalloproteinase 3 (Fragment).
GN Name-TIMP3;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RP MEDLINE=22873000; PubMed=14510686;
RX DOI=10.1046/j.1365-2052.2003.01050.x;

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RA Paton I.R., Smith J., Burt D.W.;
RT "Mapping the ABCA4, IMPDH2 and TIMP3 genes in chicken.";
RL Anim. Genet. 34:395-396(2003).
DR EMBL; AY326267; AAF9480.1; -; Genomic_DNA.
DR GO; GO:0005578; C:extracellular matrix (sensu Metazoa); IEA.
DR GO; GO:0008191; F:metalloendopeptidase inhibitor activity; IEA.
DR InterPro; IPR001820; Prot_inh_TIMP.
DR PANTHER; PTHR1844; Prot_inh_TIMP; 1.
DR Pfam; PF00965; TIMP; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2030 MW; DA8D6B493259F1F3 CRC64;

Query Match 30.2%; Score 29; DB 2; Length 17;
Best Local Similarity 54.5%; Pred. No. 1.9e+03;
Matches 6; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 8 YLTTAASP GK 18
DB 6 YLITGRVTEGK 16

RESULT 3
086865 YVIRU PRELIMINARY; PRT; 15 AA.
ID 086865;
AC 086865;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE LCMV viral protein protein (Fragment).
GN Name-LCMV viral protein;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
OX NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidis D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
RT choriomeningitis virus.";
RT J. Virol. 69:2187-2193(1995).
DR EMBL; S75741; AAB33667.1; -; mRNA.
FT NON_TER 15
SQ SEQUENCE 15 AA; 1599 MW; 2D3720F4F776C1A7 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 15;
Best Local Similarity 62.5%; Pred. No. 2.4e+03;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 4 EPHGYLT 11
DB 6 DPGGYCLT 13

RESULT 4
07M2X3 BOVIN PRELIMINARY; PRT; 20 AA.
ID 07M2X3;
AC 07M2X3;
DT 01-MAR-2004 (TREMBLrel. 26, Created)
DT 01-MAR-2004 (TREMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Collagen alpha 5(IV) chain (Fragment).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;
OC Pecora; Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP PROTEIN SEQUENCE.
RP PubMed=1869555;
RA Gunwar S., Ballesster F., Kalluri R., Timoneda J., Chonko A.M.,
RA Edwards S.J., Noelken M.E., Hudson B.G.;

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RT "Glomerular basement membrane. Identification of dimeric subunits of
RT the noncollagenous domain (hexamer) of collagen IV and the Goodpasture
RT antigen."
RL J. Biol. Chem. 266:15318-15324 (1991).

DR FJR, E39419, E39419.
FT NON_TER 1
FT NON_TER 20
SQ SEQUENCE 20 AA; 2050 MW; 384855916F0939C8 CRC64;

Query Match 29.2%; Score 28; DB 2; Length 20;
Best Local Similarity 66.7%; Pred. No. 3.3e+03;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVLIT 11
DB 10 HGFLIT 15

RESULT 5
021922_9CAUD PRELIMINARY; PRT; 16 AA.

ID 021922_021923;
AC 021922; 021923;
DT 01-JAN-1998 (TrEMBLrel. 05, Created)
DT 01-JAN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Integrase (Fragment).

GN NameInt;
OS Streptococcus thermophilus bacteriophage Sf121.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Siphoviridae.
NCBI_TaxID=64186;

RN NUCLEOTIDE SEQUENCE.
RX MEDLINE=98008989; PubMed=9344917; DOI=10.1006/viro.1997.8769;
RA Brutin A., Foley S., Brusow H.;

RT "The site-specific integration system of the temperate Streptococcus
RT thermophilus bacteriophage phfSf121."
RL Virology 237:148-158 (1997).

DR EMBL, AF013584; AAC48909.1; -; Genomic DNA.
EMBL, AF013587; AAC48910.1; -; Genomic DNA.
FT NON_TER 1
SQ SEQUENCE 16 AA; 1856 MW; 8FA82D3270B9A959 CRC64;

Query Match 28.1%; Score 27; DB 2; Length 16;
Best Local Similarity 57.1%; Pred. No. 3.8e+03;
Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFEPHG 7
DB 10 NALKPHG 16

RESULT 6
09UC80_HUMAN PRELIMINARY; PRT; 19 AA.

ID 09UC80_HUMAN PRELIMINARY;
AC 09UC80;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
DE 21.5 kDa stone matrix protein (SC 1.15.1.1) (Superoxide dismutase
DE (Mn/Fe) (Fragment)).

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.

NCBI_TaxID=9606;
RN [1]

RP PROTEIN SEQUENCE.
RA Binette J.P., Binette M.B.;

RT "Sequencing of proteins extracted from stones."
RL Submitted (JUL-1995) to the EMBL/GenBank/DBD databases.

CC -1- FUNCTION: Destructive radicals which are normally produced within the
CC cells and which are toxic to biological systems (By similarity).
CC -1- CATALYTIC ACTIVITY: 2 superoxide + 2 H(+) = O(2) + H(2O(2)).

CC -1- SIMILARITY: Belongs to the iron/manganese superoxide dismutase
CC family.

DR HSP; P09223; 1D70.
DR GO; GO:0046872; F:metal ion binding; IEA.
DR GO; GO:0016491; F:oxidoreductase activity; IEA.
DR GO; GO:0004784; F:superoxide dismutase activity; IEA.
DR GO; GO:0006801; P:superoxide metabolism; IEA.
DR InterPro: IPR001189; SODismutase.
DR Pfam: PF00081; Sod_Fe_N; 1.
KW Oxidoreductase.

SQ SEQUENCE 19 AA; 2116 MW; A0D0DAB848E87894 CRC64;

Query Match 28.1%; Score 27; DB 2; Length 19;
Best Local Similarity 66.7%; Pred. No. 4.5e+03;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 DAFEPH 6
DB 12 DALQPH 17

RESULT 7
07M4S4_HUMAN PRELIMINARY; PRT; 20 AA.

ID 07M4S4_HUMAN PRELIMINARY;
AC 07M4S4;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granulocyte inhibitory protein.

OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.

NCBI_TaxID=9606;
RN [1]

RP PROTEIN SEQUENCE.
RA Hoeft W.H., Haeg-Weber M., Georgopoulos A., Block L.H.;

RT "Physicochemical characterization of a polypeptide present in uremic
RT serum that inhibits the biological activity of polymorphonuclear
RT cells."
RL Proc. Natl. Acad. Sci. U.S.A. 87:6353-6357 (1990).

RN [2]
RP PROTEIN SEQUENCE.

RX PubMed=2385596;
RA Hoeft W.H., Haeg-Weber M., Georgopoulos A., Block L.H.;

RT "Physicochemical characterization of a polypeptide present in uremic
RT serum that inhibits the biological activity of polymorphonuclear
RT cells."
RL Proc. Natl. Acad. Sci. U.S.A. 87:6353-6357 (1990).
DR PIR; A36016; A36016.
DR HSP; P01625; IEK3.
SQ SEQUENCE 20 AA; 2046 MW; A13201D587F1EEB7 CRC64;

Query Match 28.1%; Score 27; DB 2; Length 20;
Best Local Similarity 62.5%; Pred. No. 4.8e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 11 TAVSPKG 18
DB 10 TLVSFPG 17

RESULT 8
047554_ECOLI PRELIMINARY; PRT; 19 AA.

ID 047554_ECOLI PRELIMINARY;
AC 047554;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Colicin A (Fragment).

OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

```
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93339568; PubMed=7687969; DOI=10.1016/0378-1097(93)90042-Z;
RA Gell V., Llobes R., Zaai S.A.U., Van Spaendonk R.M.L., Rollin C.,
  Benedetti H., Lazdunski C.;
RT "Recognition of the colicin A N-terminal epitope ICI1 in vitro and in
  vivo in Escherichia coli by its cognate monoclonal antibody.";
RL FEMS Microbiol. Lett. 109:335-342(1993).
DR EMBL, X73248; CAA51711.1; -, Genomic_DNA.
KW plasmid.
FT NON TER
SQ SEQUENCE 19 AA; 2082 MW; B1D35A74B858881A CRC64;

Query Match 27.6%; Score 26.5; DB 2; Length 19;
Best Local Similarity 46.7%; Pred. No. 5.5e+03;
Matches 7; Conservative 0; Mismatches 5; Indels 3; Gaps 1;

QY 6 HGVL--TAVSPG 17
DB 2 HGRYLRACVDPG 16

RESULT 9
O53183 RHOSO PRELIMINARY; PRT; 12 AA.
ID O53183;
AC O53183;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Beta-subunit of nitrite hydratase (Fragment).
OS Rhodococcus sp.
OC Bacteria; Actinobacteria; Actinomycetales;
OC Corynebacteriaceae; Nocardiaceae; Rhodococcus.
OX NCBI_TaxID=1831;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=N-774;
RX MEDLINE=95072315; PubMed=7765511;
RA Hashimoto Y., Nishiyama M., Horiuchi S., Beppu T.;
RT "The nitrite hydratase gene from Rhodococcus sp. N-774 requires its
  downstream region for efficient expression.";
RL Biotech. Biochem. 58:1859-1865(1994).
DR EMBL, D30033; BAA06273.1; -, Genomic_DNA.
DR GO; GO:0018822; F:nicotinic hydratase activity; IEA.
DR GO; GO:0006807; P:nitrogen compound metabolism; IEA.
DR InterPro; IPR003168; NHase, beta.
DR Pfam; PF02211; NHase_beta; 1.
FT NON TER
SQ SEQUENCE 12 AA; 1323 MW; 7A5DEF7D993B587B CRC64;

Query Match 27.1%; Score 26; DB 2; Length 12;
Best Local Similarity 61.5%; Pred. No. 4.1e+03;
Matches 8; Conservative 0; Mismatches 3; Indels 2; Gaps 1;

QY 1 DAFPHGYLTAA 13
DB 2 DLFE--GYLEPA 12

RESULT 10
Q86867 SVIRU PRELIMINARY; PRT; 15 AA.
ID Q86867;
AC Q86867;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE S-RNA product protein (Fragment).
GN Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
```

```
OX NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidde D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
  choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL, S75749; AAB33670.1; -, mRNA.
FT NON TER
SQ SEQUENCE 15 AA; 1598 MW; 2D3F82F4F776C1A7 CRC64;

Query Match 27.1%; Score 26; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 5.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYCLT 11
DB 7 PGYCLT 13

RESULT 11
Q86869 SVIRU PRELIMINARY; PRT; 15 AA.
ID Q86869;
AC Q86869;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE S-RNA product protein (Fragment).
GN Name=S-RNA product;
OS Lymphocytic choriomeningitis virus.
OC Viruses; ssRNA negative-strand viruses; Arenaviridae; Arenavirus;
OC Old world arenaviruses.
OX NCBI_TaxID=11623;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=95190990; PubMed=7533851;
RA Moskopidde D., Zinkernagel R.M.;
RT "Immunobiology of cytotoxic T-cell escape mutants of lymphocytic
  choriomeningitis virus.";
RL J. Virol. 69:2187-2193(1995).
DR EMBL, S75753; AAB33673.1; -, mRNA.
DR InterPro; IPR001535; Arena_glycoprot.
DR Pfam; PF00798; Arena_glycoprot; 1.
FT NON TER
SQ SEQUENCE 15 AA; 1571 MW; 2D25ABF4F776C1A7 CRC64;

Query Match 27.1%; Score 26; DB 2; Length 15;
Best Local Similarity 71.4%; Pred. No. 5.2e+03;
Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYCLT 11
DB 7 PGYCLT 13

RESULT 12
UC16 MAIZE STANDARD; PRT; 15 AA.
ID UC16 MAIZE;
AC P80622;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Unknown protein from 2D-PAGE of etiolated coleoptile (Spot 308)
  (Fragment).
OS Zea mays (Maize).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC PACCAD clade; Panicoideae; Andropogoneae; Zea.
OX NCBI_TaxID=4577;
RN [1]
RP PROTEIN SEQUENCE.
RC TISSUE=Coleoptile;
```

RA Touzet P., Riccardi F., Morin C., Dameray C., Huet J.-C.,
 RA Pernot J.-C., Zivy M., de Vienne D.,
 RT "The maize two dimensional gel protein database: towards an integrated
 RT genome analysis program."
 RL Theor. Appl. Genet. 93:997-1005(1996).
 CC -1- MISCELLANEOUS: On the 2D-gel the determined pI of this unknown
 CC protein is: 5.9, its MW is: 18.6 kDa.

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 CC Maize-2DPAGE; P80622; COLEOPTILE.
 DR Gramene; P80622; -.
 DR MaizeDB; 123948; -.
 KW Direct protein sequencing.
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 1796 MW; D3JA518F7440BE7 CRC64;

 QY Query Match 26.0%; Score 25; DB 1; Length 15;
 Db Best Local Similarity 62.5%; Pred. No. 7.5e+03;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 10 LTPAVSP 17
 Db 8 VTAFAVEPG 15

 RESULT 13
 Q71UK9 HALCO
 ID Q71UK9 HALCO PRELIMINARY; PRT; 15 AA.
 AC Q71UK9;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE Lyalin (Fragment).
 OS Halictis corrugata (Pink abalone).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Orthogastropoda;
 OC Vetigastropoda; Halictoidae; Halictidae; Halictis.
 OX NCBI_TaxID=6453;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA MEDLINE=98333704; PubMed=9724763; DOI=10.1073/pnas.95.18.10676;
 RA Metz B.C., Robles-Sikisaka R., Vacquier V.D.;
 RT "Nonymymous substitution in abalone sperm fertilization genes
 RT exceeds substitution in introns and mitochondrial DNA."
 RL Proc. Natl. Acad. Sci. U.S.A. 95:10676-10681(1998).
 DR EMBL; AF076830; AAC33932.1; -; genomic_DNA.
 FT NON TER 1 1
 FT NON TER 15 15
 SQ SEQUENCE 15 AA; 2083 MW; 3168BDCD2921B6D CRC64;

 QY Query Match 26.0%; Score 25; DB 2; Length 15;
 Db Best Local Similarity 57.1%; Pred. No. 7.5e+03;
 Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

 QY 3 FBPHGYL 9
 Db 6 FIPHKYI 12

 RESULT 14
 Q9JHM3 RAT
 ID Q9JHM3 RAT PRELIMINARY; PRT; 16 AA.
 AC Q9JHM3;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
 DE MHC class I antigen (Fragment).
 GN Name=Rtl;

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=LEW;
 RX MEDLINE=20424521; PubMed=10970104; DOI=10.1007/s002510000201;
 RA Lambrecht-Washington D., Fischer Lindahl K., Womigelt K.;
 RT "Promoter structures suggest independent translocations of ancestral
 RT rat Rtl A and mouse H2-K class I genes."
 RL Immunogenetics 51:873-877(2000).
 DR EMBL; AF210330; AAF74411.1; -; genomic_DNA.
 FT NON TER 16 16
 FT NON TER 16 16
 SQ SEQUENCE 16 AA; 1635 MW; 647FF5119E02977D CRC64;

 QY Query Match 26.0%; Score 25; DB 2; Length 16;
 Db Best Local Similarity 62.5%; Pred. No. 8.1e+03;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

 QY 9 LTPAVSP 16
 Db 9 LWAALAP 16

 RESULT 15
 Q9HEQ1 PARBR
 ID Q9HEQ1 PARBR PRELIMINARY; PRT; 17 AA.
 AC Q9HEQ1;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Alpha-tubulin (Fragment).
 GN Name=TUB1;
 OS Paracoccidioides brasiliensis.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
 OC Oryziales; Mucorales; Paracoccidioides.
 OX NCBI_TaxID=121759;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=PB18;
 RA Kasuga T., White T.J., Taylor J.W.;
 RT "The molecular clock in fungi in the class Plecomycetes."
 RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY013314; AAG40955.1; -; genomic_DNA.
 DR GO; GO:0005874; C:microtubule; IEA.
 DR GO; GO:0005198; F:structural molecule activity; IEA.
 DR GO; GO:0007018; F:microtubule-based movement; IEA.
 DR Interpro; IPR002452; Alpha_tubulin.
 DR PANTHER; PTHR11588:SP1; Alpha_tubulin; 1.
 FT NON TER 1 1
 FT NON TER 17 17
 SQ SEQUENCE 17 AA; 2039 MW; B8E787547655F90A CRC64;

 QY Query Match 26.0%; Score 25; DB 2; Length 17;
 Db Best Local Similarity 66.7%; Pred. No. 8.6e+03;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

 QY 4 EPHGYL 9
 Db 12 QPDGYL 17

 RESULT 16
 Q9HEQ2 AJRDE
 ID Q9HEQ2 AJRDE PRELIMINARY; PRT; 17 AA.
 AC Q9HEQ2;
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Alpha-tubulin (Fragment).
 GN Name=TUB1;

```

OS Afellomyces dermatitidis (Blastomyces dermatitidis).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Afellomycetaceae; Afellomyces.
OK NCBI_TaxID=5039;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC60915;
RA Kaesga T., White T.J., Taylor J.W.;
RT "The molecular clock in fungi in the class Plecomycetes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013313; AAG40954.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002452; Alpha_tubulin.
DR PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2039 MW; E8E787547655F90A CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 2; Length 17;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 EPHGYL 9
DB 12 QPDGYL 17

RESULT 17
ID Q9HEQ3 AJECA PRELIMINARY; PRT; 17 AA.
AC Q9HEQ3
DT 01-MAR-2001 (TrEMBLrel. 16, Created)
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Alpha-tubulin (Fragment).
GN Name=TRUB1;
OS Afellomyces capsulata (Histoplasma capsulatum).
OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
OC Onygenales; Afellomycetaceae; Afellomyces.
OX NCBI_TaxID=5037;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=ATCC26032;
RA Kaesga T., White T.J., Taylor J.W.;
RT "The molecular clock in fungi in the class Plecomycetes.";
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY013312; AAG40953.1; -; Genomic_DNA.
DR GO; GO:0005874; C:microtubule; IEA.
DR GO; GO:0005198; P:structural molecule activity; IEA.
DR GO; GO:007018; P:microtubule-based movement; IEA.
DR InterPro; IPR002452; Alpha_tubulin.
DR PANTHER; PTHR11588:SF1; Alpha_tubulin; 1.
FT NON_TER 1
FT NON_TER 17
SQ SEQUENCE 17 AA; 2039 MW; E8E787547655F90A CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 2; Length 17;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 4 EPHGYL 9
DB 12 QPDGYL 17

RESULT 18
ID Q4Z3U7 PLABE PRELIMINARY; PRT; 19 AA.
AC Q4Z3U7
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)

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DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB101818.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OK NCBI_TaxID=5821;
RN (1)
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlson J.M., Kooij T.W.A.,
RA Bertman M., Florens L., Jansen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Omond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jansz C.J., Barrett B., Turner C.M.R., Waters A.P., Sindén R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -! CAUTION: The sequence shown here is derived from an
EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
preliminary data.
CC EMBL; CA101000743; CAH5036.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 19 AA; 2375 MW; C416C96CE878PAD3 CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 2; Length 19;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGVL 9
DB 2 HGVL 5

RESULT 19
ID VMO2 CHICK STANDARD; PRT; 20 AA.
AC Q9P649;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Vitelline membrane outer layer protein II (VMO-II) (Fragment).
OC Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN (1)
RP PROTEIN SEQUENCE.
RC TISSUE=Egg yolk;
RC MEDLINE=92392373; PubMed=1520265;
RA Kido S., Morimoto A., Kim F., Doi Y.;
RT "Isolation of a novel protein from the outer layer of the vitelline
membrane.";
RL Biochem. J. 286:17-22(1992).
CC -! FUNCTION: Exact function not known, component of the outer
membrane of the vitelline layer of the egg.
CC -! PTM: All cysteine residues of the mature protein are involved in
disulfide bonds.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
between the Swiss Institute of Bioinformatics and the EMBL outstation -
the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.
CC -----
CC PIR; S23981; S23981.
CC Direct protein sequencing.
FT NON_TER 20
FT NON_TER 20
SQ SEQUENCE 20 AA; 2327 MW; 45FC7989AB7527C7 CRC64;

Query Match
Best Local Similarity 26.0%; Score 25; DB 1; Length 20;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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Matches 4; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

QY 6 HGXYLTAAY 14
 ||| : :
 Db 12 HGXYIRSKV 20

RESULT 20

Q8W61 HUMAN

ID Q8W61 HUMAN PRELIMINARY; PRT; 20 AA.

AC Q8W61; 08W61;

DT 01-MAR-2002 (TREMBlrel. 20, Created)

DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)

DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)

DE C10orf118 protein (Fragment).

GN NameC10orf118;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;

OC Homo.

OC NCBI_Taxid=9606;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G., Schuler G.D.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Mullaly S.J.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,

RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Liver;

RA Strausberg R.L.

RA Buterfield Y.S.N. to the EMBL/GenBank/DBJ databases.

RA EMBL; BC020842; AAH20842.1; -; mRNA.

FT NON_TER 1 1

SQ SEQUENCE 20 AA; 1979 MW; EA861D9AF6E26F10 CRC64;

QY 1 DAFPHGYLTAAY 13
 ||| : :
 Db 7 DVSAPGPGFETAA 19

RESULT 21

Q9TWL3 BOMMO

ID Q9TWL3 BOMMO PRELIMINARY; PRT; 20 AA.

AC Q9TWL3;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)

DE INITIATORIN (Fragment).

OS Bombyx mori (Silk moth).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditytata; Bombycoidea;

RP PROTEIN SEQUENCE.

RX MEDLINE=95218779; PubMed=7703988; DOI=10.1016/0965-1748(94)90134-1;

RA Aigaki T., Kasuga H., Nagaoka S., Osana M.,

RT "Purification and partial amino acid sequence of initiator, a

RT prostatic endopeptidase of the silkworm, Bombyx mori."

RT Insect Biochem. Mol. Biol. 24:969-975(1994).

SQ SEQUENCE 20 AA; 2205 MW; 8B8047E96CFE1BA CRC64;

QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18

RESULT 22

Q99JV2 MOUSE

ID Q99JV2 MOUSE PRELIMINARY; PRT; 20 AA.

AC Q99JV2;

DT 01-JUN-2001 (TREMBlrel. 17, Created)

DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)

DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)

DE Cank protein (Fragment).

GN Name=Cank;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;

OC Muridae; Murinae; Mus.

OC NCBI_Taxid=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;

RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,

RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalón D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

RA Fahy J., Helton E., Ketterman M., Madan A., Rodriguez S., Sanchez A.,

RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smalhus D.E.,

RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.,

RT "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

RL [2]

RN NUCLEOTIDE SEQUENCE.

RC STRAIN=FVB/N; TISSUE=Mammary tumor. C3;

RG NIH MGC Project;

RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.

DR MGI; BC005653; AAH05653.1; -; mRNA.

DR MGI; MGI:107461; Cank.

DR GO; GO:0005615; C:extracellular space; TMS.

FT NON_TER 1 1

SQ SEQUENCE 20 AA; 2223 MW; F203F6A80A7A0429 CRC64;

QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
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 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18QY 5 PHGYLTAAY 14
 ||| : :
 Db 9 PHSPMTVAI 18

QY 9 LTTAAVSPGK 18
: ||| |||
DB 1 VPSAARPGK 10

RESULT 23

06LC78_RAT PRELIMINARY; PRT; 10 AA.
AC 06LC78_1
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE P120/ecto-ATPase (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=96224094; PubMed=8621519; DOI=10.1074/jbc.271.15.8809;
RA Najjar S.M., Boisclair Y.R., Nabih Z.T., Philippe N., Imai Y.,
RA Suzuki Y., Suh D.S., Ooi G.T.;
RT "Cloning and characterization of a functional promoter of the rat
RT p120 gene, encoding a substrate of the insulin receptor tyrosine
RT kinase.";
RL J. Biol. Chem. 271:8809-8817(1996).
DR EMBL; U27208; AAB05593.1; -; Genomic_DNA.
FT NON_TER 1 10
SQ SEQUENCE 10 AA; 1001 MW; 438CBG35BDC1A727 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 10;
Best Local Similarity 62.5%; Pred. No. 7.2e+03;
Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLTTAAV 14
: ||| |||
DB 1 GLLTAAV 8

RESULT 24
005328_9SPHN PRELIMINARY; PRT; 12 AA.
AC 005328_1
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Catechol 2,3-dioxygenase (Fragment).
GN Name=phnB;
OS Sphingomonas chungbukensis.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Sphingomonadales;
OC Sphingomonadaceae; Sphingomonas.
OX NCBI_TaxId=56193;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DJ77;
RX MEDLINE=97242176; PubMed=9125165; DOI=10.1006/bbrc.1997.6279;
RA Shin H.J., Kim S.J., Kim Y.C.;
RT "Sequence analysis of the phnD gene encoding 2-hydroxymuconic
RT semialdehyde hydrolase in Pseudomonas sp. strain DJ77.";
RL Biochem. Biophys. Res. Commun. 232:288-291(1997).
DR EMBL; U83881; AAC45092.1; -; Genomic_DNA.
DR GO; GO:0016702; F:oxidoreductase activity, acting on single d. .; IEA.
KW Dioxxygenase.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1277 MW; 2981743D4D0042C8 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 12;
Best Local Similarity 50.0%; Pred. No. 8.7e+03;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 10 LTTAAVSPG 17
: ||| |||
DB 3 LTGVIRPG 10

RESULT 25

047335_ECOLI PRELIMINARY; PRT; 14 AA.
AC 047335_1
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE KdsA methyltransferase (kasugamycin sensitivity).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=88107880; PubMed=3122846; DOI=10.1016/0300-9084(87)90210-0;
RX van Gemen B., Koels H.J., Plooy C.A.M., Bodlaender J.,
RA van Knippenberg P.H.;
RT "Characterization of the kdsA gene of Escherichia coli determining
RT kasugamycin sensitivity.";
RL Biochimie 69:841-848(1987).
DR EMBL; X06536; CAA29785.1; -; Genomic_DNA.
DR PIR; S00843; S00843.
DR GO; GO:0008168; P:methyltransferase activity; IEA.
DR GO; GO:0016740; P:transferase activity; IEA.
KW Methyltransferase; Transferase.
SQ SEQUENCE 14 AA; 1571 MW; 670799ABR3D70D14 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 1e+04;
Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LTTAAVSPGK 18
: ||| |||
DB 5 LTRRLSPGK 14

RESULT 26
07M2K5_RABIT PRELIMINARY; PRT; 15 AA.
AC 07M2K5_1
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Phosphoglucosyltransferase (EC 5.4.2.2) (Fragment).
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OX NCBI_TaxId=9986;
RN [1]
RP PROTEIN SEQUENCE.
RX MEDLINE=90282481; PubMed=2162150;
RA Marchase R.B., Richardson K.L., Strihsman C., Drake R.R., Haley B.E.;
RT "Resolution of phosphoglucosyltransferase and the 62-kDa acceptor for the
RT glucosylphosphotransferase.";
RL Arch. Biochem. Biophys. 280:122-129(1990).
DR PIR; S10741; S10741.
DR GO; GO:0004614; P:phosphoglucosyltransferase activity; IEA.
FT NON_TER 15 15
SQ SEQUENCE 15 AA; 1452 MW; 8252201C5D34C0C4 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 15;
Best Local Similarity 50.0%; Pred. No. 1.1e+04;
Matches 5; Conservative 2; Mismatches 3; Indels 0; Gaps 0;

Db 4 GILLTASHMP 13

RESULT 27

077489_TUPGL PRELIMINARY; PRT; 16 AA.
 AC 077489;
 DT 01-NOV-1998 (TReMBLrel. 08, Created)
 DT 01-NOV-1998 (TReMBLrel. 08, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE D4 dopamine receptor (D4DR) (Fragment).
 OS Tupia glis (Tree shrew).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Scandentia; Tupaiidae; Tupia.
 NCBI_TaxID=9395;
 RX [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Inoue-Murayama M., Takenaka O., Murayama Y.;
 RT "origin and divergence of tandem repeats of primate D4 dopamine
 receptor genes";
 RL Primates 39:217-224(1998).
 DR EMBL; AB016198; BAA32036.1; -; Genomic_DNA.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KW Receptor.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 16 AA; 1577 MW; 3865ABE77FB63E09 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 16;
 Best Local Similarity 66.7%; Pred. No. 1.2e+04;
 Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPH 6
 DB 8 DPEGPH 13

RESULT 28

056385_9CYAN PRELIMINARY; PRT; 16 AA.
 AC 056385;
 DT 10-MAY-2005 (TReMBLrel. 30, Created)
 DT 10-MAY-2005 (TReMBLrel. 30, Last sequence update)
 DT 10-MAY-2005 (TReMBLrel. 30, Last annotation update)
 DE Cpca (Fragment).
 OS uncultured Cyanobacterium.
 OC Bacteria; Cyanobacteria; environmental samples.
 NCBI_TaxID=1211;
 RX [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Kim S.-G., Rhee S.-K., Ahn C.-Y., Bae J.-W., Park Y.-H., Oh H.-M.;
 RT "Profiling cyanobacterial abundance and diversity based on cpba
 sequences during bloom in Daechung Reservoir, Korea.";
 RL Submitted (FEB-2005) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY942913; AAK82532.1; -; Genomic_DNA.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 16 AA; 1575 MW; F70724E0948D995A CRC64;

Query Match 25.0%; Score 24; DB 2; Length 16;
 Best Local Similarity 62.5%; Pred. No. 1.2e+04;
 Matches 5; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LITAAVPG 17
 DB 9 VSAADSPG 16

RESULT 29

086WJ4_HUMAN PRELIMINARY; PRT; 18 AA.
 AC 086WJ4;
 DT 01-JUN-2003 (TReMBLrel. 24, Created)

DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)

DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)

DE Cyclin-dependent kinase inhibitor (Fragment).

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;

OC Homo.

NCBI_TaxID=9606;

RX [1]

RN NUCLEOTIDE SEQUENCE.

RC TISSUE=Heart;

RA Balda G., Pomyskala H., Olopade O.I.;

RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF488410; AA049471.1; -; mRNA.

DR HSSP; P55271; ID95.

DR GO; GO:0016301; F:Kinase activity; IEA.

KW Cyclin; Kinase.

FT NON_TER

FT NON_TER

SQ SEQUENCE 18 AA; 2003 MW; AD99FCC7D27538E7 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 18;
 Best Local Similarity 83.3%; Pred. No. 1.3e+04;
 Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 7 GYLTA 12
 DB 10 GYLTA 15

RESULT 30

08TDB3_HUMAN PRELIMINARY; PRT; 19 AA.
 AC 08TDB3;
 DT 01-JUN-2002 (TReMBLrel. 21, Created)
 DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)
 DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
 DE Transhyretin amyloidosis variant A1205 (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
 OC Homo.
 NCBI_TaxID=9606;
 RX [1]
 RN NUCLEOTIDE SEQUENCE.
 RA Booth D., Byde A., Peys M., Hawkins P.;
 RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF485252; AAL92041.1; -; Genomic_DNA.
 DR HSSP; P02766; 1P41.
 DR GO; GO:0005386; F:carrier activity; IEA.
 DR GO; GO:0005496; F:steroid binding; IEA.
 DR GO; GO:0006810; P:transport; IEA.
 DR InterPro; IPR000895; Transhyretin.
 DR Pfam; PF00576; Transhyretin; 1.
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 19 AA; 1988 MW; F564E31C43209399 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 19;
 Best Local Similarity 36.4%; Pred. No. 1.4e+04;
 Matches 4; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 5 PHGYLTA 15
 DB 8 PYSYSTSVVT 18

RESULT 31

09PRY1_TORCA PRELIMINARY; PRT; 20 AA.
 AC 09PRY1;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)

```

DE AGRIN receptor 190 kDa SUBUNIT-ALPHA-dystroglycan homolog
DE (Fragment)
OC Torpedo californica (Pacific electric ray).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Chondrichthyes;
OC Elasmobranchii; Squalea; Hypnosqualea; Pristigaster; Batoidae;
OC Torpediniformes; Torpedinidae; Torpedinidae; Torpedo.
OX NCBI_TaxID=787;
(1)
RP PROTEIN SEQUENCE.
RX MEDLINE=94242436; PubMed=8185951; DOI=10.1016/0896-6273(94)90324-7;
RA Bove M.A., Deyat K.A., Leszyk J.D., Fallon J.R.;
RT "Identification and purification of an agrin receptor from Torpedo
RT postsynaptic membranes: a heteromeric complex related to the
RT dystroglycans";
RL Neuron 12:1173-1180 (1994).
FT NON_TER 1 1
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2239 MW; 038622F02D189F90 CRC64;

Query Match 25.0%; Score 24; DB 2; Length 20;
Best Local Similarity 41.7%; Pred. No. 1.5e+04;
Matches 5; Conservative 1; Mismatches 6; Indels 0; Gaps 0;

QY 6 HGILTAAVSPG 17
DB 1 HEYFMAAYKKG 12

RESULT 32
Q7M1V9 LYCES
ID Q7M1V9 LYCES PRELIMINARY; PRT; 16 AA.
AC Q7M1V9;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE Multicystatin (Fragment).
OS Lycopericon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids;
OC Lamiales; Solanales; Solanaceae; Solanum; Lycopersicon.
OX NCBI_TaxID=4081;
(1)
RP PROTEIN SEQUENCE.
RA Jacinto T., Fernandes K.V.S., Machado O.L.T., Siqueira-Junior C.L.;
RT "Leaves of transgenic tomato plants overexpressing proycsteinin
RT accumulate high levels of cystatin.";
RL Plant Sci. 138:35-42 (1998).
DR PIR; A59155; A59155.
FT NON_TER 1 1
FT NON_TER 16 16
SQ SEQUENCE 16 AA; 1789 MW; CAF40110AD660AB9 CRC64;

Query Match 24.5%; Score 23.5; DB 2; Length 16;
Best Local Similarity 50.0%; Pred. No. 1.4e+04;
Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 8 YLLT-AAVSPGK 18
DB 1 YITFPAATDAGK 12

RESULT 33
Q9UCG2 HUMAN
ID Q9UCG2 HUMAN PRELIMINARY; PRT; 19 AA.
AC Q9UCG2;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE Pre-alpha 2-plasmin inhibitor (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.

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OX NCBI_TaxID=9606;
(1)
RP PROTEIN SEQUENCE.
RX MEDLINE=93243387; PubMed=8484741;
RA Bangert K., Johnson A.H., Christensen U., Thorsen S.;
RT "Different N-terminal forms of alpha 2-plasmin inhibitor in human
RT plasma.";
RL Biochem. J. 291:623-625 (1993).
SQ SEQUENCE 19 AA; 2068 MW; 01F3298DD3141992 CRC64;

Query Match 24.5%; Score 23.5; DB 2; Length 19;
Best Local Similarity 44.4%; Pred. No. 1.7e+04;
Matches 8; Conservative 1; Mismatches 4; Indels 5; Gaps 1;

QY 4 EPHGYLTRA----VSP 16
DB 2 EPLGRQLTSGPNQEQVSP 19

RESULT 34
LSK1 LETUMA
ID LSK1 LETUMA STANDARD; PRT; 11 AA.
AC P04428;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Leucosulfakinin-1 (Leucosulfakinin-1) (LSK-1).
OS Leucophaea maderae (Maderia cockroach).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Orthopteroidea; Dictyoptera; Blattaria; Blaberioidea;
OC Blaberidae; Leucophaea.
OX NCBI_TaxID=6988;
(1)
RP PROTEIN SEQUENCE.
RX MEDLINE=86315858; PubMed=3749893;
RA Nachman R.J., Holman G.M., Haddon W.F., Ling N.;
RT "Leucosulfakinin, a sulfated insect neuropeptide with homology to
RT gastrin and cholecystokinin.";
RL Science 234:71-73 (1986).
CC -1- FUNCTION: Changes the frequency and amplitude of contractions of
CC the hinge. Inhibits muscle contraction of hindgut.
CC -1- SIMILARITY: Belongs to the gastrin/cholecystokinin family.
CC -----
CC This Swiss-Prot entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.
CC -----
DR PIR; A01622; GMBOL.
DR InterPro; IPR001651; Gastrin.
DR PROSITE; PS00259; GASTRIN; 1.
KW Amidation; Direct protein sequencing; Hormone; Sulfation.
FT MOD_RES 6 6
FT MOD_RES 11 11
FT MOD_RES 11 11
SQ SEQUENCE 11 AA; 1459 MW; 7E4B0680E865AAB CRC64;

Query Match 24.0%; Score 23; DB 1; Length 11;
Best Local Similarity 33.3%; Pred. No. 1.2e+04;
Matches 3; Conservative 4; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFEPHYGL 9
DB 1 EQFEDYGHM 9

RESULT 35
Q4YEX5 PLAB
ID Q4YEX5 PLAB PRELIMINARY; PRT; 12 AA.
AC Q4YEX5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

```

Hypothetical protein (Fragment).
 GN ORFNames=PB404919.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAI01005812; CAI03444.1; -; Genomic_DNA.
 KW Hypothetical protein.
 FT NON_TER
 SQ SEQUENCE 12 AA; 1389 MW; 9843P11441059D1 CRC64;
 Query Match 24.0%; Score 23; DB 2; Length 12;
 Best Local Similarity 50.0%; Pred. No. 1.3e+04;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 QY 4 EPHGYL 9
 Db 2 EPHGYL 7
 RESULT 36
 ADFB TENMO STANDARD; PRT; 13 AA.
 ID ADFB TENMO
 AC P83109;
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 10-OCT-2003 (Rel. 42, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Antidiuretic factor B (ADFB).
 OS Tenebrio molitor (Yellow mealworm).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Coleoptera; Polyphaga; Cucujiformia;
 OC Tenebrionidae; Tenebrion.
 ON NCBI_TaxID=70671;
 RN [1]
 RP PROTEIN SEQUENCE, FUNCTION, TISSUE SPECIFICITY, MASS SPECTROMETRY, AND
 RP SYNTHESIS.
 RC TISSUE=Head;
 RC MEDLINE=22465067; PubMed=12576082; DOI=10.1016/S0196-9781(02)00273-5;
 RA Rigenheer R.A., Wehert U.M., Nicolson S.W., Schoofs L., Schegg K.M.,
 RA Hull J.J., Schooley D.A.;
 RT "Isolation, identification and localization of a second beetle
 RT antidiuretic peptide."
 RL Peptides 24:27-34(2003).
 CC -1- FUNCTION: Inhibitor of fluid secretion by Malpighian tubules. Uses
 CC GMP as second messenger. May function as an antidiuretic hormone.
 CC -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Brain. Appears to be mainly expressed in two
 CC pairs of bilaterally symmetrical cells in the protocerebrum.
 CC -1- MASS SPECTROMETRY: MW=1560.33; METHOD=MALDI; RANGE=1-13;
 CC NOT-Ref.1.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 CC Direct protein sequencing: Hormone; Neuropeptide.
 KW EMBL/CAI01001600; CAH96718.1; -; Genomic_DNA.
 SQ SEQUENCE 13 AA; 1562 MW; 0240A4504B8A632B CRC64;

Query Match 24.0%; Score 23; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.4e+04;
 Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AFEPHG 8
 Db 5 SYKPHY 11
 RESULT 37
 Q9UDC6 HUMAN
 ID Q9UDC6 HUMAN PRELIMINARY; PRT; 13 AA.
 AC Q9UDC6;
 DT 01-MAY-2000 (TRENBEREL. 13, Created)
 DT 01-MAY-2000 (TRENBEREL. 13, Last sequence update)
 DT 01-JUN-2002 (TRENBEREL. 21, Last annotation update)
 DE ENDOTHELIUM-derived RELATING factor, nitric oxide synthase
 DE (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
 OC Homo.
 ON NCBI_TaxID=9606;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=93054573; PubMed=1385404;
 RA Janssens S.P., Simionchi A., Quettermous T., Bloch D.B., Bloch K.D.;
 RT "Cloning and expression of a cDNA encoding human endothelium-derived
 RT relating factor/nitric oxide synthase."
 RL J. Biol. Chem. 267:22694-22694(1992).
 FT NON_TER
 FT NON_TER
 SQ SEQUENCE 13 AA; 1390 MW; 3231B6DFEC7EB867 CRC64;
 Query Match 24.0%; Score 23; DB 2; Length 13;
 Best Local Similarity 66.7%; Pred. No. 1.4e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 QY 2 AFEPHG 7
 Db 2 AFDPGP 7
 RESULT 38
 Q4Y227 PLABE
 ID Q4Y227 PLABE PRELIMINARY; PRT; 16 AA.
 AC Q4Y227;
 DT 13-SEP-2005 (TRENBEREL. 31, Created)
 DT 13-SEP-2005 (TRENBEREL. 31, Last sequence update)
 DT 13-SEP-2005 (TRENBEREL. 31, Last annotation update)
 DE Hypothetical protein.
 GN ORFNames=PB103937.00.0;
 OS Plasmodium berghei.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_TaxID=5821;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Hall N., Karrae M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
 RA Barriman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
 RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
 RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
 RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
 RA Jense C.J., Barrrell B., Turner C.M.R., Waters A.P., Sinden R.S.;
 RT "A comprehensive survey of the Plasmodium life cycle by genomic,
 RT transcriptomic, and proteomic analyses."
 RL Science 307:82-86(2005).
 CC -1- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL/CAI01001600; CAH96718.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 16 AA; 2063 MW; 22B78003D41CB8FD CRC64;

Query Match 24.0%; Score 23; DB 2; Length 16;
Best Local Similarity 80.0%; Pred. No. 1.7e+04;
Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 6 HGYL 10
|
|
|
|
Db 8 HNYL 12

RESULT 39

Q6R9U8_HUMAN
AC Q6R9U8; PRT; 17 AA.
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Microcephalin (Fragment).
GN Name=MCPhl;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX PubMed=15056608; DOI=10.1093/hmg/ddh127;
RA Wang Y.O., Su B.;
RT "Molecular evolution of microcephalin, a gene determining human brain
RT size.";
RT Hum. Mol. Genet. 13:1131-1137(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Wang Y., Su B.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY506298; AAS88661.1; -; Genomic DNA.
DR EMBL; AY506299; AAS88662.1; -; Genomic DNA.
DR EMBL; AY506300; AAS88663.1; -; Genomic DNA.
DR EMBL; AY506304; AAS88667.1; -; Genomic DNA.
DR EMBL; AY506307; AAS88670.1; -; Genomic DNA.
DR EMBL; AY506308; AAS88671.1; -; Genomic DNA.
DR EMBL; AY506309; AAS88672.1; -; Genomic DNA.
DR EMBL; AY506311; AAS88674.1; -; Genomic DNA.
DR EMBL; AY506312; AAS88675.1; -; Genomic DNA.
DR EMBL; AY506314; AAS88677.1; -; Genomic DNA.
DR EMBL; AY506315; AAS88678.1; -; Genomic DNA.
DR EMBL; AY506316; AAS88679.1; -; Genomic DNA.
DR EMBL; AY506317; AAS88680.1; -; Genomic DNA.
DR EMBL; AY506318; AAS88681.1; -; Genomic DNA.
DR EMBL; AY506320; AAS88683.1; -; Genomic DNA.
DR EMBL; AY506321; AAS88684.1; -; Genomic DNA.
DR EMBL; AY506327; AAS88689.1; -; Genomic DNA.
DR EMBL; AY506328; AAS88691.1; -; Genomic DNA.
DR EMBL; AY506330; AAS88693.1; -; Genomic DNA.
DR EMBL; AY506294; AAS88657.1; -; Genomic DNA.
FT NON TER 1
SQ SEQUENCE 17 AA; 1931 MW; 7364BAF1C785E59 CRC64;

Query Match 24.0%; Score 23; DB 2; Length 17;
Best Local Similarity 57.1%; Pred. No. 1.8e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 5 PHGYLT 11
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|
Db 10 PENYLS 16

RESULT 40

Q29395_CANFA
ID Q29395_CANFA PRELIMINARY; PRT; 17 AA.
AC Q29395;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)

DR Beta-galactosidase (Fragment).

GN Name=GLBI;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Carnivora; Fissipedia; Canidae;
OC Canis.
OX NCBI_TaxID=9615;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=97049323; PubMed=8894053;
RA Venta P.J., Brouillette J.A., Yuzbasliyan-Gurkan V., Brewer G.J.;
RT "Gene-specific universal mammalian sequence-tagged sites: application
RT to the canine genome.";
RL Biochem. Genet. 34:321-341(1996).
DR EMBL; L77671; AAA97424.1; -; Genomic DNA.
FT NON TER 1
FT NON TER 17
SQ SEQUENCE 17 AA; 1878 MW; FDCB86FF9F037BB2 CRC64;

Query Match 24.0%; Score 23; DB 2; Length 17;
Best Local Similarity 33.3%; Pred. No. 1.8e+04;
Matches 4; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

Qy 4 BPHGYLTAAVS 15
: || : || :
Db 5 QPHSTVKTREVA 16

RESULT 41

Q424N4_PLABE
ID Q424N4_PLABE PRELIMINARY; PRT; 18 AA.
AC Q424N4;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DE Hypothetical protein (Fragment).
GN ORFNames=PB101450.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karris M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertram M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford K., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.B., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Jance C.J., Bartell B., Turner C.M.R., Waters A.P., Sinden R.S.;
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses.";
RL Science 307:82-86(2005).
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CA0100618; CAH94749.1; -; Genomic DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 18 AA; 2268 MW; FA8DE02CB603F78B CRC64;

Query Match 24.0%; Score 23; DB 2; Length 18;
Best Local Similarity 62.5%; Pred. No. 1.9e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 YLLTAAS 15
|
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|
Db 3 YLLTISYS 10

RESULT 42

Q6LD80_9MURI
ID Q6LD80_9MURI PRELIMINARY; PRT; 18 AA.
AC Q6LD80;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TREMBlrel. 27, last sequence update)
 DE 05-JUL-2004 (TREMBlrel. 27, last annotation update)
 DB Thrombopoietin receptor (Fragment).
 GN Name=Mpl; Synonyms=c-mpl1;
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NC NCB1_TaxID=10095;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=516571; PubMed=7862460;
 RA Alexander W.S., Dunn A.R.;
 RT "Structure and transcription of the genomic locus encoding murine c-
 Mpl, a receptor for thrombopoietin."
 RL Oncogene 10:795-803(1995).
 DR EMBL; S76842; AAB33462.1; -, mRNA.
 DR MGI; MGI:97076; MGI.
 DR GO; GO:0004872; F:receptor activity; IEA.
 KM Receptor.
 FT NON_TER
 SQ SEQUENCE 18 AA; 1808 MW; E01CB44E83834E2 CRC64;
 QY Query Match 24.0%; Score 23; DB 2; Length 18;
 Best local Similarity 75.0%; Pred. No. 1.9e+04;
 Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;
 DB 4 EPHG 7
 1 QPHG 4
 RESULT 43
 Q7ZNF73_SH1V1
 ID Q7ZNF73_SH1V1 PRELIMINARY; PRT; 18 AA.
 AC Q7ZNF73;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)
 DE Truncated p24 protein (Fragment).
 GN Name=gag;
 OS Human immunodeficiency virus 1.
 OC Viruses; Retrovirdae; Retroviridae; Lentivirus;
 OC Primate lentivirus group.
 NC NCB1_TaxID=11676;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=99TCD.MN044;
 RA Vidal N., Koyalta D., Richard V., Leclache C., Ndinaromtan T.,
 RA Djimengar A., Delaporte E., Peeters M.;
 RT "High genetic diversity of HIV-1 strains in Chad, West Central
 Africa."
 RL J. Acquir. Immune Defic. Syndr. 33:139-246(2004).
 DR EMBL; AJ491020; CAD36428.1; -, Genomic_DNA.
 FT NON_TER
 SQ SEQUENCE 18 AA; 1978 MW; 1FP3DSBB656A776F CRC64;
 QY Query Match 24.0%; Score 23; DB 2; Length 18;
 Best local Similarity 40.0%; Pred. No. 1.9e+04;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
 DB 7 GYLLTAAPV 16
 4 GQVHQHIS 13
 RESULT 44
 Q95G13_AB1AL
 ID Q95G13_AB1AL PRELIMINARY; PRT; 19 AA.
 AC Q95G13;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, last sequence update)
 DT 01-OCT-2003 (TREMBlrel. 25, last annotation update)

DE ATP-dependent protease subunit (Fragment).
 OS Abies alba (Edeltanne) (European silver fir).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Abies.
 NC NCB1_TaxID=53372;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Liepelt S., Kuhnkamp V., Anzidei M., Venztramin G.G., Ziegenhagen B.;
 RL Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF367975; AAK53398.1; -, Genomic_DNA.
 DR GO; GO:0009507; C:chloroplast; IEA.
 DR GO; GO:0008233; F:peptidase activity; IEA.
 KM Chloroplast; Protease.
 FT NON_TER
 SQ SEQUENCE 19 AA; 1958 MW; 7CA63B7278AE394 CRC64;
 QY Query Match 24.0%; Score 23; DB 2; Length 19;
 Best local Similarity 37.5%; Pred. No. 2.1e+04;
 Matches 6; Conservative 2; Mismatches 8; Indels 0; Gaps 0;
 DB 2 AFEPHGVLTAAPVPG 17
 4 ATRARAYGVDAVABG 19
 RESULT 45
 PL1_LUPLU
 ID PL1_LUPLU STANDARD; PRT; 20 AA.
 AC P83363;
 DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, last sequence update)
 DT 01-FEB-2005 (Rel. 46, last annotation update)
 DE Protein PR-L1 (Fragment).
 OS Lupinus luteus (European yellow lupin).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
 OC Rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;
 OC Lupinus.
 NC NCB1_TaxID=3873;
 RN [1]
 RP PROTEIN SEQUENCE, AND INDUCTION.
 RC STRAIN=cv. Ventus; TISSUE=Root tip;
 RA Przymsinski R., Gwozdz E.A.;
 RT "Heavy metal-induced polypeptides in lupin roots are similar to
 pathogenesis-related proteins."
 RL J. Plant Physiol. 154:703-708(1999).
 CC -1- INDUCTION: By heavy metal ions.
 CC -1- SIMILARITY: Belongs to the BetyI family.
 CC -----
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 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC removed.
 CC -----
 DR InterPro; IPR000916; Bet_v1.
 DR PROSITE; PS00451; PATHOGENESIS BETV1; PARTIAL.
 KM Direct protein sequencing; Pathogenesis-related protein;
 KM Plant defense.
 FT NON_TER
 SQ SEQUENCE 20 AA; 2204 MW; 063D76EB9BD26C85 CRC64;
 QY Query Match 24.0%; Score 23; DB 1; Length 20;
 Best local Similarity 50.0%; Pred. No. 2.2e+04;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
 DB 11 TAAPVPG 18
 10 TSTVAPAK 17
 RESULT 46

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PL6_LUPLU          STANDARD;          PRT;          20 AA.
ID   PL6_LUPLU
AC   P63368;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DE   01-FEB-2005 (Rel. 46, Last annotation update)
DE   Protein PR-L6 (Fragment).
OC   Lupinus luteus (European Yellow lupin).
OC   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC   Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC   rosids; eustosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;
OC   Lupinus.
OX   NCBI_TaxID=3873;
RN   [1]
RP   PROTEIN SEQUENCE, AND INDUCTION.
RC   STRAIN=cv. Ventus, TISSUE=Root tip;
RA   Przybylski R., Gwozdz E.A.;
RT   "Heavy metal-induced polypeptides in lupin roots are similar to
RT   pathogenesis-related proteins."
RL   J. Plant Physiol. 154:703-708(1999).
CC   -1- INDUCTION: By heavy metal ions.
CC   -1- SIMILARITY: Belongs to the BetyI family.
CC   -----
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   use as long as its content is in no way modified and this statement is not
CC   removed.
CC   -----
DR   InterPro; IPR000916; Bet_v_1.
DR   PROSITE; PS00451; PATHOGENESIS_BETV1; PARTIAL.
KW   Direct protein sequencing; Pathogenesis-related protein;
KW   Plant defense.
FT   NON_TER          20
SQ   SEQUENCE          20 AA; 2190 MW; 063D60824BD26C85 CRC64;

Query Match          24.0%; Score 23; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY          11 TAAVSPGK 18
DB          10 TSTVAPAK 17

RESULT 47
O9BRP3_HUMAN        PRT;          20 AA.
ID   O9BRP3;
AC   O9BRP3;
DT   01-JUN-2001 (TrEMBLrel. 17, Created)
DT   01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DE   01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE   MAFG protein.
GN   Name=MAFG;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC   Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Straubeberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins B.S., Wagner L., Shennan C.M., Schuler G.D.,
RA   Altshul S.F., Zeeberg K.H., Buettow K.H., Schaffer C.P., Bhat N.K.,
RA   Hopkins R.P., Jordan H., Moore T., Max S.I., Wang J., Heish F.,
RA   Ditschenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Ueda T.B., Toshlyuk S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA   Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

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RA   Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahy J., Helton E., Kerteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Sheychenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butlerfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences."
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [2]
RP   NUCLEOTIDE SEQUENCE.
RC   TISSUE=Lung;
RA   Straubeberg R.;
RL   Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.
DR   EMBL; BC06143; AA06143.1; -, mRNA.
DR   Ensembl; ENSG00000197048; Homo sapiens.
SQ   SEQUENCE          20 AA; 2080 MW; DEB42194EE428F84 CRC64;

Query Match          24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY          11 TAAVSPGK 18
DB          13 TQQLSPGE 20

RESULT 48
O9RAU5_STRSL        PRELIMINARY;      PRT;          20 AA.
ID   O9RAU5;
AC   O9RAU5;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DE   01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
DE   Aminopeptidase N (Fragment).
OS   Streptococcus salivarius.
OC   Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC   Streptococcus.
OX   NCBI_TaxID=1304;
RN   [1]
RP   PROTEIN SEQUENCE.
RX   MEDLINE=95081020; PubMed=7989254;
RA   Midwinter R.G., Pritchard G.G.;
RT   "Aminopeptidase N from Streptococcus salivarius subsp. thermophilus
RT   NCDO 575: purification and properties."
RL   J. Appl. Bacteriol. 77:288-295(1994).
SQ   SEQUENCE          20 AA; 2328 MW; 55FB0E4BC6EFD2CD CRC64;

Query Match          24.0%; Score 23; DB 2; Length 20;
Best Local Similarity 40.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

QY          1 DAFEPHGYLL 10
DB          9 ESFIPENTYXL 18

RESULT 49
O81IS2_MOUSE        PRELIMINARY;      PRT;          9 AA.
ID   O81IS2;
AC   O81IS2;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DE   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   HCFc1 protein (Fragment).
GN   Name=Hcfc1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC   Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]

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RP NUCLEOTIDE SEQUENCE.
 RA Reichwald K., Petz U., Rosenthal A., Platzer M.,
 RL Submitted (NOV-2002) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AY184361; AAO24116.1; -, mRNA.
 FT NON TER 9
 SQ SEQUENCE 9 AA; 847 MW; CB74C775A2CDC5BD CRC64;

Query Match 22.9%; Score 22; DB 2; Length 9;
 Best Local Similarity 57.1%; Pred. No. 2.2e+06;
 Matches 4; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 10 LTAAVSP 16
 : |||||
 DB 1 MASAVSP 7

RESULT 50
 Q9MJ05_PODCU PRELIMINARY; PRT; 10 AA.
 ID Q9MJ05_PODCU PRELIMINARY; PRT; 10 AA.
 AC Q9MJ05;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Name=cytb;
 OS Podospora curvicolle.
 OC Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
 NCBI_TaxId=48157;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20150243; PubMed=10684923; DOI=10.1093/nar/28.6.1299;
 RA Saguez C., Lecellier G., Koll F.;
 RT "Intronic GIV-YIG endonuclease gene in the mitochondrial genome of
 Podospora curvicolle: evidence for mobility."
 RT Nucleic Acids Res. 28:1299-1306(2000).
 DR EMBL, AJ249984; CAB72447.1; -, Genomic_DNA.
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 FT NON TER 10
 SQ SEQUENCE 10 AA; 1200 MW; C31A23B437B0772 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 10;
 Best Local Similarity 55.6%; Pred. No. 1.5e+04;
 Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 AFEPHGL 10
 : |||||
 DB 1 AIVPEWYLL 9

RESULT 51
 Q9QV21_9MURI PRELIMINARY; PRT; 10 AA.
 ID Q9QV21_9MURI PRELIMINARY; PRT; 10 AA.
 AC Q9QV21;
 DT 01-MAY-2000 (TREMBlrel. 13, Created)
 DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
 DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
 DE Neurotrophic factor.
 OS Rattus sp.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Charchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Rattus.
 NCBI_TaxId=10118;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=95056708; PubMed=7967227;
 RA Yasukura T., Omori K., Mikami T., Inoue M., Uyama M., Inagaki C.;
 RT "Purification and characterization of neurotrophic factor for retinal
 RT cholinergic neurons derived from cultured hippocampal neurons."
 Jpn. J. Pharmacol. 65:153-162(1994).

SQ SEQUENCE 10 AA; 1145 MW; 58922952D6DDC767 CRC64;
 Query Match 22.9%; Score 22; DB 2; Length 10;
 Best Local Similarity 62.5%; Pred. No. 1.5e+04;
 Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLTPAAS 15
 : |||||
 DB 1 YLTPAQVN 8

RESULT 52
 Q86D31_TRYCR PRELIMINARY; PRT; 11 AA.
 ID Q86D31_TRYCR PRELIMINARY; PRT; 11 AA.
 AC Q86D31;
 DT 01-JUN-2003 (TREMBlrel. 24, Created)
 DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
 DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)
 DE Histone H1 (Fragment).
 OS Trypanosoma cruzi.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;
 OC Schizotrypanum.
 NCBI_TaxId=5693;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22557728; PubMed=12670512; DOI=10.1016/S0020-7519(02)00264-3;
 RA Sturm N.R., Vargas N.S., Westendorp S.J., Zingales B.,
 RA Campbell D.A.;
 RT "Evidence for multiple hybrid groups in Trypanosoma cruzi."
 RT Int. J. Parasitol. 33:269-279(2003).
 DR EMBL, AF545076; AAP21906.1; -, Genomic_DNA.
 FT NON TER 11
 FT NON TER 11
 SQ SEQUENCE 11 AA; 1174 MW; CDD1B21E7772CDD CRC64;

Query Match 22.9%; Score 22; DB 2; Length 11;
 Best Local Similarity 50.0%; Pred. No. 1.7e+04;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

QY 9 LTPAAVSPGK 18
 : |||||
 DB 1 MPDAVAPPK 10

RESULT 53
 Q9MJ03_PODCU PRELIMINARY; PRT; 14 AA.
 ID Q9MJ03_PODCU PRELIMINARY; PRT; 14 AA.
 AC Q9MJ03;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
 DE Cytochrome b (Fragment).
 OS Name=cytb;
 OS Podospora curvicolle.
 OC Mitochondrion.
 OC Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 OC Sordariomycetidae; Sordariales; Lasiosphaeriaceae; Podospora.
 NCBI_TaxId=48157;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=20150243; PubMed=10684923; DOI=10.1093/nar/28.6.1299;
 RA Saguez C., Lecellier G., Koll F.;
 RT "Intronic GIV-YIG endonuclease gene in the mitochondrial genome of
 Podospora curvicolle: evidence for mobility."
 RT Nucleic Acids Res. 28:1299-1306(2000).
 DR EMBL, AJ249985; CAB72449.1; -, Genomic_DNA.
 DR GO: GO:0005739; C:mitochondrion; IEA.
 KW Mitochondrion.
 FT NON TER 1
 FT NON TER 14
 SQ SEQUENCE 14 AA; 1603 MW; 2972D7731A723B43 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;
 Best Local Similarity 55.6%; Pred. No. 2.2e+04;

Matches 5; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 2 APEPHGYLT 10
| | | |
DB 2 AIVPEWYLL 10

RESULT 54
Q5OSJ7 TRIMA
ID Q5OSJ7 TRIMA PRELIMINARY; PRT; 14 AA.

AC Q5OSJ7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE HspB2 protein (Fragment).

GN Name=mkbp;
OS Trichechus manatus (Caribbean manatee) (West Indian manatee).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Afrotheria; Sirenia; Trichechidae; Trichechus.
OX NCBI_TaxId=9778;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doerwald L., van Rieede T., Dirks R.P., Madsen O., Rexwinkel R.,
RA van Geneen S.T., Martens G.J., de Jong W.W., Lubsen N.H.;
RT "Sequence and functional conservation of the intergenic region between
RT the head-to-head genes encoding the small heat shock proteins alphaB-
RT crystalin and HspB2 in the mammalian lineage."
RL J. Mol. Evol. 59:674-686(2004).
DR EMBL; AJ617824; CAB9475.1; -; Genomic_DNA.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1419 MW; 2F09350ABC6DE8F7 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTA 12
| | | |
DB 7 PHAHPATA 14

RESULT 55
Q5OSJ5 CYCDI
ID Q5OSJ5 CYCDI PRELIMINARY; PRT; 14 AA.

AC Q5OSJ5;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE HspB2 protein (Fragment).

GN Name=mkbp;
OS Cyclops didactylus (Silky anteater).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Xenarthra; Myrmecophagidae; Cyclopes.
OX NCBI_TaxId=84074;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doerwald L., van Rieede T., Dirks R.P., Madsen O., Rexwinkel R.,
RA van Geneen S.T., Martens G.J., de Jong W.W., Lubsen N.H.;
RT "Sequence and functional conservation of the intergenic region between
RT the head-to-head genes encoding the small heat shock proteins alphaB-
RT crystalin and HspB2 in the mammalian lineage."
RL J. Mol. Evol. 59:674-686(2004).
DR EMBL; AJ617820; CAB9454.1; -; Genomic_DNA.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1419 MW; 2F09350ABC6DE8F7 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTA 12
| | | |
DB 7 PHAHPATA 14

RESULT 56
Q5OSJ7 SPAEH
ID Q5OSJ7 SPAEH PRELIMINARY; PRT; 14 AA.

AC Q5OSJ7;
DT 01-FEB-2005 (TrEMBLrel. 29, Created)
DT 01-FEB-2005 (TrEMBLrel. 29, Last sequence update)
DE 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE HspB2 protein (Fragment).

GN Name=mkbp;
OS Spalax leucodon ehrenbergi (Ehrenberg's mole rat).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Spalacinae; Nannospalax.
OX NCBI_TaxId=30637;

RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Doerwald L., van Rieede T., Dirks R.P., Madsen O., Rexwinkel R.,
RA van Geneen S.T., Martens G.J., de Jong W.W., Lubsen N.H.;
RT "Sequence and functional conservation of the intergenic region between
RT the head-to-head genes encoding the small heat shock proteins alphaB-
RT crystalin and HspB2 in the mammalian lineage."
RL J. Mol. Evol. 59:674-686(2004).
DR EMBL; AJ617819; CAB9448.1; -; Genomic_DNA.
FT NON_TER 14
SQ SEQUENCE 14 AA; 1449 MW; 2F09351BF6DE8F7 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 14;
Best Local Similarity 50.0%; Pred. No. 2.2e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 5 PHGYLTA 12
| | | |
DB 7 PHAHPATA 14

RESULT 57
GSTBL_PSEUO
ID GSTBL_PSEUO STANDARD; PRT; 15 AA.

AC P82999;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 10-MAY-2005 (Rel. 47, Last annotation update)
DE Glutathione S-transferase (BC 2.5.1.18) (Fragment).

OS Pseudomonas sp. (strain M1).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_TaxId=95619;

RN [1]
RP PROTEIN SEQUENCE, FUNCTION, CATALYTIC ACTIVITY, SUBUNIT, AND
RP SUBCELLULAR LOCATION.
RX MEDLINE=21896940; PubMed=11900268; DOI=10.1016/S0923-2508(01)01293-1;
RA Santos P.M., Mignogna G., Heidegger H.J., Zennaro E.;

RT "Occurrence and properties of glutathione S-transferases in phenol-
RT degrading Pseudomonas strains";
RL Res. Microbiol. 153:89-98(2002).

CC -1- FUNCTION: Conjugation of reduced glutathione to a wide number of
CC exogenous and endogenous hydrophobic electrophiles.
CC -1- CATALYTIC ACTIVITY: RX + glutathione = HX + R-S-glutathione.
CC -1- SUBUNIT: Monomer and homodimer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to the GST superfamily.

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CC the European Bioinformatics Institute. There are no restrictions on its
CC use as long as its content is in no way modified and this statement is not
CC removed.

DR GO; GO:0005737; C:cytoplasm; NMS.
DR GO; GO:0004364; F:glutathione transferase activity; NMS.
DR GO; GO:0008152; P:metabolism; IC.

KM Direct protein sequencing; Transferase.

FT NCN TER 15 15
SQ SEQUENCE 15 AA; 1817 MW; 0E2A0FCSF55CBAC2 CRC64;

Query Match 22.9%; Score 22; DB 1; Length 15;
Best Local Similarity 55.6%; Pred. No. 2.3e+04;
Matches 5; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 8 YLTPAVSP 16
DB 3 YLTPVHSP 11

RESULT 58

005694 MOUSE
ID Q05694_MOUSE PRELIMINARY; PRT; 15 AA.

AC Q05694;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Proline-rich protein (Fragment).

GN Name=Mp6;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]

NP NUCLEOTIDE SEQUENCE.

RC STRAIN=BALB/C;
RA MEDLINE=92030206; PubMed=1747160;
RA Roberts S.G.B., Layfield R., McDonald C.J.;

RT "The mouse proline-rich protein Mp6 promoter binds isoprenaline-inducible peroxid nuclear proteins via a highly conserved NFkB/rel-like site."
RL Nucleic Acids Res. 19:5205-5211(1991).

DR EMBL; X61126; CAA43438.1; -; Genomic_DNA.

FT NCN TER 15 15
SQ SEQUENCE 15 AA; 1557 MW; C0FF9514A8F70BE4 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 15;
Best Local Similarity 83.3%; Pred. No. 2.3e+04;
Matches 5; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 9 LTPAV 14
DB 5 LTPAAL 10

RESULT 59

069353_HHV2 PRELIMINARY; PRT; 15 AA.
ID Q69353;
AC Q69353;

DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DE HSV-2 (333) N terminus of 17.8 kd protein gene (0.642 mu). (Fragment).

OS Human herpesvirus 2 (HHV-2) (Human herpes simplex virus 2).

OC Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
OC Alphaherpesvirinae; Simplexvirinae.

OC NCBI_TaxID=10310;

RN [1]

RP NUCLEOTIDE SEQUENCE.
RC MEDLINE=5033906; PubMed=6092683;
RA Draper K.G., Frink R.J., Devl G.B., Swain M., Galloway D., Wagner B.K.;

RT "Herpes simplex virus types 1 and 2 homology in the region between 0.58 and 0.68 map units."
RL J. Virol. 52:615-623(1984).

DR EMBL; X03360; AAA45840.1; -; Genomic_DNA.
FT NCN TER 15 15
SQ SEQUENCE 15 AA; 1603 MW; 20B04DC0BA4507FE CRC64;

Query Match 22.9%; Score 22; DB 2; Length 15;
Best Local Similarity 66.7%; Pred. No. 2.3e+04;
Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 2 APERHG 7
DB 2 APERSG 7

RESULT 60

09TRR1_RABIT PRELIMINARY; PRT; 16 AA.
ID 09TRR1;
AC 09TRR1;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Fibronectin 47 kDa fragment (Fragment).

OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Lagomorpha; Leporidae;
OC Oryctolagus.
OC NCBI_TaxID=9986;
RN [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=92283375; PubMed=1597256;
RA Lebot H., Faussier J.L., Akiyama S.K., Staub A., Black D., Kubler M.D., Ruch J.V.;

RT "The carboxy-terminal extension of the collagen binding domain of RT fibronectin mediates interaction with a 165 kDa membrane protein involved in odontoblast differentiation."
RL Differentiation 49:109-118(1992).

FT NCN TER 1 1
FT NON TER 16 16
SQ SEQUENCE 16 AA; 1764 MW; B196CAAC53F5739 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 16;
Best Local Similarity 42.9%; Pred. No. 2.5e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 5 PHGYLT 11
DB 10 PYGHXT 16

RESULT 61

09QZY3_MOUSE PRELIMINARY; PRT; 16 AA.
ID 09QZY3;
AC 09QZY3;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE R29144/1 (Fragment).

GN Name=R29144/1;

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.

OC NCBI_TaxID=10090;

RN [1]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=129;
RX MEDLINE=9930555; PubMed=10400995; DOI=10.1093/hmg/8.8.1479;
RA Smith D.P., Spicer J., Smith A., Swift S., Ashworth A.;

RT "The mouse Peutz-Jeghers syndrome gene Lkb1 encodes a nuclear protein kinase."
RL Hum. Mol. Genet. 8:1479-1485(1999).

DR EMBL; AF145697; AAD5370.1; -; Genomic_DNA.
FT NCN TER 1 1
SQ SEQUENCE 16 AA; 1518 MW; D6C720E4BF0A1D2 CRC64;

Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 9 LITAAVSP 16
|:|:|
RT 1 LIVAAAP 8

RESULT 62
ID 06LC11_HUMAN PRELIMINARY; PRT; 17 AA.
AC 06LC11;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Na⁺-phosphate cotransporter type II (Fragment).
GN Name=NPT2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=93317607; PubMed=8327470;
RA Mageruin S., Werner A., Markovitch D., Sorribas V., Stange G.,
RA Biber J., Murer H.;
RT "Expression cloning of human and rat renal cortex Na/Pi cotransport.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:5979-5983 (1993).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=96393539; PubMed=8693007; DOI=10.1073/pnas.93.14.7409;
RA Hartman C.M., Hewson A.S., Kos C.H., Hilleker H., Soumounou Y.,
RA Murer H., Tenenhouse H.S.;
RT "Structure of murine and human renal type II Na⁺-phosphate
cotransporter genes (NPT2 and NPT2).";
RL Proc. Natl. Acad. Sci. U.S.A. 93:7409-7414 (1996).
DR EMBL; U56692; AAD14864.1; -; Genomic_DNA.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1796 MW; 20ECDPFB839C6D26D CRC64;

Query Match 22.9%; Score 22; DB 2; Length 17;
Best Local Similarity 37.5%; Pred. No. 2.7e+04;
Matches 3; Conservative 4; Mismatches 1; Indels 0; Gaps 0;

QY 9 LITAAVSP 16
|:|:|:|
DB 8 VFTSALT 15

RESULT 63
ID 07MOD8_MOUSE PRELIMINARY; PRT; 17 AA.
AC 07MOD8;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Probable integrin alpha3 beta1 (Fragment).
GN Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognath;
OC Muridae; Murinae; Mus.
NCBI_TaxID=10090;

RP PROTEIN SEQUENCE.
RA McCormick J.I., Johnstone R.M.;
RT "Identification of the integrin alpha(3)beta(1) as a component of a
partially purified A-system amino acid transporter from Ehrlich cell
RT plasma membranes";
RL Biochem. J. 311:743-751 (1995).
RN [2]
RP PROTEIN SEQUENCE.
RX PubMed=7487928;

RA McCormick J.I., Johnstone R.M.;
RT "Identification of the integrin alpha 3 beta 1 as a component of a
RT partially purified A-system amino acid transporter from Ehrlich cell
RT plasma membranes";
RL Biochem. J. 311 (Pt 3):743-751 (1995).
DR PIR; S59512; S59512.
FT NON_TER 1 1
FT NON_TER 17 17
SQ SEQUENCE 17 AA; 1917 MW; 2A106ECB15011902 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 17;
Best Local Similarity 80.0%; Pred. No. 2.7e+04;
Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 13 AVSPG 17
|:|:|
DB 13 AVNPG 17

RESULT 64
ID 075MP5_HUMAN PRELIMINARY; PRT; 18 AA.
AC 075MP5;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein UBR2H (Fragment).
GN Name=UBR2H;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
NCBI_TaxID=9606;

RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22737999; PubMed=12853948; DOI=10.1038/nature01782;
RA Hillier L.W., Fulton R.S., Fulton L.A., Graves T.A., Pepin K.H.,
RA Wagner-McPherson C., Layman D., Maas J., Jaeger S., Walker R.,
RA Wyllie K., Sekhon M., Becker M.C., O'Laughlin M.D., Schaller M.B.,
RA Fewell G.A., Delahunty K.D., Miner T.L., Nash W.E., Cordes M., Du H.,
RA Sun H., Edwards J., Bradshaw-Cordum H., Ali J., Andrews S., Isak A.,
RA Vandrunt A., Nguyen C., Du F., Lamar B., Courtney L., Kalicki J.,
RA Ozeresky P., Bielicki L., Scott K., Holmes A., Harkins R., Harris A.,
RA Strong C.M., Hou S., Tomlinson C., Dauphin-Kohlberg S.,
RA Kozlowski-Reilly A., Leonard S., Rohlfing T., Rock S.M.,
RA Tiro-Wollam A.M., Abbott A., Mink P., Maupin R., Stromatt C.,
RA Latreille P., Miller N., Johnson D., Murray J., Woessner J.P.,
RA Wendt M.C., Yang S.-P., Schultz B.R., Wallis J.W., Spieth J.,
RA Bieri T.A., Nelson J.O., Berkowicz N., Wohldmann P.E., Cook L.L.,
RA Hickenbotham M.T., Bidred J., Williams D., Bedell J.A., Mardis E.R.,
RA Clifton S.W., Chisose S.L., Marra M.A., Raymond C., Haugen E.,
RA Gillett W., Zhou Y., James R., Phelps K., Iadonoto S., Bub K.,
RA Simme B., Levy R., Clendenning J., Kaul R., Kent W.J., Porey T.S.,
RA Baertsch R.A., Brent M.R., Keibler E., Flicker P., Bork P., Suyama M.,
RA Bailey J.A., Portnoy M.B., Torrents D., Chimala A.T., Gish W.R.,
RA Eddy S.J., McPherson J.D., Olson M.V., Bichter E.B., Green B.D.,
RA Waterston R.H., Wilson R.K.;
RT "The DNA sequence of human chromosome 7.";
RL Nature 424:157-164 (2003).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RA Haakenson W., Kyung K.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
RN [3]
RP NUCLEOTIDE SEQUENCE.
RA Waterston R.;
RL Submitted (NOV-2001) to the EMBL/Genbank/DBJ databases.
RN [4]
RP NUCLEOTIDE SEQUENCE.
RA Wilson R.;
RL Submitted (JAN-2004) to the EMBL/Genbank/DBJ databases.
DR EMBL; AC073320; AAS07548.1; -; Genomic_DNA.
KW Hypothetical protein.

FT NON TER 18 18
SQ SEQUENCE 18 AA; 2004 MW; 7616C1121A8730F0 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 18;
Best Local Similarity 100.0%; Pred. No. 2.8e+04;
Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 15 SPQK 18
DB 5 SPQK 8

RESULT 65

05C123_SCHUA
ID 05C123_SCHUA PRELIMINARY; PRT; 19 AA.
AC 05C123;
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
DE 10-MAY-2005 (TrEMBLrel. 30, Last annotation update)
DS Hypothetical protein.
OS Schistosoma japonicum (Blood fluke).
OC Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeiidae;
OC Schistosomatoidea; Schistosomatidae; Schistosoma.
OX NCBI_TaxID=6182;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Han Z.
RL Submitted (MAR-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY610763; AX26652.1; -; mRNA.
KM Hypothetical protein.
SQ SEQUENCE 19 AA; 2259 MW; FE2492FB8464550 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;
Best Local Similarity 42.9%; Pred. No. 3e+04;
Matches 3; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

QY 6 HGYLTRA 12
DB 12 HNYLVSS 18

RESULT 66

04YGN5_PLABE
ID 04YGN5_PLABE PRELIMINARY; PRT; 19 AA.
AC 04YGN5;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)
DS Hypothetical protein (Fragment).
GN ORFName=PB403349.00.0;
OS Plasmodium berghei.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5821;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall N., Karras M., Raine J.D., Carlton J.M., Kool J.T.W.A.,
RA Bertrman M., Florens L., Janssen C.S., Pain A., Christophides G.K.,
RA James K., Rutherford J., Harris B., Harris D., Churcher C.,
RA Quail M.A., Ormond D., Doggett J., Trueman H.E., Mendoza J.,
RA Bidwell S.L., Rajandream M.A., Carucci D.J., Yates J.R., Kafatos F.C.,
RA Janse C.J., Barrett B., Turner C.M.R., Waters A.P., Sinden R.S.,
RT "A comprehensive survey of the Plasmodium life cycle by genomic,
RT transcriptomic, and proteomic analyses."
RL Science 307:82-86(2005).
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.

DR EMBL; CAI01005269; CAI02832.1; -; Genomic_DNA.
KW Hypothetical protein.
FT NON TER 1
SQ SEQUENCE 19 AA; 2184 MW; 9014FEFF1869BD28 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;

Best Local Similarity 44.4%; Pred. No. 3e+04;
Matches 4; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 6 HGYLTRA 14
DB 11 NGVILAAI 19

RESULT 67

04W2E7_SEUTH
ID 04W2E7_SEUTH PRELIMINARY; PRT; 19 AA.
AC 04W2E7;
DT 13-SEP-2005 (TrEMBLrel. 31, Created)
DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
DE Putative Signal Transducer and Activator of Transcription
DE (Fragment).
GN Name=stat5A;
OS Manis temminckii (ground pangolin).
OC Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Laurasiatheria; Pholidota; Manidae; Manis.
OX NCBI_TaxID=302418;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Bick G.N., Jacobs D.S., Matchee C.R.;
RT "A phylogenetic perspective of the evolution of echolocation and
RT historical biogeography of extant bats (Chiroptera)."
RL Submitted (NOV-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ865445; CA126367.1; -; Genomic_DNA.
FT NON TER 1
SQ SEQUENCE 19 AA; 1910 MW; 8B83C620FC87B5C8 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;
Best Local Similarity 62.5%; Pred. No. 3e+04;
Matches 5; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 10 LTAIVSPG 17
DB 8 LGASPSPG 15

RESULT 68

07TBG5_ADE08
ID 07TBG5_ADE08 PRELIMINARY; PRT; 19 AA.
AC 07TBG5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DE 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DS Fiber (Fragment).
OS Human adenovirus 8 (HAdV-8).
OC Viruses; dsDNA viruses, no RNA stage; Adenoviridae; Mastadenovirus.
OX NCBI_TaxID=31545;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA STRAIN=H16;
RC PubMed=12560390; DOI=10.1136/jcp.56.2.120;
RA Adhikary A.K., Nunaga J., Kaburaki T., Kawashima H., Araie M.,
RA Ikeda Y., Ogino T., Suzuki E., Ushijima H., Mukoyama A., Matsuno S.,
RA Inada T., Okabe N.;
RT "Genetic Characterization of Adenovirus Type 8 Isolated in Hiroshima
RT City over a 15-year Period."
RL J. Clin. Pathol. 56:120-125(2003).
DR EMBL; AB102672; BAC78838.1; -; Genomic_DNA.
FT NON TER 19
SQ SEQUENCE 19 AA; 2364 MW; AC340337188B135F CRC64;

Query Match 22.9%; Score 22; DB 2; Length 19;
Best Local Similarity 75.0%; Pred. No. 3e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 5 PHGY 8
DB 1; 1; 1

Db 16 PYGY 19

RESULT 69
PL3_LUPLU STANDARD; PRT; 20 AA.
ID PL3_LUPLU
AC P83365;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 01-FEB-2005 (Rel. 46, Last annotation update)
DE Protein PR-L3 (Fragment).
OS Lupinus luteus (European yellow lupin).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons;
OC rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Genisteae;
OC lupinus.
OX NCBI_TaxID=3873;
RN [1]
RP PROTEIN SEQUENCE, AND INDUCTION.
RC STRAIN=cv. Ventus; TISSUE=Root tip;
RA Przyusinski R., Gwozdz B.A.;
RT "Heavy metal-induced polypeptides in lupin roots are similar to
pathogenesis-related proteins."
RL J. Plant Physiol. 154:703-708(1999).
CC -1- INDUCTION: By heavy metal ions.
CC -1- SIMILARITY: Belongs to the Betyr family.

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the European Bioinformatics Institute. There are no restrictions on its
use as long as its content is in no way modified and this statement is not
removed.

DR InterPro; IPR000916; Bet v 1.
DR PROSITE; PS00451; PATHOGENESIS_BETV1, PARTIAL.
KW Plant protein sequencing; Pathogenesis-related protein;
KW Plant defense.
FT NON_TER 20 20
SQ SEQUENCE 20 AA; 2218 MW; 063BADEB9BD26C85 CRC64;

Query Match 22.9%; Score 22; DB 1; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+04;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

Qy 11 TAAVSPK 18
| | | | |
Db 10 TTTVAPAK 17

RESULT 70
Q8NFW3_HUMAN PRELIMINARY; PRT; 20 AA.
ID Q8NFW3_HUMAN
AC Q8NFW3;
DT 01-OCT-2002 (TrEMBLrel. 22, Created)
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
DE Synovial sarcoma SYT/SSX1 fusion protein (Fragment).
GN Name=SYT/SSX1 fusion;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Tamborini E., Ague V., Pierotti M.A., Piliotti S., Rosal J.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF402619; AAM595901.1; -; mRNA.
FT NON_TER 1 20
SQ SEQUENCE 20 AA; 2377 MW; F1534C73F9108B83 CRC64;

Query Match 22.9%; Score 22; DB 2; Length 20;

Best Local Similarity 75.0%; Pred. No. 3.1e+04;
Matches 3; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 5 PHGYLTA 8
| | | | |
Db 4 PYGY 7

RESULT 71
Q6UCN3_ECOLI PRELIMINARY; PRT; 20 AA.
ID Q6UCN3_ECOLI
AC Q6UCN3;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 01-FEB-2005 (TrEMBLrel. 29, Last annotation update)
DE Afac (Fragment).
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=DABC18, DABC19, DABC213, DABC714, DABC7, DABC5, DABC20,
RC DABC162, DABC72a, DABC72b, DABC11a, DABC11b, DABC218, DABC712,
RC ECOR37, DABC9, ECOR50, IH1128, C1845, and ECOR64;
RX PubMed=15014151; DOI=10.1093/molbev/mh118;
RA Bacchar-Paramo P., Clermont O., Blanc-Potard A.B., But H.,
le Bougenec C., Denamur E.;
RT "A Specific Genetic Background Is Required for Acquisition and
RT Expression of Virulence Factors in Escherichia coli.";
RL Mol. Biol. Evol. 21:1085-1094(2004).
DR EMBL; AY525515; AAT00550.1; -; Genomic DNA.
DR EMBL; AY525516; AAT00552.1; -; Genomic DNA.
DR EMBL; AY525517; AAT00554.1; -; Genomic DNA.
DR EMBL; AY525518; AAT00556.1; -; Genomic DNA.
DR EMBL; AY525519; AAT00558.1; -; Genomic DNA.
DR EMBL; AY525520; AAT00560.1; -; Genomic DNA.
DR EMBL; AY525521; AAT00562.1; -; Genomic DNA.
DR EMBL; AY525522; AAT00564.1; -; Genomic DNA.
DR EMBL; AY525523; AAT00566.1; -; Genomic DNA.
DR EMBL; AY525524; AAT00568.1; -; Genomic DNA.
DR EMBL; AY525525; AAT00570.1; -; Genomic DNA.
DR EMBL; AY525526; AAT00572.1; -; Genomic DNA.
DR EMBL; AY525527; AAT00574.1; -; Genomic DNA.
DR EMBL; AY525528; AAT00576.1; -; Genomic DNA.
DR EMBL; AY525529; AAT00578.1; -; Genomic DNA.
DR EMBL; AY525530; AAT00580.1; -; Genomic DNA.
DR EMBL; AY525531; AAT00582.1; -; Genomic DNA.
DR EMBL; AY525532; AAT00584.1; -; Genomic DNA.
DR EMBL; AY525533; AAT00586.1; -; Genomic DNA.
DR EMBL; AY525534; AAT00588.1; -; Genomic DNA.
DR EMBL; AY525514; AAT00548.1; -; Genomic DNA.
FT NON_TER 1 1
SQ SEQUENCE 20 AA; 2282 MW; A3406B687822556D CRC64;

Query Match 22.9%; Score 22; DB 2; Length 20;
Best Local Similarity 50.0%; Pred. No. 3.1e+04;
Matches 5; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 5 PHGYLTA 14
| | | | |
Db 9 PAGIFLRTV 18

RESULT 72
Q9PRR9_YAVES PRELIMINARY; PRT; 16 AA.
ID Q9PRR9_YAVES
AC Q9PRR9;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE NA/K adenosine triphosphatase alpha subunit (Fragment).
OS Anas (ducks).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Aves; Neognathae; Anseriformes; Anatidae.
 RX NCBI_TaxID=8835;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=96074588; PubMed=7488178;
 RA Bol'dyrev A.A., Lopina O.D., Kenney M., Johnson P.;
 RT "Characterization of the subunit isoforms of duck salt gland Na/K
 RT adenosine triphosphatase.";
 RL Biochem. Biophys. Res. Commun. 216:1048-1053(1995).
 SO SEQUENCE 16 AA; 1784 MW; 1A338D2CE6B820 CRC64;

Query Match 22.4%; Score 21.5; DB 2; Length 16;
 Best Local Similarity 41.7%; Pred. No. 3e+04;
 Matches 5; Conservative 1; Mismatches 1; Indels 5; Gaps 1;

QY 1 DAFEP-----HG 7
 DB 3 DKYEPTXSHG 14

RESULT 73
 Q5GK34_COXBU
 ID Q5GK34_COXBU PRELIMINARY; PRT; 18 AA.
 AC Q5GK34;
 DT 10-MAY-2005 (TrEMBLrel. 30, Created)
 DT 10-MAY-2005 (TrEMBLrel. 30, Last sequence update)
 DE Malate oxidoreductase (Fragment).
 OS Coxilla burnetii.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Legionellales;
 OC Coxiellaceae; Coxiella.
 RN NCBI_TaxID=777;
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=Q212;
 RA Roux V., glazunova O., Raoult D.;
 RT "Multiplex Sequence Typing (MST): a New Method for Coxiella Isolates
 RT Characterization."
 RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF502662; AF586373.1; -; genomic_DNA.
 FT NON TER 1
 SQ SEQUENCE 18 AA; 2356 MW; 4660304A2F63A47 CRC64;

Query Match 22.4%; Score 21.5; DB 2; Length 18;
 Best Local Similarity 71.4%; Pred. No. 3.4e+04;
 Matches 5; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

QY 3 FEPHGYL 9
 DB 8 WEPH-YL 13

RESULT 74
 Q8AW46_BRARE
 ID Q8AW46_BRARE PRELIMINARY; PRT; 20 AA.
 AC Q8AW46;
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Activated leukocyte cell adhesion molecule (Fragment).
 GN Name=alcam; ORNames=alcam-001;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 RN NCBI_TaxID=7955;
 RP NUCLEOTIDE SEQUENCE.
 RA Skuce C.;
 RL Submitted (DEC-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF645788; CAD58771.1; -; Genomic DNA.
 ENSEMBL; ENSDARG0000029359; Danio rerio.

DR ZFIN; ZDB-GENE-990415-30; alcam.
 FT NON TER 20
 SQ SEQUENCE 20 AA; 2022 MW; 9435BD622E7DF308 CRC64;

Query Match 22.4%; Score 21.5; DB 2; Length 20;
 Best Local Similarity 50.0%; Pred. No. 3.8e+04;
 Matches 6; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

QY 7 GYLLTAAY-SPG 17
 DB 9 GAFIAAAYVAFG 20

RESULT 75
 Q84U84_SOYBN
 ID Q84U84_SOYBN PRELIMINARY; PRT; 9 AA.
 AC Q84U84;
 DT 01-JUN-2003 (TrEMBLrel. 24, Created)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
 DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
 DE Flavonoid 3'-hydroxylase (Fragment).
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
 OC eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 RN NCBI_TaxID=3847;
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=22474238; PubMed=12586717;
 RA Zebala G., Vodkin L.;
 RT "Cloning of the pleiotropic T locus in soybean and two recessive
 RT alleles that differentially affect structure and expression of the
 RT encoded flavonoid 3'-hydroxylase."
 RL Genetics 163:295-309(2003).
 DR EMBL; AF499732; AA047848.1; -; mRNA.
 FT NON TER 1
 SQ SEQUENCE 9 AA; 978 MW; 25A0B685AB42C1F7 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 9;
 Best Local Similarity 37.5%; Pred. No. 2.2e+06;
 Matches 3; Conservative 3; Mismatches 2; Indels 0; Gaps 0;

QY 5 PHGYLTA 12
 DB 2 PHVYSMS 9

RESULT 76
 Q7MAX1_9ZYGO
 ID Q7MAX1_9ZYGO PRELIMINARY; PRT; 10 AA.
 AC Q7MAX1;
 DT 01-MAR-2004 (TrEMBLrel. 26, Created)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
 DE Nuclease Bhl (BC 3.1.-.-) (Fragment).
 OS Basidiobolus haplosporius.
 OC Basidiobolaceae; Basidiobolus.
 OC Eukaryota; Fungi; Zygomycota; Zygomycetes; Entomophthorales;
 OC Basidiobolaceae; Basidiobolus.
 RN NCBI_TaxID=90248;
 RP PROTEIN SEQUENCE.
 RA Desai N., Shankar V.;
 RL Submitted (FEB-2000) to the PIR data bank.
 DR PIR; A59173; A59173.
 FT NON TER 1
 FT NON TER 1
 SQ SEQUENCE 10 AA; 1066 MW; 53B96C2721B87727 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 10;
 Best Local Similarity 80.0%; Pred. No. 2.2e+04;
 Matches 4; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 7 GYLLT 11

Db 5 GHLLT 9

RESULT 77

07KZ15 HUMAN
ID 07KZ15 HUMAN PRELIMINARY; PRT; 10 AA.

AC 07KZ15;

DT 05-JUL-2004 (TrEMBLrel. 27, Created)

DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)

DE Collagen alpha 2(I) (Fragment).

GN Name=collagen alpha 2(I);

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homiidae;

OC Homo.

OC NCBI_TaxID=9606;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=91291136; PubMed=2064612;

RA Bateman J.F., Hammag M., Chan D., Cole W.G.;

RT "Characterization of a type I collagen alpha 2(I) glycine-586 to

RT valine substitution in osteogenesis imperfecta type IV. Detection of

RT the mutation and prenatal diagnosis by a chemical cleavage method.";

RL Biochem. J. 276:765-770(1991).

DR EMBL; 839878; AAB19314.1; -; mRNA.

KW Collagen.

FT NON_TER 1 1

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 912 MW; D0028676DCD40D CRC64;

Query Match 21.9%; Score 21; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.2e+04;

Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 12 AAVSPG 17

Db 3 AAVAPG 8

RESULT 78

09R7J8 HELPY

ID 09R7J8 HELPY PRELIMINARY; PRT; 10 AA.

AC 09R7J8;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-JUN-2000 (TrEMBLrel. 13, Last sequence update)

DE Vacuolating cytotoxin (Fragment).

GN Name=vaca;

OS Helicobacter pylori (Campylobacter pylori).

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteraceae; Helicobacter.

OC NCBI_TaxID=210;

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=Kobe 500;

RA Shitazaka D.;

RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AB017599; BAA33412.1; -; Genomic_DNA.

FT NON_TER 1 1

FT NON_TER 10 10

SQ SEQUENCE 10 AA; 1018 MW; 414390C76879CDD7 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 10;

Best Local Similarity 66.7%; Pred. No. 2.2e+04;

Matches 4; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 2 AAPPNG 7

Db 4 AFGPG 9

RESULT 79

086D32 TRYCR

ID 086D32 TRYCR PRELIMINARY; PRT; 11 AA.

AC 086D32;

DT 01-JUN-2003 (TrEMBLrel. 24, Created)

DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)

DE Histone H1 (Fragment).

OS Trypanosoma cruzi.

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma;

OC Schizotrypanum.

OC NCBI_TaxID=5693;

OX [1]

RP NUCLEOTIDE SEQUENCE.

RX MEDLINE=22557728; PubMed=12670512; DOI=10.1016/S0020-7519(02)00264-3;

RA Sturm N.R., Vargas N.S., Westenderger S.J., Zingales B.,

RA Campbell D.A.;

RT "Evidence for multiple hybrid groups in Trypanosoma cruzi.";

RL Int. J. Parasitol. 33:269-279(2003).

RN [2]

RP NUCLEOTIDE SEQUENCE.

RC STRAIN=NR c13, SC43 c11, Tulahuen c12, CM17, M5631, CB8 c13, and

RC M4167;

RA Westenderger S.J., Sturm N.R., Campbell D.A.;

RT "Extensive heterozygosity of hybrid groups of Trypanosoma cruzi.";

RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF545075; AAF21903.1; -; Genomic_DNA.

DR EMBL; AY540674; AAX92650.1; -; Genomic_DNA.

DR EMBL; AY540676; AAX92654.1; -; Genomic_DNA.

DR EMBL; AY540677; AAX92655.1; -; Genomic_DNA.

DR EMBL; AY540678; AAX92658.1; -; Genomic_DNA.

DR EMBL; AY540679; AAX92660.1; -; Genomic_DNA.

DR EMBL; AY540680; AAX92662.1; -; Genomic_DNA.

DR EMBL; AY540672; AAX92647.1; -; Genomic_DNA.

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1114 MW; CCCLB31E772CDD CRC64;

Query Match 21.9%; Score 21; DB 2; Length 11;

Best Local Similarity 71.4%; Pred. No. 2.5e+04;

Matches 5; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 12 AAVSPK 18

Db 4 AAVPPK 10

RESULT 80

09TRW5 BOVIN

ID 09TRW5 BOVIN PRELIMINARY; PRT; 11 AA.

AC 09TRW5;

DT 01-MAY-2000 (TrEMBLrel. 13, Created)

DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)

DE 25 kDa protein P25, peptide P4 (Fragment).

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Laurasiatheria; Cetartiodactyla; Ruminantia;

OC Pecora; Bovidae; Bovinae; Bos.

OC NCBI_TaxID=9913;

OX [1]

RP PROTEIN SEQUENCE.

RX MEDLINE=91372400; PubMed=1909972; DOI=10.1016/0014-5793(91)80903-G;

RA Takahashi M., Tomizawa K., Ishiguro K., Sato K., Onori A., Sato S.,

RA Shitazuchi A., Uchida T., Imahori K.;

RT "A novel brain-specific 25 kDa protein (p25) is phosphorylated by a

RT Ser/Thr-Pro kinase (TPK II) from tau protein kinase fractions.";

RL FEBS Lett. 289:37-43(1991).

FT NON_TER 1 1

FT NON_TER 11 11

SQ SEQUENCE 11 AA; 1276 MW; CAF72DAF65A76AA9 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 11;

Best Local Similarity 42.9%; Pred. No. 2.5e+04;

Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 1 DAFPHG 7
: |||
Db 2 ERDPSC 8

RESULT 81
09K670_BACHD
ID 09K670_BACHD PRELIMINARY; PRT; 12 AA.
AC 09K670;
DT 01-OCT-2000 (TrEMBLrel. 15, Created)
DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
DE 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE BH3862 protein.
GN OrderedLocuNames=BH3862;
OS Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132; DOI=10.1093/nar/28.21.4317;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kohara S.,
RA Horikoshi K.,
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
halodurans and genomic sequence comparison with Bacillus subtilis.";
RL EMBL/ BAO00004/ BAB07581.1; -; Genomic_DNA.
DR F84132; F84132.
KM Complete proteome.
SQ SEQUENCE 12 AA; 1463 MW; 44B501F695321A7 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 57.1%; Pred. No. 2.7e+04;
Matches 4; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 8 YLITAAV 14
: |||||
: :
Db 3 YLITKII 9

RESULT 82
088575_9PICO
ID 088575_9PICO PRELIMINARY; PRT; 12 AA.
AC 088575;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=FA;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL/ M80883/ AAA73154.1; -; mRNA.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8

Db 5 HGY 7
: |||

RESULT 83
088576_9PICO
ID 088576_9PICO PRELIMINARY; PRT; 12 AA.
AC 088576;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DE 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=MHG;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL/ M80884/ AAA73155.1; -; mRNA.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8
: |||
Db 5 HGY 7

RESULT 84
088577_9PICO
ID 088577_9PICO PRELIMINARY; PRT; 12 AA.
AC 088577;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxID=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NO;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence.";
RL J. Virol. 66:1951-1958(1992).
DR EMBL/ M80885/ AAA73156.1; -; mRNA.
FT NON_TER 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8
: |||
Db 5 HGY 7

RESULT 85

Q88578_9PICO
ID Q88578_9PICO PRELIMINARY; PRT; 12 AA.
AC Q88578;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last annotation update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxId=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=NO;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipson H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80886; AAA73157.1; -; mRNA.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8
DB 5 HGY 7

RESULT 86
Q88579_9PICO
ID Q88579_9PICO PRELIMINARY; PRT; 12 AA.
AC Q88579;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxId=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=VL;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipson H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80887; AAA73158.1; -; mRNA.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8
DB 5 HGY 7

RESULT 87
Q88580_9PICO
ID Q88580_9PICO PRELIMINARY; PRT; 12 AA.
AC Q88580;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxId=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=Vilynsk;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipson H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80888; AAA73159.1; -; mRNA.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8
DB 5 HGY 7

RESULT 88
Q88581_9PICO
ID Q88581_9PICO PRELIMINARY; PRT; 12 AA.
AC Q88581;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;
OC Cardiovirus.
OX NCBI_TaxId=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=WW;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.E., Calenoff M.A., Simpson S., Jensen K., Lipson H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
attenuates neurovirulence."
RL J. Virol. 66:1951-1958(1992).
DR EMBL; M80889; AAA73160.1; -; mRNA.
FT NON_TER 12 12
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908E7B5871 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 12;
Best Local Similarity 100.0%; Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 6 HGY 8
DB 5 HGY 7

RESULT 89
Q88582_9PICO
ID Q88582_9PICO PRELIMINARY; PRT; 12 AA.
AC Q88582;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
DE Theiler's murine encephalomyelitis virus 5' flank and 5' end cds.
DE (Fragment).
OS Theiler's encephalomyelitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Picornaviridae;

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OC Cardiovirus.
OX NCBI_TaxId=12124;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=TO;
RX MEDLINE=92194426; PubMed=1548749;
RA Pritchard A.B., Calenoff M.A., Simpson S., Jensen K., Lipton H.L.;
RT "A single base deletion in the 5' noncoding region of Theiler's virus
RT attenuates neurovirulence."
RL J Virol 66:1951-1958(1992).
DR EMBL, M80890; AAA73161.1; -; mRNA.
FT NON_TER
SQ SEQUENCE 12 AA; 1321 MW; F79B7D908B7B5871 CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 12;
Pred. No. 2.7e+04;
Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HGY 8
Db 5 HGY 7

RESULT 90
O18990 ATBBE
ID 018990_ATBBE PRELIMINARY; PRT; 13 AA.
AC 018990
DT 01-JUN-1998 (TrEMBLrel. 05, Created)
DT 01-JUN-1998 (TrEMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Granzyme B (Fragment).
OS Ateles belzebuth chamek (Chamek spider monkey).
OC Bakayote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Platyrrhini; Cebidae;
OC Aellinae; Ateles.
OX NCBI_TaxId=118643;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=98267189; PubMed=9601975; DOI=10.1007/s004120050282;
RA Canavez P., Moreira M.A.M., Bonvicino C.R., Parham P., Senanez H.N.;
RT "Comparative gene assignment in Ateles paniscus chamek (Platyrrhini,
RT Primates) and man: association of three separate human syntenic groups
RT and evolutionary considerations."
RL Chromosoma 107:73-79(1998).
DR EMBL, AF029165; AAB84196.1; -; Genomic_DNA.
DR InterPro, IPR001254; Peptidase_S1_S6.
DR PROSITE, PS00134; TRYPsin_HIS; UNKNOWN_1.
FT NON_TER
SQ SEQUENCE 13 AA; 1394 MW; C0FF86BFAE5EDDD CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 13;
Pred. No. 2.9e+04;
Matches 4; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 8 YLTAA 13
Db 2 YLTAA 7

RESULT 91
O7M1A2 BACNO
ID 07M1A2_BACNO PRELIMINARY; PRT; 13 AA.
AC 07M1A2
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE 40k extracellular proteinase (Fragment).
OS Bacteroides nodosus (Bacteroides nodosus).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Cardiobacteriales;
OC Cardiobacteriaceae; Dichelobacter.
OX NCBI_TaxId=870;
RN [1]

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RP PROTEIN SEQUENCE.
RX MEDLINE=92263812; PubMed=1814046;
RA Gong Y.H., Moses E.;
RT "Overexpression of an extracellular bacteroides nodosus protease in
RT E.coli and isolation and characterization of its promoter."
RL Acta Microbiol. Sin. 31:433-437(1991).
DR PIR, PC1008; PC1008.
FT NON_TER
SQ SEQUENCE 13 AA; 1483 MW; 158DA695392221E4 CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 13;
Pred. No. 2.9e+04;
Matches 5; Conservative 2; Mismatches 5; Indels 0; Gaps 0;

Qy 2 AFEPHG YLTAA 13
Db 1 AFNIRNHLTSLA 12

RESULT 92
O6ZYT7 9CARY
ID 06ZYT7_9CARY PRELIMINARY; PRT; 14 AA.
AC 06ZYT7
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Cytochrome b6/f complex subunit VI (Fragment).
GN Name=petL;
OS Silene acaulis.
OC Chloroplast.
OC Bakayote; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllales; Caryophyllaceae; Silene.
OX NCBI_TaxId=269082;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Popp M.;
RT "Disentangling the reticulate history of polyploids in Silene
RT (Caryophyllaceae)."
RL Theiss (2004), Department of Evolutionary Biology, Systematic Botany,
RL Uppsala university, Uppsala, Sweden.
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=leaf;
RA Popp M., Erikson P., Eggens F., Oxejman B.;
RT Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
RL EMBL, AJ634219; CAG24647.1; -; Genomic_DNA.
DR GO; GO:0009507; Chloroplast; IEA.
DR GO; GO:0009512; Cytochrome b6f complex; IEA.
DR GO; GO:0016021; C:integral to membrane; IEA.
DR GO; GO:0005489; P:electron transporter activity; IEA.
DR GO; GO:0006118; P:electron transport; IEA.
DR InterPro, IPR007802; PetL.
DR Pfam, PF05115; PetL; 1.
KW Chloroplast.
FT NON_TER
SQ SEQUENCE 14 AA; 1532 MW; 06428D1B688740DB CRC64;

Query Match
Best Local Similarity 21.9%; Score 21; DB 2; Length 14;
Pred. No. 3.2e+04;
Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 7 GYLTA 12
Db 9 GYLTA 14

RESULT 93
O7L222 ANAPL
ID 07L222_ANAPL PRELIMINARY; PRT; 14 AA.
AC 07L222

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DT 01-MAR-2004 (TReMBLrel. 26, Created)
 DT 01-MAR-2004 (TReMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TReMBLrel. 26, Last annotation update)
 DE Ovaractin (Fragment).
 OS Anas platyrhynchos (Domestic duck).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
 NCBI_TaxID=8839;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=86111792; PubMed=3511043;
 RA Nagase H., Harris Jr., E.D., Brew K.;
 RT "Nadence for a thiol ester in duck ovaractin (ovomacroglobulin).";
 RL J. Biol. Chem. 261:1421-1426(1986).
 DR PIR: S00150; S00150.
 FT NON_TER 1
 FT NON_TER 14
 FT NON_TER 14
 SQ SEQUENCE 14 AA; 1600 MW; 1BDD822683DE95DB CRC64;

Query Match 21.9%; Score 21; DB 2; Length 14;
 Best Local Similarity 45.5%; Pred. No. 3.4e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 4 EPHGYLLTAAY 14
 ID 4 EPGYVLMVPAV 14

RESULT 94
 Q6ZYT6_9CARY PRELIMINARY; PRT; 15 AA.
 ID Q6ZYT6;
 DT 05-JUL-2004 (TReMBLrel. 27, Created)
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)
 DE Cytochrome b6/f complex subunit VI (Fragment).
 GN Name=petl;
 OS Silene uralensis.
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Caryophyllales; Caryophyllaceae; Silene.
 NCBI_TaxID=269082;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaf;
 RA Pop M.;
 RT "Disentangling the reticulate history of polyploids in Silene (Caryophyllaceae).";
 RL Thesis (2004), Department of Evolutionary Biology, Systematic Botany, Uppsala university, Uppsala, Sweden.
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Leaf;
 RA Pop M.;
 RT "Disentangling the reticulate history of polyploids in Silene (Caryophyllaceae).";
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF634220; CAG24649.1; -; Genomic_DNA.
 DR GO:0009507; Chloroplast; IEA.
 DR GO:0009512; Cytochrome b6 complex; IEA.
 DR GO:0016021; C:integral to membrane; IEA.
 DR GO:0005489; P:electron transporter activity; IEA.
 DR GO:0006118; P:electron transport; IEA.
 DR InterPro: IPR007802; Petl.
 DR Pfam: PF05115; Petl; 1.
 DR Chloroplast.
 FT NON_TER 15
 FT NON_TER 15
 SQ SEQUENCE 15 AA; 1645 MW; C716428D1B688740 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 66.7%; Pred. No. 3.4e+04;
 Matches 4; Conservative 1; Mismatches 1; Indels 0; Gaps 0;
 Qy 7 GYLTLTA 12

Db 9 GYLTLTA 14

RESULT 95
 Q9SQ16_ORYSA PRELIMINARY; PRT; 15 AA.
 ID Q9SQ16_ORYSA
 AC Q9SQ16;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2003 (TReMBLrel. 24, Last annotation update)
 DE Translation elongation factor (Fragment).
 OS Oryza sativa (Rice).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
 OC Eriaroidae; Oryzaceae; Oryza.
 NCBI_TaxID=4530;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RA Li Z.-Y., Chen S.-Y.;
 RT "Inducible expression of translation elongation factor 1A gene in rice seedlings in response to environmental stresses.";
 RL Acta Bot. Sin. 41:800-806(1999).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RA Li Z.-Y., Chen S.-Y.;
 RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AF067195; AAC79991.1; -; mRNA.
 DR Gramene; Q9SQ16; -;
 DR GO:0003746; P:translation elongation factor activity; IEA.
 KW Elongation factor.
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1514 MW; 95B5C46F069C9775 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 33.3%; Pred. No. 3.4e+04;
 Matches 5; Conservative 3; Mismatches 7; Indels 0; Gaps 0;

Qy 4 EPHGYLLTAAYSPK 18
 ID 1 DPTGAKVTKAAKK 15

RESULT 96
 Q9QV62_9MURI PRELIMINARY; PRT; 15 AA.
 ID Q9QV62_9MURI
 AC Q9QV62;
 DT 01-MAY-2000 (TReMBLrel. 13, Created)
 DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
 DE Differentiation enhancing factor, DEF (Fragment).
 OS Mus sp.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
 OC Muridae; Murinae; Mus.
 NCBI_TaxID=10095;
 RN [1]
 RP PROTEIN SEQUENCE.
 RX MEDLINE=93312351; PubMed=8323566;
 RA Sparatore B., Patrone M., Passalacqua M., Pessino A., Falchetto R., Melloni B., Pontremoli S.;
 RT "Characterization of the biological role of murine erythroleukemia cells 'differentiation enhancing factor' using antisense oligodeoxynucleotides.";
 RT Biochem. Biophys. Res. Commun. 193:941-947(1993).
 RL Biochem. Biophys. Res. Commun. 193:941-947(1993).
 FT NON_TER 1
 FT NON_TER 1
 FT NON_TER 1
 SQ SEQUENCE 15 AA; 1706 MW; 53329477F40FB99 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 15;
 Best Local Similarity 100.0%; Pred. No. 3.4e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYL 10
 Db 11 GYL 14

RESULT 97

KTIC AREMA STANDARD; PRT; 16 AA.

AC 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DE 10-MAY-2005 (Rel. 47, Last annotation update)
 OS taurocyamine kinase (EC 2.7.3.4) (Fragment).
 OC Arenicola marina (lugworm) (Rock worm).
 OC Eukaryota; Metazoa; Annelida; Polychaeta; Scolecida; Capitellida;
 OC Arenicolidae; Arenicola.
 NC NCB1_TaxID=6344;
 RN 11
 RP PROTEIN SEQUENCE.
 RX MEDLINE=75184095; PubMed=166684;
 RA Brevet A., Zetoun Y., Pradel L.A.;
 RT "Comparative structural studies of the active site of ATP: guanidine
 phosphotransferases. The essential cysteine tryptic peptide of
 taurocyamine kinase from Arenicola marina.";
 RL Biochim. Biophys. Acta 393:1-9(1975).
 CC -1- CATALYTIC ACTIVITY: ATP + taurocyamine = ADP + N-
 phosphotaurocyamine.
 CC -1- SIMILARITY: Belongs to the ATP:guanido phosphotransferase family.

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 between the Swiss Institute of Bioinformatics and the EMBL outstation
 CC the European Bioinformatics Institute. There are no restrictions on its
 use as long as its content is in no way modified and this statement is not
 removed.

CC PIR; A11488; A11488.
 DR InterPro: IPR000749; ATP-Gua_Pyrans.
 DR PROSITE: PS00112; GUNNIDC_KINASE, 1.
 KM Direct protein sequencing; Kinase; Transferase.
 FT ACT_SITE 7
 FT NON_TER 1
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1636 MW; CF05B7326D427E94 CRC64;

Query Match 21.9%; Score 21; DB 1; Length 16;
 Best Local Similarity 45.5%; Pred. No. 3.6e+04;
 Matches 5; Conservative 1; Mismatches 5; Indels 0; Gaps 0;

Qy 7 GYLTAAGPG 17
 Db 2 GYLGTCTPTNG 12

RESULT 98

Q44543 ANAVA PRELIMINARY; PRT; 16 AA.

AC 044543;
 DT 01-NOV-1996 (TRMBLrel. 01, Created)
 DT 01-JAN-1999 (TRMBLrel. 09, Last sequence update)
 DT 01-MAR-2003 (TRMBLrel. 23, Last annotation update)
 DE Recombled functional n1fd gene encoding alpha nitrogenase, partial
 cds. (Fragment).
 OS Anabaena variabilis.
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Anabaena.

NCBI_TaxID=11172;
 RN 11
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=89327123; PubMed=2502534;
 RA Brueca J.S., Hale M.A., Carrasco C.D., Golden J.W.,
 RT "Extension of an 11-kilobase-pair DNA element from within the n1fd gene
 in anabaena variabilis heterocysts.";
 RL J. Bacteriol. 171:4138-4145(1989).
 DR EMBL; M29073; AAA22009.1; -; Genomic_DNA.

DR HSSP; P00466; 1QGU.
 FT NON_TER 1
 FT NON_TER 16
 SQ SEQUENCE 16 AA; 1999 MW; 46724FFC7E701577 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 16;
 Best Local Similarity 100.0%; Pred. No. 3.6e+04;
 Matches 3; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 6 HG 8
 Db 13 HG 15

RESULT 99

Q14316 HUMAN PRELIMINARY; PRT; 17 AA.

AC 014316;
 DT 01-NOV-1996 (TRMBLrel. 01, Created)
 DT 01-JUN-2003 (TRMBLrel. 24, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Factor IX protein (Fragment).
 GN Name-factor IX;
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homidae;
 OC Homo.
 NC NCB1_TaxID=9606;
 RN 11
 RP NUCLEOTIDE SEQUENCE.
 RX MEDLINE=88327116; PubMed=3416069;
 RA Reitema P.A., Bertina R.M., Ploos van Amstel J.K., Riemens A.,
 RA Brier E.;
 RT "The putative factor IX gene promoter in hemophilia B Leyden.";
 RL Blood 72:1074-1076(1988).
 DR EMBL; X55008; CAB38245.2; -; Genomic_DNA.
 DR HSSP; P00734; 1UMA.
 FT NON_TER 17
 FT NON_TER 17
 SQ SEQUENCE 17 AA; 1807 MW; 73B87873A971A4F1 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 17;
 Best Local Similarity 100.0%; Pred. No. 3.9e+04;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 7 GYL 10
 Db 14 GYL 17

RESULT 100

Q7R0U2 PLAYO PRELIMINARY; PRT; 17 AA.

AC 07R0U2;
 DT 01-MAR-2004 (TRMBLrel. 26, Created)
 DT 01-MAR-2004 (TRMBLrel. 26, Last sequence update)
 DT 01-MAR-2004 (TRMBLrel. 26, Last annotation update)
 DE Hypothetical protein.
 GN Name=PY00998;
 OS Plasmodium yoelii yoelii.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.

NCBI_TaxID=73239;
 RN 11
 RP NUCLEOTIDE SEQUENCE.
 RC STRAIN=17XNL;
 RX MEDLINE=22255706; PubMed=12368865; DOI=10.1038/nature01099;
 RA Carlton J.M., Anguioni S.V., Sub B.B., Kooij T.W., Pertea M.,
 RA Silva J.C., Ermolaeva M.D., Allen J.E., Selengut J.D., Koo H.L.,
 RA Peterson J.D., Pop M., Kosack D.S., Stummay M.F., Bidwell S.L.,
 RA Shallow S.J., van Aken S.B., Riedmiller S.B., Feldblyum T.V.,
 RA Cho J.K., Quackenbush J., Sedegah M., Shoatli A., Cummings L.M.,
 RA Florens L., Yates J.R. III, Raine J.D., Sinden R.E., Harris M.A.,
 RA Cunningham D.A., Preiser P.R., Bergman L.W., Valdivia A.B.,
 RA van Lin L.H., Janse C.J., Waters A.P., Smith H.O., White O.R.,

RA Salzberg S.L., Venter J.C., Fraser C.M., Hoffman S.L., Gardner M.J.,
 RA Carucci D.J.;
 RT "Genome sequence and comparative analysis of the model rodent malaria
 RT parasite Plasmodium yoelii yoelii.";
 RL Nature 419:512-519(2002).
 CC -!- CAUTION: The sequence shown here is derived from an
 CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
 CC preliminary data.
 DR EMBL; AABL01000269; EAA19799.1; -; Genomic_DNA.
 KW Hypothetical protein.
 SQ SEQUENCE 17 AA; 2102 MW; CF0CCD41BA198092 CRC64;

Query Match 21.9%; Score 21; DB 2; Length 17;
 Best Local Similarity 60.0%; Pred. No. 3.9e+04;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 3 FEPRG 7
 | : | | |
 Db 11 FDPRG 15

Search completed: January 20, 2006, 19:11:12
 Job time : 61.8846 secs